(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 21 March 2002 (21,03,2002)

PCT

(10) International Publication Number WO 02/22675 A2

- (51) International Patent Classification7: C07K 14/415
- (21) International Application Number: PCT/US01/28506
- (22) International Filing Date:

14 September 2001 (14.09.2001)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data: 60/232,778

60/300,183

15 September 2000 (15.09.2000) US 22 June 2001 (22.06.2001) US

- (71) Applicants (for all designated States except US): SYNGENTA PARTICIPATIONS AG [CH/CH]; Schwarzwaldalle 215, CH-4058 Basel (CH). UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL [US/US]; 300 Bynum Hall, Campus Box 4100, Chapel Hill, NC 27599-4100 (US).
- (71) Applicants and
- (72) Inventors: GLAZEBROOK, Jane [US/US]; 4503 Ocean Valley Lane, San Diego, CA 92130 (US). WANG, Xun

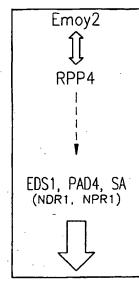
[—/US]; 12524 Caminito Vista Soledad, San Diego, CA 92121 (US). **DANGL, Jeffrey, L.** [US/US]; 601 Jones Ferry Road, Apt. B, Carrboro, NC 27510 (US). **EUL-GEM, Thomas** [US/US]; 605 Jones Ferry Road, Apt. VV1, Carrboro, NC 27510 (US). **ZHU, Tong** [—/US]; 5260 Caminito Exquisito, San Diego, CA 92130 (US).

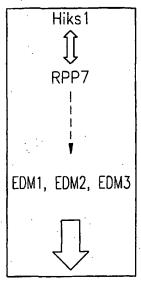
- (74) Agent: VIKSNINS, Ann, S.; Schwegman, Lunberg, Woessner & Kluth, P.O. Box 2938, Minneapolis, MN 55402 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,

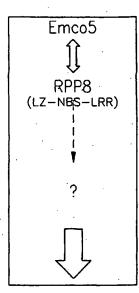
[Continued on next page]

(54) Title: PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

RPP-DEPENDENT DEFENSE PATHWAYS







RESISTANCE

(57) Abstract: Methods to identify genes, the expression of which is altered in response to pathogen infection, are provided, as well as the genes identified thereby.





CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD , TG).

 with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

Published:

 without international search report and to be republished upon receipt of that report For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

5

10

Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. application Serial No. 60/232,778, filed on September 15, 2000, and of U.S. application Serial No. 60/300,183, filed on June 22, 2001, the disclosures of which are incorporated by reference herein.

Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to stress, e.g., to pathogen exposure.

15

20

25

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (avr) gene that triggers specific recognition by a corresponding host resistance (R) gene. R gene specificity is generally quite narrow, in most cases only pathogens carrying a particular avr gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. R genes have been studied extensively in recent years. For a review of R genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

30

35

One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component

of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (nahG), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger genefor-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

5

10

15

20

25

30

Genes such as NDR1 and EDS1, as well as DND1 and the lesion-mimic genes, likely act in signal transduction pathways downstream from R-avr recognition. NDR1 and EDS1 are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen Pseudomonas syringae and the oomycete pathogen Peronospora parasitica. Curiously, ndr1 mutants are susceptible to one set of avirulent pathogens, whereas eds1 mutants are susceptible to a non-overlapping set (Aarts et el., 1998). The five cloned R genes that require EDS1 all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of R genes that contain sequences similar to the cytoplasmic domains of Drosophila Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require NDR1 belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, RPP8, that does not require EDS1 or NDR1, so

the correlation between R gene structure and requirement for EDS1 or NDR1 is not perfect. Nevertheless, these results show that R genes differ in their requirements for downstream factors and that these differences are correlated with R gene structural type.

5

10

15

20

25

30

NDR1 encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires NDR1 to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of NDR1 is to hold R proteins close to the membrane. EDS1 encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that EDS1 is involved in synthesis or degradation of a signal molecule. EDS1 expression is inducible by SA and pathogen infection, suggesting that EDS1 may be involved in signal amplification (Falk et al., 1999).

It has been extremely difficult to isolate mutations in genes other than the R genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the avr gene avrRpt2 in plants carrying the corresponding resistance gene RPS2. Expression of avrRpt2 in this background is lethal, as it triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by RPP genes (recognition of P. parasitica) mediate specific recognition of Peronospora isolates and trigger defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, RPP7 and RPP8 (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either EDS1 or NDR1, and that RPP7 resistance was also not compromised by mutations in EIN2, JAR1 or COI1, which affect ethylene or jasmonic acid signaling, or in coi1/npr1 or coi1/NahG backgrounds. The authors suggested that RPP7 initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

5

10

15

20

25

30

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of PR gene expression and enhanced disease resistance. Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include npr1, in which expression of PR genes in response to SA is blocked; cpr1, cpr5, and cpr6, which constitutively express PR genes; the npr1 suppressor ssi1; pad4, which has a defect in SA accumulation; and eds5, which has a defect in PR1 expression.

Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). NPR1 appears to be a positive regulator of *PR* gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al., 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that NPR1 acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

PAD4 appears to act upstream from SA. In pad4 plants infected with a virulent P. syringae strain, SA levels, synthesis of the antimicrobial compound camalexin, and PR1 expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in pad4 plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in pad4 do not affect SA levels, camalexin synthesis, or PR1 when plants are infected with an avirulent P. syringae strain (Zhou et al., 1998). Taken together, these results suggest that PAD4 is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

10

15

20

25

30

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The jar1 and coil mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). COII has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coi1* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jarl* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires NPR1 (Pieterse et al., 1996). This was unexpected in light of the fact that NPR1 was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SAdependent signal is received, NPR1 mediates a resistance response characterized by PRI expression, whereas if the ISR signal is received, NPRI mediates a different resistance response. It is difficult to imagine how this could occur, unless NPR1 is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in NPR1 could function in proteinprotein interactions between NPR1 and adapter proteins. Identification of proteins that interact with NPR1, and characterization of plants with loss-offunction mutations affecting those proteins, would be very helpful for understanding how NPR1 acts in each pathway. It would also be worthwhile to determine if the ssil or cpr6 mutations suppress the ISR defect of nprl mutants.

Relevance to disease resistance

10

15

20

25

30

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In Arabidopsis, the SA pathway mutants npr1 and pad4 show enhanced susceptibility to P. syringae and P. parasitica (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of NPRI caused increased resistance to P. syringae and P. parasitica in a dosage dependent manner (Cao et al., 1998). Moreover, NPRI-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Thus, what is needed is the systematic identification of genes useful to confer resistance to pathogens.

10

15

20

25

30

Summary of the Invention

The invention provides an isolated nucleic acid molecule (polynucleotide), e.g., DNA, comprising a plant or fungal nucleotide sequence, the expression of which is altered in response to stress, e.g., pathogen infection. For example, the invention provides a nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in combination with other sequences, to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth. In one embodiment of the invention, the promoter employed to express the nucleotide sequence of the invention may be one that mediates rapid and transient transcription after pathogen infection. Thus, the invention also provides an isolated nucleic acid molecule comprising a plant nucleotide sequence which alters, e.g., increases or decreases, the transcription of plant genes, e.g., open reading frames, in response to stress, e.g., pathogen infection.

As described herein, Arabidopsis plants of differing genotypes were infected with different strains of an oomycete, P. parasitica. RNA was isolated from each plant/pathogen pair and employed to prepare probes which were hybridized to a gene chip having nucleic acid sequences (probe sets) corresponding to approximately 8,200 Arabidopsis genes. Genes were then identified that were upregulated or downregulated in response to infection, including genes that were dependent on RPP7 or RPP8, which act via unconventional signaling cascades and are not dependent on defense regulators such as EDS1, NDR1, PAD4, NPR1, RAR1, PBS3 or salicyclic acid (SA). Among the genes showing strong Peronospora-induced expression changes, clusters of genes were identified that were specifically upregulated by RPP7 or RPP8, or both. In particular in one analysis, the expression of 184 genes (SEQ ID NOs:1-211 and 792) related to 217 probe sets was upregulated by either RPP7 or RPP8, or both, while in another analysis the expression of genes related to 194 probe sets (SEQ ID NOs:212-399 and 793) was

5

10

15

20

25

30

upregulated by either RPP7 or RPP8, or both. Further, as described below, promoters of genes that were rapidly and transiently transcribed after P. parasitica infection and were RPP7/8-dependent were significantly enriched with both novel sequence motifs and potential binding sites of known transcription factors. Specifically, the promoters were significantly enriched with two novel sequence motifs (referred to as "motif 1" and "motif 2"), one of which was similar to binding sites for Myb transcription factors, sequence motifs related to WRKY binding sites, and two other novel sequence motifs ("motif 3" and "motif 4"). Moreover, comparisons between expression signatures of wild type plants as well as the RPP7 loss of function mutants, and edm1, edm2 and edm3 mutants, allow for predictions regarding the RPP7 pathway hierarchy.

In addition, more than 200 genes (SEQ ID NOs:75, 214, 228, 301, 339, 400-684, 792-795) were identified that were specifically controlled by the RPP4-dependent pathway, which mediates resistance of the Arabidopsis ecotype Col-0 to the Peronospora isolate Emoy2. According to their response to SA, an important mediator of local and systemic defense responses, and the protein biosynthesis inhibitor cycloheximide (CHX), these genes were further subcategorized into immediate early and secondary response genes. A set of immediate early SA responsive genes (SEQ ID NOs:150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615, and 526) was found to consist exclusively of regulatory genes. Such genes are likely controlled by transcription factors acting closely downstream of SA. One highly conserved motif in the promoters of these immediate early genes was similar to binding sites of WRKY transcription factors (SEQ ID NOs:757-765). Other conserved promoter motifs appeared to be novel and may facilitate the cloning of their cognate transcription factors. A cluster of SA/CHX super-induced genes was found to show elevated expression ground states in the npr1 mutant (SEQ ID NOs:214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447 and 551) suggesting an NPR1-dependent derepression mechanism in the control of some SA responsive immediate early genes.

Thus, the invention provides an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to a pathogen that induces a response mediated by *R* genes, including pathogens such as bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones (1997), which is specifically incorporated by

5

10

15

20

25

30

reference herein). For example, the plant or fungal nucleotide sequence encodes a polypeptide that is substantially similar to an Arabidopsis polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to infection by an oomycete such as Peronospora, and is RPP4-, RPP7-, and/or RPP8-dependent. These sequences can be identified by employing an array of nucleic acid samples, e.g., a plurality of oligonucleotides, each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid from pathogen-infected (e.g., wild-type) plant cells and to nucleic acid from uninfected plant cells or plant cells having a mutation which alters the response to pathogen infection. Thus, genes, the expression of which are altered by pathogen infection, can be systematically identified. Preferably, the nucleotide sequence is from plant DNA, either a dicot or a monocot, which encodes a polypeptide that is substantially similar to an Arabidopsis polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. More preferably, the nucleotide sequence is from plant DNA that is substantially similar to an Arabidopsis nucleic acid segment having any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. The term "substantially similar", when used herein with respect to a polypeptide means a polypeptide corresponding to a reference polypeptide, wherein the polypeptide has substantially the same structure and function as the reference polypeptide, e.g., where only changes in amino acid sequence are those which do not affect the polypeptide function. When used for a polypeptide or an amino acid sequence, the percentage of identity between the substantially similar and the reference polypeptide or amino acid sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, where the reference polypeptide is an Arabidopsis polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. However, the percent of identity between the substantially similar and the reference polypeptide may be less than 65% as long as the two polypeptides have the same or similar function, e.g., catalyze the same or similar reaction. Another indication that two polypeptides are substantially similar to

each other is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence corresponding to a reference nucleotide sequence, wherein the corresponding sequence is from a gene that encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by a gene comprising the reference nucleotide sequence. The term "substantially similar" is specifically intended to include nucleotide sequences wherein the sequence has been 10 modified to optimize expression in particular cells. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 15 96%, 97%, 98%, up to at least 99%, wherein the reference sequence is preferably any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or http://www hto.usc.edu/software/seqaln/index.html). The localS program, version 1.16, is preferably used with following parameters: match: 1, mismatch penalty: 0.33, 20 open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM 25 EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 30 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the isolated nucleic acid molecules of the invention also include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*,

5

10

15

20

25

30

including, but not limited to, plants other than Arabidopsis, preferably cereal plants, e.g., corn, wheat or rice, as well as rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugarbeet, and in fungi. An ortholog is a gene from a different species that encodes a product having the same function as the product encoded by a gene from a reference organism. The encoded ortholog products likely have at least 70% amino acid sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or more of the Arabidopsis sequences, although it is also envisioned that orthologous genes to those disclosed herein may encode a polypeptide with less than 70%, e.g., less than 65% amino acid sequence identity, but which polypeptide has the same or similar function. Databases such GenBank or one found at http://bioserver.myongjiac.kr/rjce.html (for rice) may be employed to identify sequences related to the Arabidopsis sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the Arabidopsis sequences.

Thus, the invention preferably includes an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence that encodes a polypeptide that has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, amino acid sequence identity to an Arabidopsis polypeptide encoded by an open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795. In one embodiment, the isolated nucleic acid molecule is not SEQ ID NOs: 1-684 and 792-795. The invention also provides anti-sense nucleic acid molecules corresponding to the open reading frames or genes identified as responsive to pathogen infection. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention in either sense or antisense orientation.

Also provided is an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising a nucleic acid sequence having at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, nucleic acid sequence similarity to an *Arabidopsis* open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, the complement thereof, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795.

5

10

15

20

25

30

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are useful to provide resistance to pathogens and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules of the invention or one or more of the polypeptides encoded thereby. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant or fungal nucleotide sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. The resistance or tolerance may be accomplished by decreasing or eliminating expression of a plant gene necessary for pathogen infection and/or replication or by overexpressing a gene product that inhibits pathogen infection and/or replication. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more

5

10

15

20

25

30

preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism. Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields under conditions of pathogen infection and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also includes recombinant nucleic acid molecules which have been modified so as to comprise codons other than those present in the unmodified sequence. The recombinant nucleic acid molecules of the invention include those in which the modified codons specify amino acids that are the same as those specified by the codons in the unmodified sequence, as well as those that specify different amino acids, i.e., they encode a variant polypeptide having one or more amino acid substitutions relative to the polypeptide encoded by the unmodified sequence.

5

10

15

20

25

.30

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The present invention also provides a method to identify a gene, the expression of which is altered in response to an external stimulus, e.g., pathogen infection. The method comprises contacting a plurality of samples comprising portions or fragments of isolated nucleic acid molecules with a probe which corresponds to a population of a nucleic acid sequences, the expression of which is altered in response to an external stimulus, so as to form a binary complex. Each sample corresponds to a different gene. Then complex formation is detected or determined. The method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. For example, the method comprises contacting a solid substrate comprising a plurality of samples comprising portions or fragments of isolated plant nucleic acid with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from a pathogen infected plant so as to form a complex. Preferred pathogens are those which induce an R-gene dependent resistance response. Each individual sample comprises one or more nucleic acid sequences corresponding to a plant gene, e.g., a pool of oligonucleotides corresponding to the same gene or a portion of that gene. The plurality of samples is provided on a DNA chip. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising portions or fragments of

isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from an uninfected or mutant plant or plant cells so as to form a complex. Then complex formation with nucleic acid from infected cells and from uninfected or mutant cells is compared.

The invention also provides a method for identifying a plant cell infected with a pathogen, e.g., one that induces a RPP4-, RPP7- and/or RPP8-dependent resistance response. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with the pathogen with at least one, preferably at least two, oligonucleotides under conditions effective to amplify at least a portion of a nucleotide sequence in the isolated plant nucleic acid which is substantially similar to at least one of SEQ ID NOs: 1-684 and 792-795, so as to yield an amplified product. Then the presence of the amplified product is detected or determined. The presence of the amplified product, e.g., in an amount that is different than the amount of the corresponding amplified product from an uninfected or mutant plant, corresponding to one or more of SEQ ID NOs: 1-684 and 792-795 or an ortholog thereof, is indicative of pathogen infection.

10

15

20

25

30

The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected from SEQ ID NOs: 1-684 and 792-795 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a pathogen is compared to hybridization of the probe to nucleic acid isolated from an uninfected or mutant cell. A change in the amount of the hybridized probe in nucleic acid isolated from a cell suspected of being infected by a pathogen relative to the amount of hybridized probe in nucleic acid isolated from an uninfected or mutant cell is indicative of infection.

Also provided is an isolated nucleic acid molecule comprising a nucleotide sequence that directs transcription, e.g., a promoter, of a linked nucleic acid segment in a host cell, such as a plant cell, wherein transcription is altered, e.g., increased, in response to a pathogen infection. Preferably, the pathogen is R-dependent, and more preferably, one that triggers a response that is dependent on RPP4, RPP7 and/or RPP8, such as an oomycete (for example, Peronospora). It is preferred that the nucleotide sequence is from plant genomic

DNA which has at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, nucleotide sequence identity to a sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, e.g., SEQ ID NOs:774-788, or comprising motifs such as one of SEQ ID NOs:685-773. Thus, the invention also includes orthologs of *Arabidopsis* promoters. Preferably, the nucleotide sequence includes the promoter region from a gene corresponding to SEQ ID NOs: 1-770 and 792-795, which region preferably includes at least one copy of at least one of the following, e.g., a nucleic acid sequence comprising one of SEQ ID NOs:685-697 ("motif 1"), SEQ ID NOs:698-709 ("motif 2"), GGT/CCCA ("motif 3"), GNCCAAA ("motif 4"), or SEQ ID NOs:710-713, 714-756, or 757-773. The promoter sequence is preferably about 25 to 2000, e.g., 50 to 500 or 100 to 1400, nucleotides in length.

In one embodiment of the invention, the isolated nucleic acid molecule comprises a plant nucleotide sequence which is the promoter region for any one of SEQ ID NOs: 1-684 and 792-795, or is structurally related to the promoter for SEQ ID NOs: 1-684 and 792-795, i.e., is an orthologous promoter, and is linked to a plant structural gene or open reading frame. Hence, the present invention further provides an expression cassette or a recombinant vector containing the nucleic acid molecule, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid segment in the plant, plant tissue or plant cell.

Transcription of the linked segment is altered in response to pathogen infection, including *Peronospora* infection. For promoters with motif 1, transcription of linked segments may be altered in response to agents or other stimuli that induce Myb-like transcription factors.

Generally, the promoters of the invention may be employed to express a nucleic acid segment that is operably linked to the promoter, for example, an open reading frame or a portion thereof, an anti-sense construct or a transgene. The open reading frame may be obtained from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a

mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a positive selectable marker, a gene affecting plant agronomic characteristics, i.e., yield, standability and the like, or an environment or stress resistance gene, i.e., one or more genes that confer herbicide resistance or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like.

5

10

15

20

25

30

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of the promoter sequences from genes comprising any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

The expression cassettes or vectors of the invention may optionally include other regulatory sequences, e.g., transcription terminator sequences, introns and/or enhancers, and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may

be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell protoplast. Further, the expression cassette can be contained in a plant, plant cell or plant tissue from a dicot or a monocot. In particular, the plant may be a cereal plant.

5

10

15

25

30

The present invention further provides a method of augmenting a plant genome by contacting plant cells with an expression cassette or vector of the invention, i.e., one having a nucleotide sequence that directs transcription of a linked nucleic acid segment in a plant cell, wherein transcription of the linked segment is altered in response to a pathogen such as an oomycete, e.g., *Peronospora*, infection, and wherein the nucleic sequence is from plant DNA that has at least 65%, and more preferably at least 70%, identity to the sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the linked fragment in the cells of the plant in response to infection. The present invention also provides a plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these crossed fertile transgenic plants.

5

10

15

20

25

30

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in response to pathogen exposure, by contacting a probe comprising plant nucleic acid, e.g., cRNA, isolated from tissues of a plant contacted with the pathogen with a plurality of isolated nucleic acid samples on a plurality of solid substrates, wherein each sample is a plurality of oligonucleotides corresponding to at least a portion of a plant gene, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Then complex formation is determined or detected to determine which samples represent genes comprising promoters that are responsive to infection with the pathogen. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

A method to shuffle the nucleic acid molecules of the invention is provided. This method involves fragmentation of a (parent) nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-684 and 792-795, the ortholog thereof, or the corresponding gene thereof, followed by religation. This method allows for the production of polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule. Accordingly, the invention provides cells and transgenic plants containing nucleotide sequences produced through shuffling that encode polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are provided. This medium allows a nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs:1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence

corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795, and the corresponding gene or polypeptide encoded by the nucleic acid sequence.

5

Brief Description of the Figures

Figure 1 depicts RPP-dependent defense pathways.

Figure 2 depicts nucleotide sequences including the promoter region and motifs therein for genes, the expression of which is altered in response to pathogen infection (SEQ ID NOs: 774-788).

Figure 3 is a schematic of the overlap in genes that are induced early after *P. parasitica* infection and in a *RPP8*-specific manner, genes that are induced late after infection and in a *RPP8*-specific manner, and genes induced early and late after infection in a *RPP7*-specific manner.

15 .

10

Figure 4 shows a schematic of RPP4-pathway, RPP7-pathway and RPP8upregulated transcription factor genes.

Detailed Description of the Invention

Definitions

20

25

30

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., 1991; Ohtsuka et al., 1985; Rossolini et al., 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic

acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single-or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid", "nucleic acid molecule", "nucleic acid fragment" or "nucleic acid sequence or segment" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

5

10

15

20

25

30

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart-from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of- interest chemicals. Fragments and variants of the disclosed nucleotide sequences and proteins or partial-length proteins encoded thereby are also encompassed by the present invention. By "fragment" or "portion" is meant a full length or less than

full length of the nucleotide sequence encoding, or the amino acid sequence of, a polypeptide or protein. Alternatively, fragments or portions of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments or portions of a nucleotide sequence may range from at least about 9 nucleotides, about 12 nucleotides, about 20 nucleotides, about 50 nucleotides, about 100 nucleotides or more.

5

10

15

20

25

30

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

A "marker gene" encodes a selectable or screenable trait.

"Selectable marker" is a gene whose expression in a cell gives the cell a selective advantage. The selective advantage possessed by the cells transformed with the selectable marker gene may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a cell gives the cell both a negative and/or a positive selective advantage.

The term "chimeric" refers to any gene or DNA that contains 1) DNA

sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for example, DNA that is either heterologous or homologous to the DNA of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host organism but that is introduced by gene transfer.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

10

15

20

25

30

By "variants" is intended substantially similar sequences. For nucleotide sequences, variants include those sequences that, because of the degeneracy of the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those generated, for example, by using site-directed mutagenesis which encode the native protein, as well as those that encode a polypeptide having amino acid substitutions. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g., 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98%, sequence identity to the native (endogenous) nucleotide sequence.

"DNA shuffling" is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The

DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may have an altered biological activity with respect to the polypeptide encoded by the template DNA.

5

10

15

20

25

30

The nucleic acid molecules of the invention can be optimized for enhanced expression in plants of interest. See, for example, EPA035472; WO91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined in vitro or in vivo. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Crameri et al., 1997; Moore et al., 1997; Zhang et al., 1997; Crameri et al., 1998; and U.S. Patent Nos. 5,605,793 and 5,837,458.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the

encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

5

...10

15

20

25

30

"Recombinant DNA molecule" is a combination of DNA sequences that are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1989).

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," each refer to a sequence that originates from a source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" DNA sequence is a DNA sequence that is naturally associated with a host cell into which it is introduced.

"Wild-type" refers to the normal gene, or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or Agrobacterium binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

5

10

15

20

25

"Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

Such expression cassettes will comprise the transcriptional initiation region of the invention linked to a nucleotide sequence of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of A. tumefaciens, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

5

10

15

20

25

30

An oligonucleotide corresponding to a nucleic acid molecule of the invention may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

10 "Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and whichinfluence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, 15 promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters. However, some suitable regulatory sequences useful in the present invention will include, but are not limited to constitutive plant promoters, plant tissue-specific promoters, plant development specific promoters, inducible plant promoters and viral promoters.

20

25

30

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

5

10

15

20

25

30

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" or "signal sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA- box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate

element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

5

10

15

20

25

30

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e. further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the gene that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of ≥1% of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and

include both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al., 1989. Since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.

Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysome-inducible systems.

10

15

20

25

30

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Altered levels" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed cells or organisms.

10

15

20

25

30

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes. (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al., 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes.

Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

"Transcription stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose bisphosphate carboxylase.

"Translation stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as one or more termination codons in all three frames, capable of terminating translation. Insertion of a translation stop fragment adjacent to or near the initiation codon at the 5' end of the coding sequence will result in no translation or improper translation. Excision of the translation stop fragment by site-specific recombination will leave a site-specific sequence in the coding sequence that does not interfere with proper translation using the initiation codon.

5

10

15

20

25

The terms "cis-acting sequence" and "cis-acting element" refer to DNA or RNA sequences whose functions require them to be on the same molecule. An example of a cis-acting sequence on the replicant is the viral replication origin.

The terms "trans-acting sequence" and "trans-acting element" refer to DNA or RNA sequences whose function does not require them to be on the same molecule.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

- (a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.
- 30 (b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

5.

10

15

20

25

30

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al., 1981; the homology alignment algorithm of Needleman and Wunsch, 1970; the search-for-similarity-method of Pearson and Lipman, 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al., 1988; Higgins et al., 1989; Corpet et al., 1988; Huang et al., 1992; and Pearson et al., 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al., 1997.

Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., supra. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See http://www.ncbi.nlm.nih.gov. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

5

10

15

20

25

- (c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a nonconservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).
- (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal

alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

10

15

20

25

30

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%,

75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, 1970. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

5

10

15

20

25

30

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-

5

10

15

20

25

hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; T_m 81.5°C + 16.6 (log M) +0.41 (%GC) - 0.61 (% form) - 500/L; where M is the molarity of monovalent cations. %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. Tm is reduced by about 1°C for each 1% of mismatching; thus, Tm, hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes.

An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long robes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

5

10

15

20

25

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0. 1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5

M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

5

10

15

20

25

30

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may results form, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides of the invention may be altered in various ways including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U. S. Patent No. 4,873,192; Walker and Gaastra, 1983, and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al., 1978, herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar properties, are preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the polypeptides of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to possess the desired activity. The deletions, insertions, and substitutions of the polypeptide sequence encompassed herein are not expected to produce radical changes in the characteristics of the polypeptide. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of

doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%, more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition, individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

. 10

15

20

25

30

"Production tissue" refers to mature, harvestable tissue consisting of nondividing, terminally-differentiated cells. It excludes young, growing tissue consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

The word "plant" refers to any plant, particularly to seed plant, and "plant cell" is a structural and physiological unit of the plant, which comprises a cell wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds, tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al., 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

10

15

20

25

30

"Transformed," "transgenic," and "recombinant" refer to a host cell or organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995; and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to transgene expression in cells, e.g., after transformation with recombinant virus or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

"Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

5

10

20

25

30

"Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Significant increase" is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

"Significantly less" means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

I. The Nucleic Acid Molecules of the Invention and Polypeptide Encoded Thereby

This invention relates to isolated plant, e.g., Arabidopsis and rice, nucleic acid molecules, sequences and segments (fragments), the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those expressed molecules, sequences or segments. However, the expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic

plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

Preferred sources for the nucleic acid molecules of the invention include, but are not limited to, corn (Zea mays), Brassica sp. (e.g., B. napus, B. rapa, B. juncea), particularly those Brassica species useful as sources of seed oil, alfalfa (Medicago sativa), rice (Oryza sativa), rye (Secale cereale), sorghum (Sorghum bicolor, Sorghum vulgare), millet (e.g., pearl millet (Pennisetum glaucum), proso millet (Panicum miliaceum), foxtail millet (Setaria italica), finger millet (Eleusine coracana)), sunflower (Helianthus annuus), safflower (Carthamus tinctorius), wheat (Triticum aestivum), soybean (Glycine max), tobacco (Nicotiana tabacum), potato (Solanum tuberosum), peanuts (Arachis hypogaea), cotton (Gossypium barbadense, Gossypium hirsutum), sweet potato (Ipomoea batatus), cassava (Manihot esculenta), coffee (Cofea spp.), coconut (Cocos nucifera), pineapple (Ananas comosus), citrus trees (Citrus spp.), cocoa (Theobroma cacao), tea (Camellia sinensis), banana (Musa spp.), avocado 15 (Persea americana), fig (Ficus casica), guava (Psidium guajava), mango (Mangifera indica), olive (Olea europaea), papaya (Carica papaya), cashew (Anacardium occidentale), macadamia (Macadamia integrifolia), almond (Prunus amygdalus), sugar beets (Beta vulgaris), sugarcane (Saccharum spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (Lemna, see WO 20 00/07210, which includes members of the family Lemnaceae. There are known four genera and 34 species of duckweed as follows: genus Lemna (L. aequinoctialis, L. disperma, L. ecuadoriensis, L. gibba, L. japonica, L. minor, L. miniscula, L. obscura, L. perpusilla, L. tenera, L. trisulca, L. turionifera, L. valdiviana); genus Spirodela (S. intermedia, S. polyrrhiza, S. punctata); genus Wo~ffia (Wa. angusta, Wa. arrhiza, Wa. australina, Wa. borealis, Wa. brasiliensis, Wa. columbiana, Wa. elongata, Wa. globosa, Wa. microscopica, Wa. neglecta) and genus Wo-fiella (W1. caudata, W1. denticulata, W1. gladiata, W1. hyalina, W1. lingulata, W1. repunda, W1. rotunda, and W1. neotropica). Any other genera or species of Lemnaceae, if they exist, are also aspects of the present invention. Lemna gibba, Lemna minor, and Lemna miniscula are preferred, with Lemna minor and Lemna miniscula being most preferred. Lemna species can be classified using the taxonomic scheme described by Landolt,

25

30

Biosystematic Investigation on the Family of Duckweeds: The family of

Lemnaceae - A Monograph Study. Geobatanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (Lycopersicon esculentum), lettuce (e.g., Lactuca sativa), green beans (Phaseolus vulgaris), lima beans (Phaseolus limensis), peas (Lathyrus spp.), and members of the genus Cucumis such as cucumber (C. sativus), cantaloupe (C. cantalupensis), and musk melon 5 (C. melo). Ornamentals include azalea (Rhododendron spp.), hydrangea (Macrophylla hydrangea), hibiscus (Hibiscus rosasanensis), roses (Rosa spp.), tulips (Tulipa spp.), daffodils (Narcissus spp.), petunias (Petunia hybrida), carnation (Dianthus caryophyllus), poinsettia (Euphorbia pulcherrima), and 10 chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (Pinus taeda), slash pine (Pinus elliotii), ponderosa pine (Pinus ponderosa), lodgepole pine (Pinus contorta), and Monterey pine (Pinus radiata), Douglas-fir (Pseudotsuga menziesii); Western hemlock (Tsuga canadensis); Sitka spruce (Picea glauca); redwood (Sequoia sempervirens); true firs such as silver fir (Abies amabilis) and balsam fir (Abies balsamea); and cedars such as Western red cedar (Thuja plicata) and Alaska yellow-cedar (Chamaecyparis nootkatensis). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, 20 chickpea, etc. Legumes include, but are not limited to, Arachis, e.g., peanuts, Vicia, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, Lupinus, e.g., lupine, trifolium, Phaseolus, e.g., common bean and lima bean, Pisum, e.g., field bean, Melilotus, e.g., clover, Medicago, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, Acacia, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, 25 honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, 30 nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula,

Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

Other vegetable sources (and databases to identify orthologs of the invention) for the nucleic acid sequences of the invention include those are shown in Table 1.

Table 1

	·		Γ	
FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
			· .	
Cucurbitaceae	Cucumis sativus	Cucumber		http://www.cucurbit. rg/
	Cucumis melo	Melon		http://genome.comell edu/cgc/
	Citrullus lanatus	Watermelon		
	Cucurbita pepo	Squash – summer		
	Cucurbita maxima	Squash - winter		
	Cucurbita moschata	Pumpkin /butternut		
Total	·			http://www.nal.usda.į ov/pgdic/Map_proj/
	<u> </u>			
Solanaceae	Lycopersicon esculentum	Tomato	Genome center (www.genome.c lemson.edu) 11.6x BAC of L. cheesmanii (orginates from J. Giovannoni) available from Clemson	genome.cornell.edu/s olgenes http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=solgenes http://genome.cornell edu/tgc/ http://tgrc.ucdavis.edu/
			genome center (www.genome.c lemson.edu) EST collection	

			T	
	ł		from TIGR	
Ì	ł		(www.tigr.org/t	
· ·		1	db/lgi/index.htm	1
		ł	1)	,
į			• EST collection	
·	į .		from Clemsom	
		,	Genome Center	
		İ] .
		ł	(www.genome.c	
			lemson.edu)	1
			• TAG 99:254-	
[1	271, 1999	
•			(esculentum x	
			pennelli)	
			• TAG 89:1007-	
		j	1013, 1994	
		İ	(peruvianum)	
1		İ	Plant Cell	
			Reports 12:293-	· · · · · · · · ·
]	_	
			297, 1993	
	•		(RAPDs)	
		ļ	• Genetics	
		j	132:1141-1160,	to the factor of the second
			1992 (potato x	ĺ
		ŀ	tomato)	
' '			 Genetics 	
Ì		1	120:1095-1105,	
		İ	1988 (RFLP	,
		1	potato and	· ·
i			tomato)	
l	•	}	• Genetics	
\	i		•	and the second
			115:387-393,	1
	•	ĺ	1986	
	•		(esculentum x	
		1	pennelli	
			isozyme and	•
			cDNAs)	
	Capsicum	Pepper		http://neptune.netima
	annuum	1 11		ges.com/~chile/scienc
				e.html
F	Capsicum	Chile pepper		V(1111
·	frutescens	Cinic bobber		·
	Solanum	Form!		
1		Eggplant		
	melongena			·
}	(Nicotiana	(Tobacco)		
	tabacum)			
	(Solanum	(Potato)		
]	tuberosum)			
	(Petunia x	(Petunia)	4x BAC of Petunia	
	hybrida hort.		hybrida 7984	
1	·· rui iuu iiui i.		11VIJIUN / 704	
1	ex E. Vilm.)		available from	

Total Total Brassicaceae Brassica oleracea L. var. italica Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db-brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAc	•		I	Claman	T
Total Brassicaceae Brassica oleracea L. var. italica Brassica oleracea L. var. capitata Brassica rapa Cabbage Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis Arabidopsis Arabidopsis Daikon scheme Clemson genome Clemson genome Center (www.genome.clem son.edu) http://www.nal.usda.g ov/pgdic/Map proj/ http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=agr Total Total Chenopodiaceae Spinacia oleracea Geta vulgaris) (Sugar Beet)		Ĭ		Clemson genome	1
Total Brassicaceae Brassica oleracea L. var. italica Brassica oleracea L. var. capitata Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs on Columbia strain available from clemson genome center (www.genome.clem son.edu) Arabidopsia Total Total Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus amusus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	` .			1	
Brassicaceae Brassica oleracea L. var. italica Brassica oleracea L. var. capitata Brassica rapa Clabbage Brassica cleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs oleracea Columbia strain available from Clemson genome center (mww.genome.clem son.edu) Attp://www.nal.usda.gov/pgdic/Map proj/ http://geneous.cit.com ell.edu/cabbage/about cab.html http://geneous.cit.com ell.edu/cabbage/about cab.html http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=agr	• •				
Brassicaceae Brassica oleracea L. var. italica Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis Arabidopsis Arabidopsis Arabidopsis Total Total Daucus carota Carrot Compositae Lactuca sativa Lettuce Brassica oleracea Calbage Calbage Calbage Calbage Calbage Calbage Calbage Calbage Calbage Calbage Calbage Calbage Calliflower calbage Calba			<u> </u>	son.edu)	
Brassicaceae Brassica oleracea L. var. italica Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Attp://www.nal.usda.g ov/pgdic/Map proj/ http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=agr Www.genome.clem son.edu) Attabile from Clemson genome center (www.genome.clem son.edu) Attabile from Clemson genome come.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://www.nal.usda.g ov/pgdic/Map proj/ Compositae Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	Total	ľ			http://www.nal.usda.g
Brassicaceae Brassica oleracea L. var. italica Broccoli oleracea L. var. italica Brassica oleracea L. var. capitata Cabbage Cauliflower oleracea L. var. botrytis Raphanus sativus var. niger Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica oleracea L. var. botrytis Raphanus sativus var. niger Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassica (Oilseed rape) Brassicadb Brassica (Oilseed rape) Brassica (Oilseed ra]			•	
oleracea L. var. italica Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. botryvis Raphanus sativus var. niger (Brassica napus) Arabidopsis Arabidopsis Arabidopsis Total Total Center de de de de de de de de de de de de de			<u> </u>	<u> </u>	PB010/1/12p_p10j/
oleracea L. var. italica Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. capitata Brassica oleracea L. var. botryvis Raphanus sativus var. niger (Brassica napus) Arabidopsis Arabidopsis Arabidopsis Total Total Center de de de de de de de de de de de de de	Brassicaceae	Brassica	Broccoli		http://res.gor.go/goorg/
Var. italica dex.htm http://geneous.cit.com ell.edu/cabbage/about cab.html			Broccon	<u>'</u>	
http://geneous.cit.comell.edu/cabbage/about cab.html Brassica oleracea L. var. capitata Brassica rapa Chinese Cabbage Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Total Chenopodiaceae Spinacia oleracea (Sunflower) annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet)		I	l	}	
Brassica Cabbage cab.html		vai. italica			
Brassica oleracea L. var. capitata Cabbage Calbage Cabbage Brassica rapa Chinese Cabbage Cauliflower oleracea L. var. botrytis Daikon Sativus var. niger (Brassica napus) Total Campositae Lactuca sativa var. niger (Www.genome.clem son.edu) http://www.nal.usda.gov/pgdic/Map proj/	Ì			1	
Brassica oleracea L. var. capitata Brassica rapa Brassica clebage Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Daikon strain available from Clemson genome connell.edu/c gi-bin/WebAce/webace? db=agr Total Total Compositae Lactuca sativa Lettuce Helianthus annuus Lettuce Helianthus annuus Lettuce Gundown Lettuce Lettu			i .		
Oleracea L. var. capitata				·	cab.html
Var. capitata Brassica rapa Chinese Cabbage		1	Cabbage		
Brassica rapa Brassica Brassica Cabbage Calliflower oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis Lemson genome center (www.genome.clem son.edu) Attp://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=brassicadb http://ars- genome.cornell.edu/c gi- bin/WebAce/webace? db=agr Www.genome.clem son.edu) http://www.nal.usda.g ov/pgdic/Map_proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet)		oleracea L.	ŀ	j .	. •
Cabbage Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Daikon	<u></u>	var. capitata	İ		
Cabbage Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Daikon		Brassica rapa	Chinese		
Brassica oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome clem son.edu) Total Total Total Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)			ī		
oleracea L. var. botrytis Raphanus sativus var. niger (Brassica napus) Arabidopsis Arabidopsis Arabidopsis Arabidopsis I2x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Total Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)		Rrassica			
Var. botrytis Raphanus sativus var. niger (Brassica napus) Compositae Lactuca sativa Lettuce Helianthus annuus Chenopodiaceae (Beta vulgaris) (Sugar Beet) Compositae Carrot Compositae Carrot Chenopodiaceae (Beta vulgaris) (Sugar Beet) Compositae Carrot Compositae Carrot Chenopodiaceae (Beta vulgaris) (Sugar Beet) Compositae Carrot Compositae Carrot		1 .	Caulifiower		
Raphanus sativus var. niger (Brassica napus) Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome.cornell.edu/c gibin/WebAce/webace? db=orassicadb http://ars-genome.cornell.edu/c gibin/WebAce/webace? db=orassicadb http://ars-genome.cornell.edu/c gibin/WebAce/webace? db=orassicadb http://ars-genome.cornell.edu/c gibin/WebAce/webace? db=agr Total Total Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) http://www.nal.usda.g ov/pgdic/Map_proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Arabidopsis 12x and 6x BACs on Columbia strain available from clemson genome.cornell.edu/c gibin/WebAce/webace? db=agr bin/WebAce/webace? db=agr bin/WebAce/webace? db=agr bin/WebAce/webace? db=agr bin/WebAce/webace? db=agr					
Sativus var. niger (Brassica napus) (Oilseed rape) http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db=brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db=brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db=brassicadb http://ars-genome.cornell.edu/c gi-bin/WebAce/webace? db=agr db=a					
Niger (Brassica napus) Nittp://ars-genome.comell.edu/c gibin/WebAce/webace? Nittp://ars-genome.comell.edu/c gibin/W			Daikon	1	
Compositae Carrot Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet) Compositae Carrot Chenopodiaceae Spinacia oleracea (Sugar Beet) Compositae Compositae Carrot Compositae Carrot		sativus var.	·		
mapus) rape) genome.comell.edu/c gibin/WebAce/webace? db=brassicadb Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total http://www.nal.usda.gov/pgdic/Map_proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)		niger	<u> </u> -		:
mapus) rape) genome.comell.edu/c gibin/WebAce/webace? db=brassicadb Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total http://www.nal.usda.gov/pgdic/Map_proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)		(Brassica	(Oilseed		http://ars-
Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Daucus carota Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet)		napus)	rape)	4	r - '
Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet)					T. 1
Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet) Arabidopsis 12x and 6x BACs on Columbia strain available from gibin/WebAce/webace? db=agr http://www.nal.usda.g ov/pgdic/Map proj/				· ·	6 -
Arabidopsis 12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clem son.edu) http://www.nal.usda.g ov/pgdic/Map proj/ Umbelliferae Daucus carota Carrot Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet) Columbia strain available from Clemson genome bin/WebAce/webace? db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr db=agr		1			· ·
on Columbia strain available from Clemson genome center (www.genome.clem son.edu) Total Total Daucus carota Carrot Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet)		 	Arabidonaia		
available from Clemson genome center (www.genome.clem son.edu) Total http://www.nal.usda.g ov/pgdic/Map proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)					
Clemson genome center (www.genome.clem son.edu) Total http://www.nal.usda.g ov/pgdic/Map proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)		·	i e		۲.
Total Total Compositae Lactuca sativa Total Chenopodiaceae (Beta vulgaris) (Sunflower) (Sungar Beet) Center (www.genome.clem son.edu) http://www.nal.usda.gov/pgdic/Map_proj/ http://www.nal.usda.gov/pgdic/Map_proj/ http://www.nal.usda.gov/pgdic/Map_proj/ Chenopodiaceae Spinacia (Sunflower) Spinach (Sunflower)					
Total Total Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet) Mattp://www.nal.usda.g ov/pgdic/Map_proj/ http://www.nal.usda.g ov/pgdic/Map_proj/ http://www.nal.usda.g ov/pgdic/Map_proj/ http://www.nal.usda.g ov/pgdic/Map_proj/ Sunflower Carrot					
Total Total Compositae Lactuca sativa Helianthus annuus Total Chenopodiaceae (Beta vulgaris) (Sugar Beet) Mattp://www.nal.usda.g ov/pgdic/Map_proj/ http://www.nal.usda.g ov/pgdic/Map_proj/ http://www.nal.usda.g ov/pgdic/Map_proj/ http://www.nal.usda.g ov/pgdic/Map_proj/ Sunflower Carrot			center	db≃agr	
Total son.edu) Total http://www.nal.usda.g ov/pgdic/Map_proj/ Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus (Sunflower) annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	· .			(www.genome.clem	
Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus (Sunflower) annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)					
Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	Total				http://www.nal.usda.g
Umbelliferae Daucus carota Carrot Compositae Lactuca sativa Lettuce Helianthus (Sunflower) annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)		,			
Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)					PPorolitrah hioli
Compositae Lactuca sativa Lettuce Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	Umbelliferse	Dancus carota	Carret		
Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	Oniconniciae	Luncus curviu	Carror	·	
Helianthus annuus Total Chenopodiaceae Spinacia oleracea (Beta vulgaris) (Sugar Beet)	Correction	7	*		
Total Chenopodiaceae Spinacia Spinach oleracea (Beta vulgaris) (Sugar Beet)	Compositae				
Total Chenopodiaceae Spinacia Spinach oleracea (Beta vulgaris) (Sugar Beet)		Helianthus	(Sunflower)		**
Chenopodiaceae Spinacia Spinach oleracea (Beta vulgaris) (Sugar Beet)		annuus			
Oleracea (Beta vulgaris) (Sugar Beet)	Total				
Oleracea (Beta vulgaris) (Sugar Beet)	·				
Oleracea (Beta vulgaris) (Sugar Beet)	Chenopodiaceae	Spinacia	Spinach		·
(Beta vulgaris) (Sugar Beet)			Spinacii		
Total (Beta vuigaris) (Sugar Beet)	 		(G		
I OTAL	TD . 1	(Beta vulgaris)	(Sugar Beet)		
	Lotal	L			

		, 		
				
Leguminosae	Phaseolus	Bean	4.3x BAC available	http://ars-
•	vulgaris	ļ	from Clemson	genome.comell.edu/c
			genome center	gi-
• •	•		(www.genome.clem	bin/WebAce/webace
			son.edu)	db=beangenes
	Pisum sativum	Pea		
	(Glycine max)	(Soybean)	7.5x and 7.9x BACs	http://ars-
		` -	available from	genome.comell.edu/c
-			Clemson genome	gi-
			_	bin/WebAce/webace?
		}	(www.genome.clem	
		·	son.edu)	
Total			http://www.nal.usda	
		}	.gov/pgdic/Map pro	
	•		i/	,
			J'	
Gramineae	Zea mays	Sweet Com	Novartis BACs for	
	Lea mays	Sweet Com	Mo17 and B73 have	
[been donated to	,
		·	Clemson Genome	A Committee of the Comm
	. · ·		Center ·	
			(www.genome.clem	
. 4	(700	(P:-14 (P)	son.edu)	1
	(Zea mays)	(Field Corn)		http://www.agron.mis
Total				souri.edu/mnl/
Total	·		http://www.nal.usda	
			.gov/pgdic/Map_pro	
			<u> </u>	
T '1'	477			
Liliaceae	Allium cepa	Onion	·	
	·	Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda	
		•	.gov/pgdic/Map pro	

Preferred forage and turf grass nucleic acid sources for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Preferably, the nucleic acid sources are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence obtained or obtainable

5

10

15

20

25

30

from any plant gene which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by SEQ ID NOs. 1-684 or 789-795, or a promoter for said gene. Thus, based on the Arabidopsis nucleic acid sequences of the present invention, orthologs of those sequences may be identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the Arabidopsis coding sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular Arabidopsis sequence is used as a probe that selectively hybridizes to other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g., Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from which the probe sequence is derived. The application of these methods using the Arabidopsis coding sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art as discussed hereinabove.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ³²P, or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al., 1989. In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

II. Expression Cassettes of the Invention

5

10

15

20

25

30

The present invention also encompasses expression cassettes, preferably in the form of a recombinant vectors comprising the nucleic acid sequences of the invention. In such vectors, the expression cassette comprises regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise promoter and termination signals and preferably also comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be effective in plants. Joshi (1987) has suggested an appropriate consensus for plants and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensuses are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, e.g., as extrachromosomal molecules, and are

therefore used to amplify the nucleic acid sequences of this invention in the host cells. In a preferred embodiment, host cells for such vectors are plant cells.

A. Promoters and Enhancers

5

10

15

20

25

30

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In many cases, expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, stress-responsive, tissue-preferred and tissue-specific promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level of isothiopropylgalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP

0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Tissue-specific or tissue-preferential promoters useful in the present invention. Also useful are promoters which confer seed-specific expression, such as those disclosed by Schernthaner et al., 1988; anther (tapetal) specific promoter B6 (Huffman et al.); and pistil-specific promoters such as a modified S13 promoter (Dzelkalns et al., 1993).

5

10

20

25

30

Preferred tissue specific expression patterns include green tissue-specific, root-specific, stem-specific, and flower-specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, 1989). A preferred promoter for root-specific expression is that described by de Framond (1991; EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in U.S. Patent No. 5,625,136 (to Ciba-Geigy) and which drives expression of the maize trpA gene.

Other promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs, nos*, and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Bonchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Preferred plant promoters include, but are not limited to, a promoter such as the CaMV 35S promoter, an enhanced 35S promoter or others such as CaMV 19S, nos, Adh1, sucrose synthase, α-tubulin, ubiquitin, actin, cab, PEPCase or those associated with the R gene complex. Further suitable promoters include the U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein

protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea rbcS gene and the actin promoter from rice; seed specific promoters, such as the phaseolin promoter from beans, may also be used. Other promoters useful in the practice of the invention are known to those of skill in the art.

5

25

30

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990,) corn alcohol dehydrogenase 1 10 (Vogel et al., 1992; Dennis et al., 1984), corn light harvesting complex (Simpson, 1985; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985; Rochester et al., 1986), pea small subunit RuBP carboxylase (Poulsen et al., 1986; Cashmore et al., 1983), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone 15 isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), \alpha-tubulin, cab (Sullivan et al., 1989), 20 PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), and chalcone synthase promoters (Franken et al., 1991).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase, and fatty acid desaturases (fad 2-1)), and other genes expressed during embryo development (such as Bce4, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific

expression is the pea vicilin promoter (Czako et al., 1992. (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995, 270 (5244), 1986-8).

5

10

15

20

25

30

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674, the disclosure of which is hereby incorporated by reference. cDNA clones that are preferentially expressed in cotton fiber have been isolated (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S. Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al., 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky" expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996 and 1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid-(Aoyama, 1997) and ecdysome-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol- (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to

environmental stress or stimuli such as increased salinity. drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986). Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and air borne pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous or homologous-pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the mRNA of the native DNA sequence.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by DNA binding proteins such as zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific DNA sequence.

B. 5' and 3' Sequences

5

10

15

20

25

30

In addition to promoters, a variety of 3 transcriptional terminators are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA

polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the tml terminator, the nopaline synthase terminator, the pea rbcS E9'terminator, the terminator for the T7 transcript from the octopine synthase gene of Agrobacterium tumefaciens, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed.

The 5' regulatory region of the expression cassette may also include other enhancing sequences. Numerous sequences have been found to enhance gene expression in transgenic plants. These include sequences which have been shown to enhance expression such as intron sequences (e.g., from Adh1, bronze1 or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

30 C. Targeting Sequences

5

10

15

20

25

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle, e.g., the nucleus, may be preferred. Subcellular

localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

D. Marker Genes

10

15

20

25

30

In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the preselected nucleic acid sequence or segment. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., α-amylase, β-lactamase, phosphinothricin acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a polypeptide that becomes sequestered in the cell wall, and which polypeptide

includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

5

15

20

25

30

Elements of the present disclosure are exemplified in detail through the use of particular marker genes. However in light of this disclosure, numerous other possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth herein below. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant cell, e.g., a monocot cell.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a neo gene, which codes for kanamycin resistance and can be selected for using kanamycin, G418, a gene encoding resistance to bleomycin, and the like; a bar gene which codes for bialaphos resistance; a gene which encodes an altered EPSP synthase protein thus conferring glyphosate resistance; a nitrilase gene such as bxn from Klebsiella ozaenae which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonylurea or other ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene; a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; or a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable chloroplast transit peptide, CTP (European Patent Application 0 218 571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the bar gene from Streptomyces

hygroscopicus or the pat gene from Streptomyces viridochromogenes (U.S. Patent No. 5,550,318). The enzyme phosphinothricin acetyltransferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Screenable markers that may be employed include, but are not limited to, a β-glucuronidase or *uid*A gene (GUS) which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a -lactamase gene, which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xyl*E gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an -amylase gene; a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene, which allows for bioluminescence detection; or an aequorin gene, which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein.

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one, or as many as four, R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22

which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, Pl. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

E. Other Sequences

5

10

15

20

25

30

A vector of the invention can also further comprise plasmid DNA. Plasmid vectors include additional DNA sequences that provide for easy selection, amplification, and transformation of the expression cassette in prokaryotic and eukaryotic cells, e.g., pUC-derived vectors such as pUC8, pUC9, pUC18, pUC19, pUC23, pUC119, and pUC120, pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, or pBS-derived vectors. The additional DNA sequences include origins of replication to provide for autonomous replication of the vector, additional selectable marker genes, preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the expression cassette, and sequences that enhance transformation of . prokaryotic and eukaryotic cells.

Another vector that is useful for expression in both plant and prokaryotic cells is the binary Ti plasmid (as disclosed in Schilperoort et al., U.S. Patent No. 4,940,838) as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, cited *supra*. This binary Ti vector can be replicated in prokaryotic bacteria such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can be used to transfer the expression cassette to dicot plant cells, and under certain conditions to monocot cells, such as rice cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *colE1* replication of origin and a wide host range replicon. The binary Ti vectors carrying an

expression cassette of the invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform dicot plant cells.

Virtually any DNA may be used for delivery to recipient cells to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instance containing only the DNA element to be expressed in the plant, and the like, may be employed.

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

20 III. Transformation

5

10

15

25

30

The expression cassettes of the present invention can be introduced into a host cell, e.g., a plant cell, in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of cell, e.g., monocotyledonous or dicotyledonous, targeted for transformation. Vectors which may be used to transform plant tissue with the expression cassettes of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation, e.g., direct uptake or via electroporation. However, cells other than plant cells may be transformed with the expression cassettes of the invention.

Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), direct DNA transfer to plant cells by PEG precipitation; liposomes; electroporation (Riggs et al., 1986, Agrobacterium-mediated transformation (Hinchee et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using

devices available from Agracetus, Inc., Madison, Wis. and BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat).

5

10

In one embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994. The basic technique for chloroplast transformation involves introducing regions 15 of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous 20 recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants 25 at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant 30 selectable marker, the bacterial aadA gene encoding the spectinomycindetoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a

homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression-cassette of the present invention, wherein the vector-comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an Agrobacterium tumefaciens as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous Agrobacterium vector systems useful in carrying out the present invention are known. For example, U.S. Pat. No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an Agrobacterium strain containing the Ti plasmid. The transformation of woody plants with an Agrobacterium vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary Agrobacterium vector (i.e., one in which the Agrobacterium contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of Agrobacterium spp. Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985: Byrne et al., 1987; Sukhapinda et al., 1987; Lorz et al., 1985; Potrykus, 1985; Park et al., 1985: Hiei et al., 1994. The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An. et al., 1985. For introduction into plants, the nucleotide sequences of the invention can be inserted into binary vectors as described in the examples.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention.

Numerous transformation vectors are available for plant transformation, and the expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

5

Preferred plant cells for transformation include, but are not limited to, cells from plant such as corn (Zea mays), Brassica sp. (e.g., B. napus, B. rapa, B. juncea), particularly those Brassica species useful as sources of seed oil, alfalfa (Medicago sativa), rice (Oryza sativa), rye (Secale cereale), sorghum (Sorghum bicolor, Sorghum vulgare), millet (e.g., pearl millet (Pennisetum glaucum), proso millet (Panicum miliaceum), foxtail millet (Setaria italica), finger millet (Eleusine coracana)), sunflower (Helianthus annuus), safflower (Carthamus tinctorius), wheat (Triticum aestivum), soybean (Glycine max), tobacco 15 (Nicotiana tabacum), potato (Solanum tuberosum), peanuts (Arachis hypogaea), cotton (Gossypium barbadense, Gossypium hirsutum), sweet potato (Ipomoea batatus), cassava (Manihot esculenta), coffee (Cofea spp.), coconut (Cocos nucifera), pineapple (Ananas comosus), citrus trees (Citrus spp.), cocoa 20 (Theobroma cacao), tea (Camellia sinensis), banana (Musa spp.), avocado (Persea americana), fig (Ficus casica), guava (Psidium guajava), mango (Mangifera indica), olive (Olea europaea), papaya (Carica papaya), cashew (Anacardium occidentale), macadamia (Macadamia integrifolia), almond (Prunus amygdalus), sugar beets (Beta vulgaris), sugarcane (Saccharum spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (Lemna, see WO 25 00/07210, which includes members of the family Lemnaceae. There are known four genera and 34 species of duckweed as follows: genus Lemna (L. aequinoctialis, L. disperma, L. ecuadoriensis, L. gibba, L. japonica, L. minor, L. miniscula, L. obscura, L. perpusilla, L. tenera, L. trisulca, L. turionifera, L. valdiviana); genus Spirodela (S. intermedia, S. polyrrhiza, S. punctata); genus 30 Woffia (Wa. angusta, Wa. arrhiza, Wa. australina, Wa. borealis, Wa. brasiliensis, Wa. columbiana, Wa. elongata, Wa. globosa, Wa. microscopica, Wa. neglecta) and genus Wofiella (W1. caudata, W1. denticulata, W1. gladiata, W1. hyalina, W1. lingulata, W1. repunda, W1. rotunda, and W1. neotropica).

5

10

15

20

25

30

Any other genera or species of Lemnaceae, if they exist, are also aspects of the present invention. Lemna gibba, Lemna minor, and Lemna miniscula are preferred, with Lemna minor and Lemna miniscula being most preferred. Lemna species can be classified using the taxonomic scheme described by Landolt, Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobatanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (Lycopersicon esculentum), lettuce (e.g., Lactuca sativa), green beans (Phaseolus vulgaris), lima beans (Phaseolus limensis), peas (Lathyrus spp.), and members of the genus Cucumis such as cucumber (C. sativus), cantaloupe (C. cantalupensis), and musk melon (C. melo). Ornamentals include azalea (Rhododendron spp.), hydrangea (Macrophylla hydrangea), hibiscus (Hibiscus rosasanensis), roses (Rosa spp.), tulips (Tulipa spp.), daffodils (Narcissus spp.), petunias (Petunia hybrida), carnation (Dianthus caryophyllus), poinsettia (Euphorbia pulcherrima), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (Pinus taeda), slash pine (Pinus elliotii), ponderosa pine (Pinus ponderosa), lodgepole pine (Pinus contorta), and Monterey pine (Pinus radiata), Douglas-fir (Pseudotsuga menziesii); Western hemlock (Tsuga canadensis); Sitka spruce (Picea glauca); redwood (Sequoia sempervirens); true firs such as silver fir (Abies amabilis) and balsam fir (Abies balsamea); and cedars such as Western red cedar (Thuja plicata) and Alaska yellow-cedar (Chamaecyparis nootkatensis). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, Arachis, e.g., peanuts, Vicia, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, Lupinus, e.g., lupine, trifolium, Phaseolus, e.g., common bean and lima bean, Pisum, e.g., field bean, Melilotus, e.g., clover, Medicago, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, Acacia, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry,

nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other vegetables are in Table 1.

5

10

15

20

25

30

Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.—

Preferably, plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably rice, corn and soybean.

In a preferred embodiment, the host cells are monocot or dicot cells, including, but are not limited to, wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as Arachis, e.g., peanuts, Vicia, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, Lupinus, e.g., lupine, trifolium, Phaseolus, e.g., common bean and lima bean, Pisum, e.g., field bean, Melilotus, e.g., clover, Medicago, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia,

Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. More preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

5

10

15

20

25

30

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

The choice of plant tissue source for transformation will depend on the nature of the host plant and the transformation protocol. Useful tissue sources include callus, suspension culture cells, protoplasts, leaf segments, stem segments, tassels, pollen, embryos, hypocotyls, tuber segments, meristematic regions, and the like. The tissue source is selected and transformed so that it retains the ability to regenerate whole, fertile plants following transformation, i.e., contains totipotent cells. Type I or Type II embryonic maize callus and immature embryos are preferred *Zea mays* tissue sources. Selection of tissue sources for transformation of monocots is described in detail in U.S. Application Serial No. 08/112,245 and PCT publication WO 95/06128 (incorporated herein by reference).

For certain plant species, different antibiotic or herbicide selection markers may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982); Bevan et al., 1983), the *bar* gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the *hph* gene which confers resistance to the antibiotic hygromycin

(Blochinger & Diggelmann), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., 1983).

Thus, the present invention also provides a transformed (transgenic) plant cell, in planta or ex planta, including, but not limited to, a transformed plant cell from plants such as corn (Zea mays), Brassica sp. (e.g., B. napus, B. rapa, B. 5 juncea), particularly those Brassica species useful as sources of seed oil, alfalfa (Medicago sativa), rice (Oryza sativa), rye (Secale cereale), sorghum (Sorghum bicolor, Sorghum vulgare), millet (e.g., pearl millet (Pennisetum glaucum), proso millet (Panicum miliaceum), foxtail millet (Setaria italica), finger millet 10 (Eleusine coracana)), sunflower (Helianthus annuus), safflower (Carthamus tinctorius), wheat (Triticum aestivum), soybean (Glycine max), tobacco (Nicotiana tabacum), potato (Solanum tuberosum), peanuts (Arachis hypogaea), cotton (Gossypium barbadense, Gossypium hirsutum), sweet potato (Ipomoea batatus), cassava (Manihot esculenta), coffee (Cofea spp.), coconut (Cocos 15 nucifera), pineapple (Ananas comosus), citrus trees (Citrus spp.), cocoa (Theobroma cacao), tea (Camellia sinensis), banana (Musa spp.), avocado (Persea americana), fig (Ficus casica), guava (Psidium guajava), mango (Mangifera indica), olive (Olea europaea), papaya (Carica papaya), cashew (Anacardium occidentale), macadamia (Macadamia integrifolia), almond (Prunus amygdalus), sugar beets (Beta vulgaris), sugarcane (Saccharum spp.), 20 oats, barley, vegetables, ornamentals, and conifers; duckweed (Lemna, see WO 00/07210, which includes members of the family Lemnaceae. There are known four genera and 34 species of duckweed as follows: genus Lemna (L. aequinoctialis, L. disperma, L. ecuadoriensis, L. gibba, L. japonica, L. minor, L. 25 miniscula, L. obscura, L. perpusilla, L. tenera, L. trisulca, L. turionifera, L. valdiviana); genus Spirodela (S. intermedia, S. polyrrhiza, S. punctata); genus Woffia (Wa. angusta, Wa. arrhiza, Wa. australina, Wa. borealis, Wa. brasiliensis, Wa. columbiana, Wa. elongata, Wa. globosa, Wa. microscopica, Wa. neglecta) and genus Wofiella (W1. caudata, W1. denticulata, W1. gladiata, W1. hyalina, W1. lingulata, W1. repunda, W1. rotunda, and W1. neotropica). 30 Any other genera or species of Lemnaceae, if they exist, are also aspects of the present invention. Lemna gibba, Lemna minor, and Lemna miniscula are preferred, with Lemna minor and Lemna miniscula being most preferred. Lemna species can be classified using the taxonomic scheme described by Landolt,

Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobatanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (Lycopersicon esculentum), lettuce (e.g., Lactuca sativa), green beans (Phaseolus vulgaris), lima beans 5 (Phaseolus limensis), peas (Lathyrus spp.), and members of the genus Cucumis such as cucumber (C. sativus), cantaloupe (C. cantalupensis), and musk melon (C. melo). Ornamentals include azalea (Rhododendron spp.), hydrangea (Macrophylla hydrangea), hibiscus (Hibiscus rosasanensis), roses (Rosa spp.), tulips (Tulipa spp.), daffodils (Narcissus spp.), petunias (Petunia hybrida), 10 carnation (Dianthus caryophyllus), poinsettia (Euphorbia pulcherrima), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (Pinus taeda), slash pine (Pinus elliotii), ponderosa pine (Pinus ponderosa), lodgepole pine (Pinus contorta), and Monterey pine (Pinus radiata), Douglas-fir (Pseudotsuga 15 menziesii); Western hemlock (Tsuga canadensis); Sitka spruce (Picea glauca); redwood (Sequoia sempervirens); true firs such as silver fir (Abies amabilis) and balsam fir (Abies balsamea); and cedars such as Western red cedar (Thuja plicata) and Alaska yellow-cedar (Chamaecyparis nootkatensis). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, 20 soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, Arachis, e.g., peanuts, Vicia, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, Lupinus, e.g., lupine, trifolium, Phaseolus, e.g., common bean and lima bean, Pisum, e.g., field bean, Melilotus, e.g., clover, Medicago, e.g., alfalfa, Lotus, e.g., 25 trefoil, lens, e.g., lentil, and false indigo, Acacia, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, 30 nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, as well as from vegetables including those described in Table 1.

In a preferred embodiment, the transformed cells, include, but are not limited to, transformed wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as Arachis, e.g., peanuts, Vicia, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, Lupinus, e.g., lupine, trifolium, Phaseolus, e.g., common bean and lima bean, Pisum, e.g., field bean, Melilotus, e.g., clover, Medicago, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. Preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

30 IV. Identification of Transgenic Plants

5

15

20

25

To confirm the presence of the preselected nucleic acid segment(s) or "transgene(s)" in the regenerating plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, in situ

hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

10

15

20

25

30

The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discreet fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

5

10

15

20

25

30

Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The nonchimeric nature of the callus and the parental transformants (R₀) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R₀ plants and R₁ progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical composition, morphology, or physiological properties of the plant.

Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

30 V. Utility

5

10

15

20

25

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention

include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

10

components.

30

15 The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested 20 from the plant (e.g., improved nutritive content in human food or animal feed), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or 25 for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements

encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can be used to identify proprietary lines or varieties.

5

10

15

20

25

30

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of viruses or other pests, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

5

10

15

20

25

30

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-795 as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, nonvolatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(http://www.ncbi.nlm.nih.gov/) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following examples which is not intended to limit the scope of the invention.

Example 1

GeneChip Standard Protocol

Quantitation of total RNA

Total RNA from plant tissue is extracted and quantified.

5 1. Quantify total RNA using GeneQuant

1OD₂₆₀=40 mg RNA/ml; A260/A280=1.9 to about 2.1

2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

10 Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019)

was employed to prepare cDNAs. T7-(dT)₂₄ oligonucleotides were prepared

and purified by HPLC. (5'-

15 GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)₂₄-3'(SEQ ID NO:800).

Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

Quick spin and put on ice briefly

20 <u>Step 2. Temperature adjustment:</u>

Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

DEPC-water- 1 µl

RNA (10 μg final)-10 μl

25 T7=(dT)₂₄ Primer (100 pmol final)-1 μl pmol

5X 1st strand cDNA buffer-4 ul

0.1M DTT (10 mM final)- 2 μl

10 mM dNTP mix (500 µM final)-1 µl

Superscript II RT 200 U/µl- 1 µl

30 Total of 20 μl

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

5

DEPC-water- 91 μl

5X 2nd strand cDNA buffer- 30 μl

mM dNTP mix (250 mM final) - 3 μl

E. coli DNA ligase (10 U/μl)-1 μl

E. coli DNA polymerase 1-10 U/μl- 4 μl

RnaseH 2U/μl -1 μl

T4 DNA polymerase 5 U/μl-2 μl

0.5 M EDTA (0.5 M final)--10 μl

Total 162 µl

10 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233)
 at 14,000X, transfer 162 μl of cDNA to PLG
 - 2. Add 162 μl of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge 2 minutes
 - 3. Transfer the supernatant to a fresh 1.5 ml tube, add
- 20 Glycogen (5 mg/ml)

2

0.5 M NH4OAC (0.75xVol)

120

ETOH (2.5xVol, -20 °C)

400

- 4. Mix well and centrifuge at 14,000X for 20 minutes
- 5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
- 25 6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
 - 7. Add 44 μl DEPC H₂O

Analyze of quantity and size distribution of cDNA Run a gel using 1 µl of the double-stranded synthesis product

30 Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

Purified cDNA

22 µl

10X Hy buffer

4 µl

10X biotin ribonucleotides

 $4 \mu l$

10X DTT 4 μl
10X Rnase inhibitor mix 4 μl
20X T7 RNA polymerase 2 μl
Total 40 μl

Centrifuge 5 seconds, and incubate for 4 hours at 37°C
Gently mix every 30-45 minutes

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

10 Determine concentration and dilute to 1 μg/μl concentration

Fragmentation of cRNA

cRNA (1 μg/μl) 15 μl 5X Fragmentation Buffer* 6 μl 15 DEPC H_2O 9 μl 30 μl

*5x Fragmentation Buffer

1M Tris (pH8.1) 4.0 ml

20 MgOAc

0.64 g

KOAC

0.98 g

DEPC H₂O

Total

20 ml

Filter Sterilize

25

Array wash and staining

Stringent Wash Buffer**

Non-Stringent Wash Buffer***

SAPE Stain****

30 Antibody Stain****

Wash on fluidics station using the appropriate antibody amplification protocol **Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H₂O 910 ml,

Filter Sterilize

10

15

20

25

30

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml, Filter Sterilize, Antifoam 1.0.

****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

*****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat

IgG 6 µl, Biotinylated Ab 3.6 µl

Example 2

Identification of Arabidopsis Genes Induced by Peronospora Infection

RPP7- and RPP8- dependent genes, four Arabidopsis lines were infected with one of two different P. parasitica isolates (see Table 2). One Arabidopsis line was Col-0::RPP8 which carries the cloned RPP8 genomic clone (RPP8 mediates resistance of the ecotype La-er against Emco5; McDowell et al. 1998) and is Emco5 resistant. Wild-type Col-0 plants are Emco5 susceptible. RPP7 mediates resistance of Arabidopsis against the Peronospora isolate Hiks1, and occurs naturally in Col-0. Another Arabidopsis line had a loss of function rpp7 mutant allele (Col-0 (rpp7)) (McDowell et al., 2000). Finally, three mutants in the signaling pathway for RPP7, i.e., they lack a RPP7-mediated response, were identified, i.e., edm1, edm2 and edm3, and a line with one of the mutant alleles, i.e., edm1, was used.

RNA samples were collected from two week old seedlings at three time points, 0, 12 and 24 hours post infection with 100,000 spores/ml. Twelve hours post-inoculation was determined to be an appropriate time point for analysis of both incompatible interactions, based on trypan blue staining of HR sites and PR-1 and sen1 induction. Forty-eight hours post-inoculation was determined to be a time point where both compatible interactions exhibit dense hyphal growth and both PR-1 and sen1 expression. Three independent sets of RNA were pooled.

Table 2

	<u>Plant</u>	Peronospora isolate	Time of RNA collection		
	Col-0 (RPP7, incomp.)	Hiksl	0, 12, 48 hours		
35	Col-0 (rpp7, comp.)	Hiks1	0, 12, 48 hours		

 Col-0 (edml, comp.)
 Hiks1
 0, 12, 48 hours

 Col-0 (tgRPP8, incomp.)
 Emco5
 0, 12, 48 hours

 Col-0 (rpp8, comp.)
 Emco5
 0, 12, 48 hours

PCT/US01/28506

- RNAs were labeled as described in Example 1 and hybridized to an Affymetrix Gene Chip having sequences corresponding to about 8,200 *Arabidopsis* genes. The data collected from these chips was employed to determine:
 - 1) the difference, if any, between RPP7 and RPP8 triggered signaling (and how these profiles compare to other profiles, for example, to the profiles of RPM1 and RPS2);
 - 2) which portion of the transcriptional response is R dependent;
 - 3) which genes are either commonly or uniquely induced during two different compatible interactions;
- 4) which genes are specifically activated during the incompatible interactions
 15 (gleaned by comparison with isogenic compatible controls) and, hence, may be important for the plant's defense against *Peronospora*;
 - 5) which genes whose expression is a prerequisite for induced defense reactions against *Peronospora*; and
 - 6) which genes are specifically repressed during the incompatible interactions, which may be required for successful Oomycete infections.

Results

WO 02/22675

10

20

25

30

Genes Expressed Early and Transiently After Infection

The normalized "average difference" (AD) from the chip experiments were processed as follows. All values together with the respective gene identifiers were loaded in EXCEL. Genes having, for a given treatment, AD values of 25 or less were considered as being not expressed. To reduce spurious background fluctuation, this cut off level was elevated to 75 for most of the analyses and normalized all AD values of 75 or less. For all five infection time courses, the AD values were divided by the corresponding 0 hour time point AD value. To visualize differences in gene expression ground states between the four experimental *Arabidopsis* lines, the following ratios were calculated for the 0 hour AD values: Col-0 (from Emco5 series)/Col-0-RPP8 and rpp7/Col-0 (from Hiks1 series) and edm1/Col-0 (from Hiks1 series). These ratios indicate whether

WO 02/22675 PCT/US01/28506

a given gene is up- or down-regulated by the RPP7 or RPP8 pathway, respectively. The resulting set of 18 expression ratio series was then loaded into CLUSTER (Eisen et al., 1998). The AD values were log transformed (base 2) and filtered to include only genes in the final data set that showed at least a 3-fold expression change (which equals a 1.6-fold change of the log transformed values). These criteria were fulfilled by 464 genes that define the final data set. With this data set Average linkage clustering was performed (uncentered correlation). The resulting clustergram was displayed using TREEVIEW (Eisen et al., 1998). A second clustergram was generated in the same way applying a cut off value of 50 on the normalized AD values. This clustergram includes 619 genes (probe sets).

Based on these clustergrams, gene clusters showing distinct expression behaviors were defined. Cluster cR7/R8 (see Table 3) contained genes that are early and transiently upregulated early and transiently after *P. parasitica* infection of *Arabidopsis* in an *RPP7/8* dependent manner. Upregulation by the *RPP8* pathway was generally stronger. Strong induced expression of cR7/R8 genes was detectable 12 hours after Emco5 infection in Col-0(tgRPP8) plants (incompatible interaction), whereas no elevated expression can be observed 48 hours post infection in the same plants (as compared to untreated control plants). Only weakly elevated or no elevated expression was detected at all tested time points in Col-0 plants (compatible interaction). After Hiks1 infection, elevated expression of these genes was only observed in Col-0 plants (incompatible interaction) after 12 hours. At no other time point following Hiks1 infection was substantially elevated expression of these genes observed. The expression ground state of these genes is similar in all four *Arabidopsis* lines.

Table 3

5

10

15

20

25

20245 s at cut off = 75 18716 At 18022 at 14609 at 17014 s at 17051 s at 19640 at 14248 at 13176 at

15978 at	cut off +50
17014 s at	
14609 at	
13764 at	
16649 s at	Subcluster A
13215 s at	
17653 at	
17008 at	
15042 at	
12778_r_at	
14614 at	
17051 sat	
14248 at	Subcluster B
20245 s at	
19640 at	
18716 at	
18022_at	•
17500 s at	
13217 s at	
18928 at	

The cR7/R8 cluster was originally defined using the clustergram based on a cut off value of 75 and comprised only 9 genes. Applying a cut off value of 50, the cluster became larger, comprising 21 genes, which could be divided into two subclusters (Table 4). Subcluster cR7/R8 A includes genes strongly and transiently upregulated by the RPP8 pathway, but either not, or only faintly, upregulated by the RPP7 pathway. Members of subcluster B showed pronounced upregulation by both RPP pathways after 12 hours and also elevated expression during compatible Emco5 infections in Col-0.

10

Table 4

Subcluster A	
Gene-identifier (probe set)	Related to
15978_at	X68592.6 at
17014_s_at*	atu05206 s at
14609_at	AC002340.147 at
16649_s_at+	athorf s at
	CafferoylCoAmethyltrans s a
13215_s_at ⁺	t
17653_at	AL035679.144 at
17008_at	AC006585.212 at

AL021961.3 at

	- 1202170115_40
12778_r_at	AC006577.16_r_at
Subcluster B	
Gene-identifier (probe set)	Related to
14614_at	AC004165.66 at
17051_s_at	af098947_s_at
14248_at	PAD3_at
20245_s_at	AC005309.97 s_at
19640_at	AC004561.78_at
18716_at	X91916_at
18022_at	AJ010971_at
17500_s_at [†]	athcallga s at
13217_s_at [†]	calmodulinlike s at
18928_at	AC002333.181_at

15042 at

5

10

15

20

Thus, the predominant feature of genes of the cR7/R8 cluster is more pronounced expression along with RPP7 and RPP8 mediated Peronospora resistance in comparison to the corresponding compatible interactions. Expression of these genes peaks in around 12 hours post infection and returns to ground state by 48 hours post infection. Hence, increased transcript levels of these genes coincide with the time window of decision between disease or resistance. Within 48 hours after infection with each tested Peronospora isolate, the plant either responds with HR and hinders development of oomycete hyphae or allows successful infection.

Identification of Conserved Sequence Motifs Within cR7/R8 Upstream Regions

To identify potential *cis*-elements involved in the specific regulation of cR7/R8 genes, stretches comprising 1.1 to 1.2 kb localized directly upstream of the translation start sites of coding regions from this cluster were collected from genomic *Arabidopsis* sequences (see Figure 2). Two motif search algorithms were used to recognize conserved motifs: AlignAce (Roth et al., 1998) and MEME (Bailey and Elkan, 1994). A search with AlignAce (default settings) revealed two conserved motifs within a set of 8 promoters comprising 7 from the originally defined cR7R8 using a cut off value of 75 and the promoter of a gene encoding a putative Myb-like transcription factor (Martin &Paz-Ares, 1997)

^{*}Genes printed in **bold** were identified using a cut off value of 75; all others were identified using a cut off value of 50.

The probe sets 16649 and 13215 as well as 17500 and 13217 correspond to the same genes.

WO 02/22675

(probe set 13176, SEQ ID NO:36), which shows a similar expression behavior as cR7/R8. The AlignAce output is shown below in Table 5:

Table 5

Motif 1	MAP Score:	SEQ ID NO.	Corresponding
** * * * * * *	6.87857		Probe Set
CAACAATTAT	0 36 1	685	17014
CAACTATGTC	0 981 1	686	17014
CAACAATGAC	1 934 0	687	20245
CAACAATGAC	2 271 1	688	14609
AAACAATGAT	2 1184 1	689	14609
CAACATTGAC	3 163 0	690	17051
CAACATTGTT	3 298 0	691	17051
CAACAATGTT	4 613 1	692	19640
CAACTATGAT	4 791 0	693	19640
CAACAATGAT	4 1064 0	694	19640
CAAAAATGAT	7 397 0	695	17008
CAACATTGAT	7 415 1	696	17008
CATATCA/TA/TTGAC (Consensus)		697	N.A.

5

Motif 2 **** * **	MAP Score: 2.22382	SEQ ID NO.	Corresponding Probe Set
TTTGGGCAAAA	1 260 0		
	1 368 0	698	20245
GTTGGGTCAAA	1 739 0	699	20245
GATGGGCACAA	2 691 0	700	14609
GATGGGCCAAA	3 700 0	701	17051
GATGGGTATAA	4 344 0	702	19640
GATGGGACTAA	5 98 1	703	14248
TTTGGGCCTAA	5 971 1	704	14248
TATGGGCCCAA	5 1012 0	705	14248
CTTGGGACAAA	7 579 1	706	17008
GATGGGTCAAC	7 1009 0	707	17008
CATGGGAATAA	7 1072 1	708	17008
NATTGGGNC/ANAA		709	N.A.
(Consensus)		,	1 111 11

For each motif, examples from cR7/R8 promoters are listed. Nucleotides evaluated by AlignAce as being conserved are indicated by a "*" above the examples. Besides motifs 1 and 2, a variety of additional ones were found by AlignAce, which, however, consisted almost exclusively of Ts and As. These motifs probably do not constitute functional cis-elements. Promoter sequences

5

10

15

20

25

30

are generally enriched in As or Ts (A/T content in cR7R8 promoters is 70%) and regulatory cis-elements usually contain also Cs or Gs.

Motif 1 (CAACA/TA/TTGA/TC/T, SEQ ID NO:710) resembles the type I Myb binding site consensus (MBS;T/CAACT/GG), which is bound by animal and some plant Myb transcription factors (Yang & Klessig, 1996). The 3' portion of the motif 1 consensus allows overlap with binding sites of WRKY (TTTGACC/T; Eulgem et al., 2000) or TGA-bZIP transcription factors (TGACG; Schindler et al. 1992). Interestingly, a gene encoding a putative Myblike transcription factor (gene identification number 13176) is upregulated along with cR7/R8 genes in an RPP7/RPP8-dependent, early and transient manner. The factor encoded by this gene may be a regulator of cR7/R8 genes. Motif 1 is particularly enriched in promoters of the originally defined cR7/R8 cluster (cut off = 75). This motif, which consists of six strictly defined positions and four positions allowing two base pairs each, should occur by random roughly once per 20,000 bp in each of both possible orientations (assuming a T/A content of 70% and a G/C content of 30%. In the 8,441 bp of cR7/R8 promoter sequences, the motif occurs 9 times (roughly 20 times the statistically expected frequency). Consistent with the statistical expectation, motif 1 occurs only two times within 15,873 bp from a set of control promoters of genes showing no defense related expression (data not shown).

In the extended set of cR7/R8 genes (cut off = 50), the enrichment of motif 1 is less striking. It occurs only 9 times within 16,519 bp in total and, more importantly, none of the promoters added to the set by lowering the cut off value contains this motif. Thus, if motif 1 is involved in the specific regulation of cR7/R8 genes it cannot alone be responsible for the particular expression features of these genes, and may rather be responsible for the more pronounced R7/R8-triggered expression of members of the originally defined cluster (cut off = 75).

Motif 2 (A/TTGGGNC/ANAA; SEQ ID NO:711) does not resemble any other known plant *cis*-element. The consensus sequence consists of six strictly defined positions, two positions with two alternatives and two positions with four alternatives; and, hence, should occur by random once per 10,000 bp. Motif 2 can be found 10 times within 8,441 bp of the promoters from the originally defined cR7/R8 (cut off = 75) and 14 times within 16,519 bp of the extended

cR7/R8 promoter set. Thus, its occurrence in cR7/R8 promoters is roughly 10 times the statistical expectation. Motif 2 is absent in the 15,873 bp of promoters of genes showing no defense related expression (data not shown). It is, however, also enriched in the promoters of previously defined clusters of defense related genes, such as the PR1 regulon (SAR genes) and SOMc3 (genes up regulated in Ws-0 after infection with avirulent Noco2; data not shown). The latter two clusters may also include genes sharing expression features with cR7/R8 genes. In addition to AlignAce, a motif 2-like sequence was also recognized by MEME. Within the extended set of cR7/R8 promoters, MEME found the following sequence stretch to be conserved:

sequence stretch to be conserved:

	bits	2.2									-
		2.0									
		1.7			•					٠	
15	• • .	1.5			•	*					•
	Information	1.3					•	*			
,	content	1.1					*	*			
	(13.4 bits)	0.9		***	**.	*	*		**		
		0.7		***	***	*	*		**	*	
20	•	0.4	**	***	***	*	*		**	*	*
	•	0.2	**	***	* ***	*	*	*	**	*	*
•		0.0					•				-

Multilevel Consensus sequence T/C TTT G/C A/T/G C/T

25 CCAAG/A/CAA/GAC/A (SEQ ID NO:712)

The reverse complement of this consensus sequence is (positions with three alternatives were given as "N") given below with motif 2 for comparison:

30 MEME motif: G/T T C/T T N T T G G G N G/C A A A A/C (SEQ ID

NO:713)

Motif 2: T G G G N A N/C A A (SEQ ID NO:714)

MEME was run using the default settings of "advanced MEME" choosing the options "one motif per sequence", "narrow motifs" and "additional strand: reverse complement".

To confirm these results, Northern blots using probes of representatives of each cluster are performed. In addition, T-DNA lines are screened for knock out in Myb-like gene (AL031394.56_at) and selected members of cR7/R8, such as RNS1 (atu05206_s_at) or the gene encoding a calmodulin-like protein (identification number 13217_s_at). Also, yeast one hybrid screens are performed to clone transcription factors binding to motifs 1 and 2, or other identified motifs. Transgenic *Arabidopsis* plants carrying fusions of GUS with a representative promoter from cR7/R8 can be used to further evaluate the functional significance of motifs 1 and 2, and to perform a genetic screening for mutants impaired in regulation of cR7/R8 genes.

15 Genes Induced by *Peronospora* Infection in a Manner that Requires *RPP7* or *RPP8*

The data sets described above were employed to identify genes that were induced by *Peronospora* infection and were RPP7/8-dependent. All expression values less than 5 were set to 5. Using ratios calculated in Excel, and database sorting using Access, a subset of genes was identified whose expression depends on RPP7 or RPP8 using the following criteria:

Col Hiks1 12 hour/Col untreated > 2.5 AND Col Hiks1 12 hour > 30 AND Col Hiks1 12 hour/Col rpp7 Hiks1 12 hour > 2 OR

Col Hiks1 48 hour/Col untreated > 2.5 AND Col Hiks1 48 hour > 30

AND Col Hiks1 48 hour/Col rpp7 Hiks1 48 hour > 2

OR

Col RPP8 Emco5 12 hour/Col RPP8 no treatment > 2.5 AND Col RPP8 Emco5 12 hour > 30 AND Col RPP8 Emco5 12 hour/Col (rpp8) Emco5

30 12 hour > 2

5

10

20

OR

Col RPP8 Emco5 48 hour/Col RPP8 no treatment AND Col RPP8
Emco5 48 hour > 30 AND Col RPP8 Emco5 48 hour/Col (rpp8) Emco5
48 hour > 2

This yielded 217 probe sets ("RPP7 or 8") which correspond to sequences, the expression of which were increased by at least 2.5 fold and were RPP7- or RPP8-dependent (Table 6).

5

Table 6

	ProbeSet	Description
	12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
	12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
	12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
	12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
	12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana] gb AAD12037.1 (AC002392) putative
	12307_at (AC002392.162_AT)	receptor-like protein kinase [Arabidopsis thaliana]
	12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana] emb CAA16619.1 (AL021637) vacuolar
	12341_s_at (AL021637.176_S_AT)	sorting receptor-like protein [Arabidopsis thaliana]
-	12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum] emb CAA18468.1 (AL022347)
	12360_at (AL022347.131_AT)	serine/threonine kinase-like protein [Arabidopsis thaliana] gb AAC32192.1 (AF081067) IAA-Ala
	12500_s_at (AF081067.3_S_AT)	hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
,	12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
	12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana] emb CAB45330.1 (AL079344) nucleotide
	12556_at (AL079344.155_AT)	pyrophosphatase-like protein [Arabidopsis thaliana]
.]	125/4_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
]	1263U_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
]	12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]

	gb AAD25772.1 AC006577_8 (AC006577)
	Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453,
	gb T04815, gb T45993, gb R30138,
	gb AI099570 and gb T22281 come from this
12777_i_at (AC006577.16_I_AT)	gene. [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577)
•	Belongs to the PF 00657 Lipase/Acylhydrolase
•	with GDSL-motif family. ESTs gb T44453,
	gb T04815, gb T45993, gb R30138, gb A1099570 and gb T22281 come from this
12778_r_at (AC006577.16_R_AT)	gene. [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577)
	Belongs to the PF 00657 Lipase/Acylhydrolase
	with GDSL-motif family. ESTs gb/T44453
	gb T04815, gb T45993, gb R30138,
12779_f_at (AC006577.16_F_AT)	gb AI099570 and gb T22281 come from this
12/15_1_at (AC0003/7.10_F_A1)	gene. [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
12072_0_dt (71101_b_A1)	
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate
======================================	synthase alpha subunit [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
-	gb AAC63850.1 (U73786) ACC synthase
12892_g_at (ATACS6_G_AT)	[Arabidopsis thaliana]
	dbj BAA32419.1 (AB008104) ethylene
10005	responsive element binding factor 2
12905_s_at (ATERF2_S_AT)	[Arabidopsis thaliana]
	dbj BAA32422.1 (AB008107) ethylene
12908_s_at (ATERF5_S_AT)	responsive element binding factor 5 [Arabidopsis thaliana]
	-
12016 p of (ATUCOD) G AT	gb AAC13947.1 (AF021244) coronatine-
12916_s_at (ATHCOR1_S_AT)	induced protein 1 [Arabidopsis thaliana]
12033 + at (ATDD 1TAN D AT)	emb CAA65420.1 (X96600) pathogenesis-
12933_r_at (ATPR1TAN_R_AT)	related protein 1 [Arabidopsis thaliana]
12080 s at (AC004077 140 S AT)	gb AAC26690.1 (AC004077) putative
12909_8_at (AC004077.149_8_A1)	cytochrome P450 [Arabidopsis thaliana]
	gb AAC24083.1 (AC003114) Match to
	calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719,
	gb T22451, gb H36323 and gb AA042519
13067_s_at (AC003114.16_S_AT)	come from this gene. [Arabidopsis thaliana]
	gb AAC06158.1 (AC003680) putative
13100_at (AC003680.50_AT)	cytochrome P450 [Arabidopsis thaliana]
	gb AAB60774.1 (AC000375) ESTs
13115 at (AC000275 44 AT)	gb U75592,gb T13956,gb T43869 come from
13115_at (AC000375.44_AT)	from this gene. [Arabidopsis thaliana]

	gb AAB64047.1 (AC002333) putative
13154_s_at (AC002333.210_S_AT)	endochitinase [Arabidopsis thaliana] emb CAA20567.1 (AL031394) putative
13176_at (AL031394.56_AT)	protein [Arabidopsis thaliana] gb AAC49356.1 (U35829) thioredoxin h
13187_i_at (ATTHIRED4_I_AT)	[Arabidopsis thaliana] gb AAC49356.1 (U35829) thioredoxin h
13188_r_at (ATTHIRED4_R_AT)	[Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563)
13215_s_at (CAFFEROYLCOAMETHYLTRA NS_S_AT)	putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAD22369.1 AC006580_1 (AC006580)
13381_at (AC006580.8_AT)	NAM (no apical meristem)-like protein [Arabidopsis thaliana] gb[AAC49775.1] (AF003102) AP2 domain
13435_at (AF003102.3_AT)	containing protein RAP2.9 [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana] emb CAA23036.1 (AL035394) putative
13627_at (AL035394.196_AT)	Na+/H+-exchanging protein [Arabidopsis thaliana] gb AAB82634.1 (AC002387) putative
13631_at (AC002387.185_AT)	transketolase precursor [Arabidopsis thaliana] emb CAA18462.1 (AL022347)
13659_at (AL022347.46_AT)	serine/threonine kinase-like protein [Arabidopsis thaliana] gb AAD25552.1 AC005850_9 (AC005850)
13685_s_at (MLOLIKE2_S_AT)	Highly Similiar to Mlo proteins [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13697_at (NI16_AT)	No hits found.

13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana] gb AAD15433.1 (AC006218) putative
13818_s_at (AC006218.175_S_AT)	aspartate aminotransferase [Arabidopsis thaliana] emb CAB39611.1 (AL049480) possible
13880_s_at (AL049480.183_S_AT)	apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana] gb AAC78535.1 (AC005662) putative
14083_at (AC005662.56_AT)	embryo-abundant protein [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found.
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana] emb CAB36854.1 (AL035528) putative
14111_s_at (AL035528.279_S_AT)	disease resistance protein [Arabidopsis thaliana] gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam:
14116_at (AF077407.30_AT)	sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15. dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein
14145_at (NOVARTIS35_AT)	[Nicotiana tabacum]
14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14201_at (NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15.
14223_at (NOVARTIS9_AT)	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana] gb AAF16756.1 AC010155_9 (AC010155)
14232_at (NOVARTIS95_AT)	F3M18.20 [Arabidopsis thaliana]

14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana] gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	thaliana] gb AAC05341.1 (AC002521) unknown
14381_at (AC002521.68_AT)	protein [Arabidopsis thaliana] gb AAB61498.1 (AC000348) T7N9.22
14443_at (AC000348.23_AT)	[Arabidopsis thaliana] gb AAC02748.1 (AC002340) putative
14609_at (AC002340.147_AT)	cytochrome P450 [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana] gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase
14620_s_at (PAT1_S_AT)	[Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana] gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis
14635_s_at (PR.1_S_AT)	thaliana] emb CAA50677.1 (X71794) peroxidase
14638_s_at (PRXCB_S_AT)	[Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	thaliana]
14682_i_at (WT1012A_RC_I_AT)	No hits found.
14691_at (WT1096_AT)	No hits found.

14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15. emb CAA60521.1 (X86958) protein kinase
14763_at (X86958.1_AT)	catalytic domain (fragment) [Arabidopsis thaliana] gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase
14838_s_at (M96073.6_S_AT)	[Arabidopsis thaliana]
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana] emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein
15042_at (AL021961.3_AT)	[Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana] gb AAB53975.1 (U90522) lysine-ketoglutarate
15161_s_at (ATU90522_S_AT)	reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	dbj BAA24440.1 (AB010407)
15629_s_at (AB003280_S_AT)	phosphoglycerate dehydrogenase [Arabidopsis thaliana] gb AAD10829.1 (AF117063) putative inositol
15641_s_at (AF117063_S_AT)	polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] gb AAB80922.1 (AF022658) putative c2h2
15665_s_at (AF022658_S_AT)	zinc finger transcription factor [Arabidopsis thaliana] emb CAA67234.1 (X98676) zinc finger
15778_at (X98676.2_AT)	protein [Arabidopsis thaliana] emb CAA67234.1 (X98676) zinc finger
15779_g_at (X98676.2_G_AT)	protein [Arabidopsis thaliana] gb AAD15461.1 (AC006067) unknown
15846_at (AC006067.63_AT)	protein [Arabidopsis thaliana]

	15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
	15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
	15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
	15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] emb CAA74639.1 (Y14251) glutathione S-
	16053_i_at (Y14251.4_I_AT)	transferase [Arabidopsis thaliana]
	16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog
	16083_s_at (AF153283_S_AT)	[Arabidopsis thaliana]
	16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
	16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
	16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
	16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana] gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis
	16257_at (AC004138.105_AT)	thaliana]
	16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
	16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana] gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis
	16357_at (AF149413.38_AT)	thaliana] emb CAA20203.1 (AL031187) receptor-like
	16360_at (AL031187.126_AT)	serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
	16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
,	16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana] dbj BAA32422.1 (AB008107) ethylene
	16536_s_at (AB008107_S_AT)	responsive element binding factor 5 [Arabidopsis thaliana]

	·
16578_s_at (ATHRPRP1B_S_AT) 16609_s_at (AB008104_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana] dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcaffeoyl-Coenzyme A 3-O-methyltransferase
16649_s_at (ATHORF_S_AT)	[Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana] gb AAD23027.1 AC006585_22 (AC006585)
17008_at (AC006585.212_AT)	putative tyrosine aminotransferase [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana] gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase
17083_s_at (ATU18770_S_AT)	[Arabidopsis thaliana] gb AAC49697.1 (U66345) calreticulin
17097_s_at (ATU66345_S_AT)	[Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana] gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this
17464_at (AC000132.72_AT)	gene. [Arabidopsis thaliana] emb CAB10405.1 (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis
17485_s_at (Z97340.345_S_AT)	thaliana]

	17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
	17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
	17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-
	17511_s_at (AF067605_S_AT)	linalool synthase gp U58314 1491939 [Arabidopsis thaliana] dbj BAA28538.1 (D78606) cytochrome P450
	17522_s_at (D78606_S_AT)	monooxygenase [Arabidopsis thaliana] gb AAC49282.1 (U40856) AIG1 [Arabidopsis
	17544_s_at (ATU40856_S_AT)	thaliana] emb CAB38823.1 (AL035679) putative
	17653_at (AL035679.144_AT)	protein [Arabidopsis thaliana]
	17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana] gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator
	17775_at (AC004392.2_AT)	(GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana] gb AAB64049.1 (AC002333) putative
	17840_s_at (AC002333.223_S_AT)	endochitinase [Arabidopsis thaliana]
	17843_s_at (AC002391.150_S_AT)	gb[AAB87109.1] (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
-	17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana] emb CAA07352.1 (AJ006960) peroxidase
	17930_s_at (AJ006960.4_S_AT)	[Arabidopsis thaliana] emb[CAB59428.1] (AJ002295) inositol-1,4,5-
	18012_s_at (AJ002295_S_AT)	trisphosphate 5-Phosphatase [Arabidopsis thaliana] emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis
	18022_at (AJ010971_AT)	thaliana]
	18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana] gb AAF24959.1 AC012375_22 (AC012375)
	18216_at (X95573.2_AT)	T22C5.18 [Arabidopsis thaliana]
,	18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana] emb CAA17150.1 (AL021890) putative
	18224_s_at (AL021890.57_S_AT)	protein [Arabidopsis thaliana] gb AAB87112.1 (AC002391) putative
	18551_at (AC002391.163_AT)	cytochrome P450 [Arabidopsis thaliana]
	18567_at (AC004411.25_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

	•
18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and
18625_at (AC005278.22_AT)	gb[T20569 come from this gene. [Arabidopsis thaliana]
18716_at (X91916_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana] gb AAC33239.1 (AC005315) putative ligand- gated ion channel protein [Arabidopsis
18844_at (AC005315.131_AT)	thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana] gb AAD45127.1 AF163823 1 (AF163823)
18968_at (AF163823.4_AT)	endoxyloglucan transferase [Arabidopsis thaliana] gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis
18969_g_at (AF163823.4_G_AT)	thaliana] emb CAB41722.1 (AL049730) pEARLI 1-like
18983_s_at (AL049730.104_S_AT)	protein [Arabidopsis thaliana]
19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana] gb AAB64325.1 (AC002335) putative trypsin
19171_at (AC002335.160_AT)	inhibitor [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA68191.1 (X99923) male sterility 2- like protein [Arabidopsis thaliana] emb CAA21214.1 (AL031804) putative
19182_at (AL031804.245_AT)	protein [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]

19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like
19664_at (AL050351.172_AT)	protein [Arabidopsis thaliana] gb AAC36019.1 (AC005687) RAP2.6
19672_at (AC005687.19_AT)	[Arabidopsis thaliana] emb CAB36812.1 (AL035527) peptide
19762_at (AL035527.204_AT)	transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana] emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit
19894_at (AJ001809.1_AT)	[Arabidopsis thaliana] gb AAC79593.1 (AC005727) unknown
19914_at (AC005727.175_AT)	protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana] gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20,
19982_at (AC002986.28_AT)	gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana] gb AAD21459.1 (AC007017) similar to
19991_at (AC007017.124_AT)	harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana] emb CAA18469.1 (AL022347) serine/threonine kinase-like protein
20223_at (AL022347.145_AT)	[Arabidopsis thaliana] emb CAA18460.1 (AL022347) protein kinase-
20232_s_at (AL022347.12_S_AT)	like protein [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta- fructofuranosidase [Arabidopsis thaliana] emb CAA52619.1 (X74514) beta-
20239_g_at (X74514.2_G_AT)	fructofuranosidase [Arabidopsis thaliana] emb CAA05625.1 (AJ002584) AtMRP4
20245_s_at (AC005309.97_S_AT	
20246_s_at (AF084037.3_S_AT)	protein kinase [Arabidopsis thaliana] gb AAB82640.1 (AC002387) putative
20269_at (AC002387.237_AT)	pectinesterase [Arabidopsis thaliana] emb CAA74930.1 (Y14590) class IV chitinase
20287_at (Y14590.5_AT)	[Arabidopsis thaliana] emb CAA74930.1 (Y14590) class IV chitinase
20288_g_at (Y14590.5_G_AT)	[Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate

synthase alpha subunit [Arabidopsis thaliana] gb|AAD23617.1|AC007168 8 (AC007168) putative aspartate aminotransferase 20331_at (AC007168.86 AT) [Arabidopsis thaliana] gb|AAD25552.1|AC005850 9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis 20365_s_at (AC005850.19 S AT) thaliana] gb|AAC36163.1| (AC005314) putative serpin 20368 at (AC005314.38 AT) [Arabidopsis thaliana] emb|CAA19698.1| (AL024486) putative 20420 at (AL024486.131 AT) chitinase [Arabidopsis thaliana] emb|CAB10219.1| (Z97336) hypothetical 20429 s at (Z97336.167 S AT) protei [Arabidopsis thaliana] gb|AAC98070.1| (AC005896) putative C2H2-20620 g_at (AC005896.161_G AT) type zinc finger protein [Arabidopsis thaliana] emb|CAB41131.1| (AL049658) hypothetical 20625_at (AL049658.102_AT) protein [Arabidopsis thaliana]

The functions of RPP7 and RPP8 are independent of PAD4, NDR1. NahG, COII, and EDSI. Consequently, it is unlikely that genes whose expression is reduced in pad4 or NahG backgrounds are important for RPP7- or 5 RPP8- mediated resistance. Although data from Peronospora infection of pad4 or nahG plants was not available, data from Pseudomonas syringae (ES4326) infection of pad4 and NahG plants was available and employed to determine which genes depended on PAD4 or were interfered with by NahG. Resistance to P. syringae mediated by RPS2 requires NDR1 function. Genes whose expression 10 requires RPS2 are less likely to be important for RPP7 or RPP8 mediated resistance than genes whose expression is independent of RPS2. Gene expression data was available for wild-type plants infected with Pseudomonas syringae pv. tomato DC3000 avrRpt2, and rps2 mutant plants infected with Pseudomonas syringae pv. tomato DC3000 avrRpt2, 6 hours after infection. 15 EDM1 is required for resistance mediated by RPP7. Thus, genes whose expression requires EDM1 are likely to be important for RPP7-mediated resistance. Gene expression data was available for an edml mutant (see above).

The data from the 7 additional data sets (Col Psm ES4326 30 hour; Col Mock 30 hour; Col NahG Psm ES4226 30 hour; Col pad4 Psm ES4326 30 hour; Col water control; Col DC3000 avrRpt2 and rps2 DC3000 avrPrt2 was added to the 217 probe sets in "RPP7 or 8". The following sets were identified: edm1:

Col edm1 Hiks1 12 hour/Col Hiks1 12 hour < 0.5 OR Col edm1 Hiks1 48 hour/Col Hiks1 48 hour < 0.5.

rps2:

5

Col DC3000 avrRpt2 6 hour/Col water control > 2 AND rps2 DC3000 avrRpt2 6 hour/Col DC3000 avrRpt2 6 hour < 0.5.

pad4 or NahG:

Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col pad4 Psm

10 ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

OR

Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col NahG Psm ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

There are 8 possible combinations of these three sets. Access was used to divide the 217 probe sets into 8 sets, numbered 2-9 (considering the whole set of 217 probe sets as set 1) as shown in Tables 7 and 8:

Table 7

20	<u>Set</u>	Content	Number of probe
	sets		
	2	RPP7 or 8 not edm1 not rps2 not pad4 o rNahG	62 probe sets
·	3	edm1 not rps2 not pad4 or NahG	50 probe sets
-	4	rps2 not edm1 not pad4 or NahG	14 probe sets
25	5	pad4 or NahG not edm1 not rps2	21 probe sets
	6	edm1 and rps2 not pad4 or NahG	23 probe sets
	7	edm1 and pad4 or NahG not rps2	25 probe sets
	8	rps2 and pad4 or NahG not edm1	8 probe sets
	9	edm1 and rps2 and pad4 or NahG	14 probe sets
30	Tota	al .	217 probe sets

Table 8

2 RPP7 or 8 not edm1 not rps2 not pad4orNahG

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana] emb CAB43974.1 (AL078579) putative
12240_at (AL078579.130_AT)	protein [Arabidopsis thaliana] gb AAA17993.1 (M91192) phenylalanine
12349_s_at (X84728.6_S_AT)	ammonia-lyase [Trifolium subterraneum]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana] emb CAB45330.1 (AL079344) nucleotide
12556_at (AL079344.155_AT)	pyrophosphatase-like protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
12777_i_at (AC006577.16_I_AT)	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidops thaliana] gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657
	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815,
10770 6	gb T45993, gb R30138, gb AI099570 and
12779_f_at (AC006577.16_F_AT)	gb[T22281 come from this gene. [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana] dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5
12908_s_at (ATERF5_S_AT)	[Arabidopsis thaliana]
12933_r_at (ATPRITAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis- related protein 1 [Arabidopsis thaliana] emb CAA20567.1 (AL031394) putative
13176_at (AL031394.56_AT)	protein [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15. emb CAB39611.1 (AL049480) possible
13880_s_at	apospory-associated like protein [Arabidopsis
(AL049480.183_S_AT)	thaliana]
13966_at (AL022023:172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana] emb CAB36854.1 (AL035528) putative
14111_s_at (AL035528.279_S_AT)	disease resistance protein [Arabidopsis thaliana]

14145_at (NOVARTIS35 AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein
14143_at (140 VAR11333_A1)	[Nicotiana tabacum]
14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana] gb AAD23719.1 AC005956_8 (AC005956)
14320_at (AC005956.54_AT)	putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana] gb AAA32835.1 (M96073)
14620_s_at (PAT1_S_AT)	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana] emb CAA17549.1 (AL021961) cinnamyl
15042_at (AL021961.3_AT)	alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana] gb AAD34615.1 AF153283_1 (AF153283)
16083_s_at (AF153283_S_AT)	putative progesterone-binding protein homolog [Arabidopsis thaliana] gb AAC32915.1 (AC004138) putative
16257_at (AC004138.105_AT)	nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana] emb CAA19705.1 (AL024486) putative
16299_at (AL024486.185_AT)	protein [Arabidopsis thaliana] emb CAA54631.1 (X77500) amino acid
16522_at (X77500.2_AT)	transporter [Arabidopsis thaliana] dbj BAA32422.1 (AB008107) ethylene
16536_s_at (AB008107_S_AT)	responsive element binding factor 5 [Arabidopsis thaliana] gb AAD09952.1 (AF098947) CTF2B
17051_s_at (AF098947_S_AT)	[Arabidopsis thaliana]

VO 02/22675

PCT/US01/28506

*	•
17083_s_at (ATU18770_S_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this
17464_at (AC000132.72_AT)	gene. [Arabidopsis thaliana]
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana] emb CAA52772.1 (X74756) ATAF2
18591_at (X74756.2_AT)	[Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs
18625_at (AC005278.22_AT)	gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana] gb AAC33239.1 (AC005315) putative ligand-
18844_at (AC005315.131_AT)	gated ion channel protein [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana] gb AAC62611.1 (AF055848) subtilisin-like
18909_s_at (AF055848.2_S_AT)	protease [Arabidopsis thaliana] gb AAC16927.1 (AC002338) putative laccase
18920_at (AC002338.11_AT)	[Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAB41722.1 (AL049730) pEARLI 1- like protein [Arabidopsis thaliana] emb CAA65053.1 (X95738) proline
19158_at (X95738.2_AT)	transporter 2 [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana] emb CAB43638.1 (AL050351) NAD(P)H
.19664_at (AL050351.172_AT)	oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana] emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit
19894_at (AJ001809.1_AT)	[Arabidopsis thaliana]

gb|AAC17040.1| (AC002986) Similarity to A. thaliana gene product F21M12.20, gb|AC000132. EST gb|Z25651 comes from 19982 at (AC002986.28 AT) this gene. [Arabidopsis thaliana] gb|AAD32864.1|AC005489 2 (AC005489) 20189_at (AC005489.2 AT) F14N23.2 [Arabidopsis thaliana] emb|CAA52619.1| (X74514) beta-20238_at (X74514.2 AT) fructofuranosidase [Arabidopsis thaliana] emb|CAA52619.1| (X74514) beta-20239 g at (X74514.2 G AT) fructofuranosidase [Arabidopsis thaliana] gb|AAC95354.1| (AF084037) receptor-like 20246_s_at (AF084037.3_S_AT) protein kinase [Arabidopsis thaliana] gb|AAA32738.1| (M92353) anthranilate 20291_s_at (M92353.4 S AT) synthase alpha subunit [Arabidopsis thaliana] gb|AAD23617.1|AC007168_8 (AC007168) putative aspartate aminotransferase 20331_at (AC007168.86_AT) [Arabidopsis thaliana] gb|AAC36163.1| (AC005314) putative serpin 20368_at (AC005314.38 AT) [Arabidopsis thaliana] 20620 g at gb|AAC98070.1| (AC005896) putative C2H2type zinc finger protein [Arabidopsis thaliana] (AC005896.161 G AT) **Duplicates** 12777 and 12779 (lipase) 12889 and 20291 (ASA1) 12908 and 16536 (ERF5) 17464 and 19982 (RLK5) 18216 and 18217 (T22C5.18) 18908 and 18909 (subtilisin-like protease) 20238 and 20239 (betafructofuranosidase)

3 edm1 without rps2 without pad4orNahG

ProbeSet

Description

12091_at (AC004450.116 AT)

gb|AAC64313.1| (AC004450) unknown protein [Arabidopsis thaliana]

emb|CAA22152.1| (AL033545) extensin-like

12115 at (AL033545.26 AT)

protein [Arabidopsis thaliana]

	gb AAC32192.1 (AF081067) IAA-Ala
12500 a at (A E001067 2 G A T	hydrolase; IAA-amino acid hydrolase
12500_s_at (AF081067.3_S_AT	
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577)
	Belongs to the PF 00657
	Lipase/Acylhydrolase with GDSL-motif
	family. ESTs gb T44453, gb T04815,
10770	gb T45993, gb R30138, gb AI099570 and
12778_r_at	gb T22281 come from this gene. [Arabidopsis
(AC006577.16_R_AT)	thaliana]
10001 -	gb AAC63850.1 (U73786) ACC synthase
12891_at (ATACS6_AT)	[Arabidopsis thaliana]
12002 (ATA CO.C. C. AT)	gb AAC63850.1 (U73786) ACC synthase
12892_g_at (ATACS6_G_AT)	[Arabidopsis thaliana]
	dbj BAA32419.1 (AB008104) ethylene
12905_s_at (ATERF2_S_AT)	responsive element binding factor 2
12703_3_at (ATERT2_3_AT)	[Arabidopsis thaliana]
12916_s_at (ATHCOR1 S AT)	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
13188 r at	gb AAC49356.1 (U35829) thioredoxin h
(ATTHIRED4_R AT)	[Arabidopsis thaliana]
(emb CAA16892.1 (AL021749) 12S cruciferin
13198_i_at (ATTS0190 I AT)	seed storage protein [Arabidopsis thaliana]
(***********************************	gb AAC49775.1 (AF003102) AP2 domain
	containing protein RAP2.9 [Arabidopsis
13435_at (AF003102.3 AT)	thaliana]
	gb AAB82634.1 (AC002387) putative
13631_at (AC002387.185_AT)	transketolase precursor [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found.
14000 4 0707747	emb CAA19683.1 (AL024486) putative
14223_at (NOVARTIS9_AT)	protein [Arabidopsis thaliana]
14020 -4 OJOVA DETGOS AED	gb AAF16756.1 AC010155_9 (AC010155)
14232_at (NOVARTIS95_AT)	F3M18.20 [Arabidopsis thaliana]
14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine
MKNA_S_AI)	ammonia lyase (PAL1) [Arabidopsis
14614_at (AC004165.66 AT)	gb AAC16958.1 (AC004165) putative
14691_at (WT1096_AT)	glucosyltransferase [Arabidopsis thaliana] No hits found.
14021_ur(M11030_W1)	
	gb AAA32835.1 (M96073)
14838_s_at (M96073.6_S_AT)	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
- 110 at (1120073.0_b_A1)	gb AAB53975.1 (U90522) lysine-
•	ketoglutarate reductase/saccharopine
15161_s_at (ATU90522_S_AT)	dehydrogenase [Arabidopsis thaliana]
	and an about the fund of the same of the s

15532_r at	emb CAB45069.1 (AL078637) putative
(AL078637.191_R_AT)	protein [Arabidopsis thaliana]
(dbj BAA24440.1 (AB010407)
	phosphoglycerate dehydrogenase [Arabidopsis
15629_s_at (AB003280 S AT)	
13025_3_at (AB003280_B_A1)	thaliana]
	gb AAB80922.1 (AF022658) putative c2h2
15665 A (A E000650 G A FR)	zinc finger transcription factor [Arabidopsis
15665_s_at (AF022658_S_AT)	thaliana]
16232_s_at	emb CAB45796.1 (AL080252) putative
(AL080252.77_S_AT)	protein [Arabidopsis thaliana]
	dbj BAA32419.1 (AB008104) ethylene
	responsive element binding factor 2
16609_s_at (AB008104_S_AT)	[Arabidopsis thaliana]
16817_s_at	emb CAB51412.1 (AL096882) ACC synthase
(AL096882.91_S_AT)	(AtACS-6) [Arabidopsis thaliana]
 ' .	gb AAC49356.1 (U35829) thioredoxin h
16981_s_at (U35829.2 S AT)	[Arabidopsis thaliana]
	gb AAD23027.1 AC006585_22 (AC006585)
	putative tyrosine aminotransferase
17008_at (AC006585.212 AT)	[Arabidopsis thaliana]
	gb AAC48925.1 (U05206) ribonuclease
17014 s at (ATU05206 S AT)	[Arabidopsis thaliana]
17500 s at	emb CAB42906.1 (AL049862) calmodulin-
(ATHCALLGA_S_AT)	
(MINOREEGN_B_A1)	like protein [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450
17322_5_at (D78000_5_A1)	monooxygenase [Arabidopsis thaliana]
17652 A (AT 025670 144 AT)	emb CAB38823.1 (AL035679) putative
17653_at (AL035679.144_AT)	protein [Arabidopsis thaliana]
17744_s_at	gb AAC23646.1 (AC004684) putative
(AC004684.168_S_AT)	alcohol dehydrogenase [Arabidopsis thaliana]
17843_s_at	gb AAB87109.1 (AC002391) putative
(AC002391.150_S_AT)	cytochrome P450 [Arabidopsis thaliana]
•	emb CAB52675.1 (AJ010971) glucose-6-
	phosphate 1-dehydrogenase [Arabidopsis
18022_at (AJ010971_AT)	thaliana]
	gb AAB87112.1 (AC002391) putative
18551_at (AC002391.163_AT)	cytochrome P450 [Arabidopsis thaliana]
	gb AAF26754.1 AC007396_3 (AC007396)
18716_at (X91916_AT)	T4O12.6 [Arabidopsis thaliana]
	emb CAA72484.1 (Y11788) peroxidase
18946_at (Y11788.1_AT)	ATP24a [Arabidopsis thaliana]
_ , _ ,	gb AAB64325.1 (AC002335) putative trypsin
19171_at (AC002335.160 AT)	inhibitor [Arabidopsis thaliana]
	emb CAA68191.1 (X99923) male sterility 2-
19177_at (X99923.1_AT)	like protein [Arabidopsis thaliana]
	emb CAA21214.1 (AL031804) putative
19182_at (AL031804.245 AT)	
17102_m (AD031004.243_A1)	protein [Arabidopsis thaliana]
19284_at (AC003028.196 AT)	gb AAC27173.1 (AC003028) putative
17207_at (AC003020.190_A1)	anthocyanidin synthase [Arabidopsis thaliana]

gene.

gb|AAC36019.1| (AC005687) RAP2.6

emb|CAB36812.1| (AL035527) peptide

gb|AAC79626.1| (AC005770) putative

protease inhibitor [Arabidopsis thaliana]

emb|CAA18460.1| (AL022347) protein

emb|CAA63012.1| (X91919) LEA76 homologue typel [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gb|N97082, gb|Z27056 and gb|Z29902 come from this

kinase-like protein [Arabidopsis thaliana] emb|CAB10219.1| (Z97336) hypothetical

transporter-like protein [Arabidopsis thaliana]

[Arabidopsis thaliana]

19672_at (AC005687.19 AT)

19762_at (AL035527.204_AT)

19892 at (AC005770.30 AT) 20232 s at

(AL022347.12 S AT)

20429_s_at (Z97336.167 S AT) protei [Arabidopsis thaliana]

20641 at (X91919.1 AT)

Duplicates -12905 and 16609 (ERF2)

13188 and 16981 (thioredoxin h) 12891 and 12892 (ACC synthase) 14838 (phosphoribosyl anthranilate transferase) has a duplicate in set 2 (14620). Counted in set 2

14254 (PAL1) has a duplicate in set 2 (14256) Counted in set 2. 12778 (lipase) has duplicates in set 2 (12777 and 12779) Counted in set 2.

4 rps2 without edm1 without pad4orNahG

ProbeSet Description

emb|CAA09731.1| (AJ011674) receptor-like 12278 at (AJ011674.2 AT) protein kinase, RLK3 [Arabidopsis thaliana]

> emb|CAA18468.1| (AL022347) serine/threonine kinase-like protein

12360 at (AL022347.131 AT) [Arabidopsis thaliana]

13154 s at

gb|AAB64047.1| (AC002333) putative (AC002333.210 S AT) endochitinase [Arabidopsis thaliana] gb|AAC31756.1| (U68017) heat shock

13273_s_at (HSF4_S_AT) transcription factor 4 [Arabidopsis thaliana] gb|AAD25552.1\AC005850 9 (AC005850)

Highly Simlilar to Mlo proteins [Arabidopsis

13685 s at (MLOLIKE2_S_AT) thaliana]

14141_at (NOVARTIS31_AT) No hits found less than or equal to 1e-15.

110

emb|CAA19722.1| (AL030978) putative 15431_at (AL030978.64 AT) protein [Arabidopsis thaliana] emb|CAA74639.1| (Y14251) glutathione S-16053 i at (Y14251.4 I AT) transferase [Arabidopsis thaliana] gb[AAB87114.1] (AC002391) unknown 16995 at (AC002391.188 AT) protein [Arabidopsis thaliana] emb|CAB54517.1| (AJ238846) SGP1 18054 at (AJ238846 AT) monomeric G-protein [Arabidopsis thaliana] emb|CAA17150.1| (AL021890) putative protein [Arabidopsis thaliana] gb|AAC42241.1| (AC005395) unknown protein [Arabidopsis thaliana] emb|CAA18469.1| (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] gb|AAD25552.1|AC005850 9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana

18224 s at (AL021890.57 S AT)

19951_at (AC005395.47 AT)

20223_at (AL022347.145 AT)

20365 s at (AC005850.19 S AT)

Duplicates

12360 and 20223 (serine threonine kinase) 13685 and 20365 (similar to Mlo)

5 pad4orNahG without rps2 without edm1

ProbeSet

12307 at (AC002392.162 AT) 12332 s at (AB023448.2_S_AT)

13067 s at (AC003114.16 S AT)

13381_at (AC006580.8 AT)

13588 at (AL021961.24 AT)

13751_at (NOVARTIS127_AT) F3M18.8 [Arabidopsis thaliana]

13764 at (NOVARTIS22 AT)

Description

gb|AAD12037.1| (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana] dbj|BAA82810.1| (AB023448) basic endochitinase [Arabidopsis thaliana] gb|AAC24083.1| (AC003114) Match to calreticulin (AtCRTL) mRNA gblU27698 and DNA gb|U66344. ESTs gb|T45719, gb|T22451, gb|H36323 and gb|AA042519 come from this gene. [Arabidopsis thaliana] gb[AAD22369.1|AC006580 1 (AC006580) NAM (no apical meristem)-like protein

[Arabidopsis thaliana] emb|CAA17552.1| (AL021961)

Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

gb|AAF16751.1|AC010155 4 (AC010155)

gb|AAD39641.1|AC007591 6 (AC007591)

F9L1.6 [Arabidopsis thaliana]

gb|AAD25550.1|AC005850 7 (AC005850) 14146 at (NOVARTIS36 AT) Hypothetical protein [Arabidopsis thaliana] emb|CAA67234.1| (X98676) zinc finger 15778_at (X98676.2 AT) protein [Arabidopsis thaliana] emb|CAA67234.1| (X98676) zinc finger 15779 g at (X98676.2 G AT) protein [Arabidopsis thaliana] gb|AAD21491.1| (AC006587) unknown 15859_at (AC006587.164 AT) protein [Arabidopsis thaliana] emb|CAA20203.1| (AL031187) receptor-like serine/threonine protein kinase ARK3 16360_at (AL031187.126_AT) [Arabidopsis thaliana] 16578 s at emb|CAB68132.1| (AL137080) beta-1, 3-(ATHRPRP1B S AT) glucanase 2 (BG2) [Arabidopsis thaliana] 16914 s at emb|CAB39936.1| (AL049500) osmotin (AL049500.57_S_AT) precursor [Arabidopsis thaliana] gb|AAC49697.1| (U66345) calreticulin 17097_s_at (ATU66345 S AT) [Arabidopsis thaliana] gb|AAD36959.1|AC000107 5 (AC000107) 17278_at (AC000107.5 AT) F17F8.5 [Arabidopsis thaliana] emb|CAB10405.1| (Z97340) beta-1, 3glucanase class I precursor [Arabidopsis 17485_s_at (Z97340.345 S_AT) thaliana] gb|AAD11587.1|AAD11587 (AF071527) 19247 at (AF071527.44 AT) hypothetical protein [Arabidopsis thaliana] 20245 s at emb|CAA05625.1| (AJ002584) AtMRP4 (AC005309.97 S AT) [Arabidopsis thaliana] thaliana] emb|CAA19698.1| (AL024486) putative 20420 at (AL024486.131 AT) chitinase [Arabidopsis thaliana] emb|CAB41131.1| (AL049658) hypothetical 20625_at (AL049658.102 AT) protein [Arabidopsis thaliana] Duplicates: 15778 and 15779 (zinc finger protein) 6 edm1 and rps2 without pad4orNahG ProbeSet Description gb|AAF18681.1|AF024504 11 (AF024504) 12630_at (AF024504.13_AT) unknown protein [Arabidopsis thaliana] gb|AAC06158.1| (AC003680) putative 13100 at (AC003680.50 AT)

cytochrome P450 [Arabidopsis thaliana] gb|AAB60774.1| (AC000375) ESTs gb[U75592,gb]T13956,gb]T43869 come from 13115 at (AC000375.44 AT) from this gene. [Arabidopsis thaliana] gb|AAC49356.1| (U35829) thioredoxin h [Arabidopsis thaliana] gb|AAC49356.1| (U35829) thioredoxin h [Arabidopsis thaliana]

13187 i at

13189 s at

(ATTHIRED4 I AT)

(ATTHIRED4 S AT)

	13215_s_at (CAFFEROYLCOAMETHYLT RANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
	13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
	13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
	13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC78535.1 (AC005662) putative
	14083_at (AC005662.56_AT)	embryo-abundant protein [Arabidopsis thaliana]
		gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam:
-	14116	sugar_tr.hmm, score: 395.39) [Arabidopsis
	14116_at (AF077407.30_AT)	thaliana]
		gb AAD31062.1 AC007357_11 (AC007357)
		Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a
		member of the PF 00067 Cytochrome P450
		family. ESTs gb N65665, gb T14112,
	14040 4 (DADO ASS	gb T76255, gb T20906 and gb AI100027 come
	14248_at (PAD3_AT) 14682 i at	from this gene.
	(WT1012A_RC_I_AT)	No hits found.
	(
		gh A AD10829 11 (AF117063) putative
		gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase AtSP2
	15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
	·	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine
	15641_s_at (AF117063_S_AT) 15978_at (X68592.6_AT)	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
	15978_at (X68592.6_AT)	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1
	·	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT)	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT)	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563 29 (AC012563)
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT)	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcaffeoyl-Coenzyme A 3-O-methyltransferase
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcrifeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT) 16649_s_at (ATHORF_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcrifeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcaffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
<u>-</u>	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT) 16649_s_at (ATHORF_S_AT) 17511_s_at (AF067605_S_AT)	inositol polyphosphate 5-phosphatase AtSP2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcraffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana] emb CAB10339.1 (Z97339) hypothetical
<u>-</u>	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT) 16649_s_at (ATHORF_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcaffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana] emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
<u>-</u>	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT) 16649_s_at (ATHORF_S_AT) 17511_s_at (AF067605_S_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcaffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana] emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana] emb CAB59428.1 (AJ002295) inositol-1,4,5-
	15978_at (X68592.6_AT) 16061_s_at (AB004796_S_AT) 16091_s_at (ATHHSP83_S_AT) 16105_s_at (ATU68017_S_AT) 16649_s_at (ATHORF_S_AT) 17511_s_at (AF067605_S_AT) 17899_at (Z97339.197_AT)	inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana] emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana] gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana] gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:transcaffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana] emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]

19640_at (AC004561.78 AT)

gb|AAC95192.1| (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Duplicates

13187 and 13189 (thioredoxin h) There are two duplicates of this in set 3 (13188 and 16981) Count it in set 3.

13215 and 16649 (putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase)
13285 and 16091 (heat shock protein 83)
13217 (calmodulin-like) has a duplicate in set 3 (17500). Count in set 3

16105 (hsf4) has a duplicate in set 4 (13273) Count in set 4

7 pad4orNahG and edm1 without rps2

ProbeSet

14110_i_at (AL035528.279_I_AT)

14148_at (NOVARTIS38_AT)

14249_i_at (PAD4_I_AT)

14250_r_at (PAD4_R_AT)

14672_s_at (TSA1_S_AT)

14673_s_at (TSB2_S_AT)

14704_s_at (WT768_RC_S_AT) protein [Arabidopsis thaliana] 14709_at (WT788_AT) No hits found less than or equal

14882_at (AL022605.63_AT) 15616_s_at (ATHPRO25A S AT)

Description emb|CAB36854.1| (AL035528) putative disease resistance protein [Arabidopsis thaliana gb|AAF34713.1|AF224762 1 (AF224762) SigA binding protein [Arabidopsis thaliana] emb|CAB43438.1| (AL050300) putative protein [Arabidopsis thaliana] emb|CAB43438.1| (AL050300) putative protein [Arabidopsis thaliana] gb|AAC49117.1| (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] gb|AAA32879.1| (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] thaliana] gb|AAD15461.1| (AC006067) unknown No hits found less than or equal to 1e-15. emb|CAA18753.1| (AL022605) putative protein [Arabidopsis thaliana] emb|CAA08794.1| (AJ009696) wallassociated kinase 1 [Arabidopsis thaliana]

gb|AAD15461.1| (AC006067) unknown 15846 at (AC006067.63 AT) protein [Arabidopsis thaliana] 15847 g at gb|AAD15461.1| (AC006067) unknown (AC006067.63_G_AT) protein [Arabidopsis thaliana] emb|CAA50677.1| (X71794) peroxidase 15970_s_at (X71794.2_S_AT) [Arabidopsis thaliana] emb|CAB41718.1| (AL049730) pEARLI 1 16150_s_at (ATHPEAR_S_AT) [Arabidopsis thaliana] gb|AAD40144.1|AF149413 25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis 16357_at (AF149413.38 AT) thaliana gb|AAC04495.1| (AC003974) putative disease 16365_at (AC003974.136 AT) resistance protein [Arabidopsis thaliana] 17068 s at gb|AAA32857.1| (M84658) receptor-like (ATHRLPKA S AT) protein kinasė [Arabidopsis thaliana] emb|CAA67551.1| (X99097) peroxidase. 17413_s_at (AJ006961.4_S_AT) [Arabidopsis thaliana] gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis 17499_s_at (AF107726_S_AT) thalianal gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. 17775_at (AC004392.2 AT) [Arabidopsis thaliana] emb|CAA10955.1| (AJ222713) unnamed 18590_at (AJ222713.4 AT) protein product [Arabidopsis thaliana] gb|AAD45127.1|AF163823 1 (AF163823) endoxyloglucan transferase [Arabidopsis 18968_at (AF163823.4 AT) thalianal gb|AAD45127.1|AF163823 1 (AF163823) 18969 g_at endoxyloglucan transferase [Arabidopsis (AF163823.4 G AT) thalianal emb|CAA74930.1| (Y14590) class IV 20287 at (Y14590.5 AT) chitinase [Arabidopsis thaliana] emb|CAA74930.1| (Y14590) class IV 20288 g at (Y14590.5 G AT) chitinase [Arabidopsis thaliana] **Duplicates** 14249 and 14250 (PAD4)

14704 and 15846 and 15847 (unknown protein)

18968 and 18969 (endoxyloglucan transferase)

20287 and 20288 (class IV chitinase)
14110 (putative diseaseresistance gene) is an incomplete probe set with very low signal. It has a duplicate (14111) in set 2.
Count in set 2.
14672 (trp synthase alpha) has a duplicate in set 2 (17487)
Counted in set 2.

8 rps2 and pad4orNahG without edm1

ProbeSet Description emb|CAA23036.1| (AL035394) putative Na+/H+-exchanging protein [Arabidopsis 13627_at (AL035394.196_AT) thaliana emb|CAA18462.1| (AL022347) serine/threonine kinase-like protein 13659_at (AL022347.46 AT) [Arabidopsis thaliana] gb|AAD15433.1| (AC006218) putative 13818 s at aspartate aminotransferase [Arabidopsis (AC006218.175_S_AT) thalianal gb|AAC69381.1| (AC005398) pathogenesisrelated PR-1-like protein [Arabidopsis 14635_s_at (PR.1 S AT) thalianal 17128 s at gb|AAC69381.1| (AC005398) pathogenesis-(ATHRPRP1A S AT) related PR-1-like protein [Arabidopsis emb|CAA07352.1| (AJ006960) peroxidase 17930_s_at (AJ006960.4_S AT) [Arabidopsis thaliana] gb|AAC79593.1| (AC005727) unknown 19914_at (AC005727.175 AT) protein [Arabidopsis thaliana] gb|AAD21459.1| (AC007017) similar to harpin-induced protein hin1 from tobacco 19991_at (AC007017.124 AT) [Arabidopsis thaliana]

Duplicates:

14635 and 17128 (PR-1)

9 edm1 and rps2 and pad4orNahG

ProbeSet

Description
emb|CAA16619.1| (AL021637) vacuolar
sorting receptor-like protein [Arabidopsis
thaliana]
gb|AAC49282.1| (U40856) AIG1
12879_s_at (AIG1_S_AT)

[Arabidopsis thaliana]

12989 s at gb[AAC26690.1] (AC004077) putative (AC004077.149 S_AT) cytochrome P450 [Arabidopsis thaliana] 13697 at (NI16 AT) No hits found. 14201 at (NOVARTIS73_AT) No hits found less than or equal to 1e-15. 14202 at (NOVARTIS73 RC AT) No hits found less than or equal to 1e-15. gb|AAC02748.1| (AC002340) putative 14609 at (AC002340.147_AT) cytochrome P450 [Arabidopsis thaliana] emb|CAA50677.1| (X71794) peroxidase 14638_s_at (PRXCB S AT) [Arabidopsis thaliana] emb|CAA60521.1| (X86958) protein kinase catalytic domain (fragment) [Arabidopsis 14763 at (X86958.1 AT) thalianal gb|AAD28243.1|AF121356 1 (AF121356) 15116 f at (AF121356 F AT) peroxiredoxin TPx2 [Arabidopsis thaliana] gb|AAC49282.1| (U40856) AIG1 17544_s at (ATU40856 S AT) [Arabidopsis thaliana] 17840 s at gb|AAB64049.1| (AC002333) putative (AC002333.223 S AT) endochitinase [Arabidopsis thaliana] gb|AAC34217.1| (AC004411) putative 18567_at (AC004411.25_AT) alcohol dehydrogenase [Arabidopsis thaliana] gblAAB82640.1| (AC002387) putative 20269 at (AC002387.237 AT) pectinesterase [Arabidopsis thaliana]

Duplicates 12879 and 17544 (AIG1)

10

14201 and 14202 (Novartis 73) 14638 (peroxidase) has a duplicate in set 7 (15970). Counted in set 7.

The first set (set 2 above) do not require *EDM1* and are not affected by *rps2*, *pad4* or *NahG*. These genes are less likely to be important for resistance mediated by *RPP7* and *RPP8* than the genes in the second set (set 3 above). The genes in the second set require *EDM1* but are not affected by *rps2*, *pad4* or *NahG*. These genes are more likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the third set (set 4 above) are affected by *rps2*, do not require *EDM1*, and are not affected by *pad4* or *NahG*. The genes in the fourth (set 5 above), seventh (set 8 above) and eight (set 9 above) sets include genes that are affected by *pad4* or *NahG*, and so are less likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the sixth set (set 7 above) require *RPP7* or *RPP8* for increased expression after infection by

Peronospora and are affected by *rps2*. These genes are also less likely to be important for resistance mediated by *RPP7* and *RPP8*.

Duplicates were identified by sorting "RPP7 or 8" by description, which put duplicated genes adjacent to one another. Most duplicates were in the same set, but there were nine cases of duplicates that had one probe set in one set, and another in another set. Examination of the data revealed that in these cases, the expression values were close to the cut-offs used to define the various sets. If one copy met the criteria, e.g., for *rps2*-dependent, but the other copy did not, the gene was classified as not *rps2*-dependent. Duplicates are noted. One hundred eighty four unique genes remained (SEQ ID NOs:1-211 and 792, Table 9 and Table 10).

Table 9

5

10

SEQ ID	ProbeSet	Description
	12007_at	emb CAB16829.1 (Z99708) putative protein
1	(Z99708.249_AT)	[Arabidopsis thaliana]
	12091_at	gb AAC64313.1 (AC004450) unknown
2	(AC004450.116_AT)	
	12115_at	emb CAA22152.1 (AL033545) extensin-like
3	(AL033545.26_AT)	protein [Arabidopsis thaliana]
	12240_at	emb CAB43974.1 (AL078579) putative
4	(AL078579.130_AT)	protein [Arabidopsis thaliana]
	12278 at	emblCA A 00731 11 (A 1011674) recentor like
5	(AJ011674.2 AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
J	(110011074.2_1(1)	gb AAD12037.1 (AC002392) putative
•	12307 at	receptor-like protein kinase [Arabidopsis
6	(AC002392.162_AT)	thaliana]
	12332 s at	dbj BAA82810.1 (AB023448) basic
7	(AB023448.2 S AT)	
	12341_s_at	emb CAA16619.1 (AL021637) vacuolar
	(AL021637.176_S_A	
8	T)	thaliana]
	12349_s_at	gb AAA17993.1 (M91192) phenylalanine
9	(X84728.6_S_AT)	ammonia-lyase [Trifolium subterraneum]
		emb CAA18468.1 (AL022347)
	12360_at	serine/threonine kinase-like protein
10	(AL022347.131_AT)	- ·
	2022	emb CAA18468.1 (AL022347)
	20223_at	serine/threonine kinase-like protein
11	(AL022347.145_AT)	[Arabidopsis thaliana]

12 13	12500_s_at (AF081067.3_S_AT) 12521_at (AF049236.28_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana] gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
14	12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana] emb CAB45330.1 (AL079344) nucleotide
15	12556_at (AL079344.155_AT) 12574 at	pyrophosphatase-like protein [Arabidopsis thaliana]
16	(X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
17	12630_at (AF024504.13_AT) 12642_at	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
18	(AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577)
	·	Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and
19	12777_i_at (AC006577.16_I_AT)	gb T22281 come from this gene. [Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577)
	12778_r_at	Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and
20	(AC006577.16_R_AT	gb T22281 come from this gene. [Arabidopsis thaliana] gb AAD25772.1 AC006577_8 (AC006577) Relenge to the PE100657
		Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and
21	12779_f_at (AC006577.16_F_AT)	gb T22281 come from this gene. [Arabidopsis thaliana]
22	12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
23	17744_s_at (AC004684.168_S_A T)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
24		gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
25	20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

26	12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
	12892_g_at	gb AAC63850.1 (U73786) ACC synthase
27	(ATACS6_G_AT)	[Arabidopsis thaliana] dbj BAA32419.1 (AB008104) ethylene
	12905_s_at	responsive element binding factor 2
28	(ATERF2_S_AT)	[Arabidopsis thaliana]
	16609 s at	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2
29	(AB008104_S_AT)	[Arabidopsis thaliana]
	12908 s at	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5
30	(ATERF5_S_AT)	[Arabidopsis thaliana]
	16536 a at	dbj BAA32422.1 (AB008107) ethylene
31	16536_s_at (AB008107_S_AT)	responsive element binding factor 5 [Arabidopsis thaliana]
	12916_s_at	gb AAC13947.1 (AF021244) coronatine-
32	(ATHCOR1_S_AT) 12933 r at	induced protein 1 [Arabidopsis thaliana] emb CAA65420.1 (X96600) pathogenesis-
33	(ATPRITAN_R_AT)	
	12989_s_at	1114 A COCCOO 11 (A COO 40CC)
34	(AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
		gb AAC24083.1 (AC003114) Match to
	•	calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719,
25	13067_s_at	gb T22451, gb H36323 and gb AA042519
35	(AC003114.16_S_AT) 13100 at	come from this gene. [Arabidopsis thaliana] gb[AAC06158.1] (AC003680) putative
36	(AC003680.50_AT)	cytochrome P450 [Arabidopsis thaliana]
		gb AAB60774.1 (AC000375) ESTs
37	13115_at	gb U75592,gb T13956,gb T43869 come from from this gene. [Arabidopsis thaliana]
31	13154_s_at	nom this gene. [Arabidopsis manana]
38		gb AAB64047.1 (AC002333) putative
20	T) 13176 at	endochitinase [Arabidopsis thaliana] emb CAA20567.1 (AL031394) putative
39		protein [Arabidopsis thaliana]
40	13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h
	13188_r_at	gb AAC49356.1 (U35829) thioredoxin h
41	(ATTHIRED4_R_AT)	[Arabidopsis thaliana]
42	13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
42	16981_s_at	gb AAC49356.1 (U35829) thioredoxin h
43	(U35829.2_S_AT)	[Arabidopsis thaliana] emb CAA16892.1 (AL021749) 12S
	13198_i_at	cruciferin seed storage protein [Arabidopsis
44	(ATTS0190_I_AT)	thaliana]

45	13215_s_at (CAFFEROYLCOAM ETHYLTRANS_S_A T)	gb AAF16576.1 AC012563_29 (AC012563) I putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
,	16649_s_at	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase
46	(ATHORF_S_AT) 13217_s_at	[Arabidopsis thaliana]
47	(CALMODULINLIK E_S_AT) 17500 s at	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
48	(ATHCALLGA_S_A T)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
49	13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
50	16105_s_at (ATU68017 S AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
51	13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
52	13285_s_at (HSP83_S_AT) 16091_s_at	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
53	(ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana] gb AAD22369.1 AC006580_1 (AC006580)
54	13381_at (AC006580.8_AT)	NAM (no apical meristem)-like protein [Arabidopsis thaliana]
	13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
55	13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like
55		protein [Arabidopsis thaliana] emb CAA23036.1 (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
56	(AL035394.196_AT)	thaliana] gb AAB82634.1 (AC002387) putative
57	13631_at (AC002387.185_AT)	transketolase precursor [Arabidopsis thaliana]
58	13659_at	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
59	13685_s_at	gb AAD25552.1 AC005850_9 (AC005850) Highly Simlilar to Mlo proteins [Arabidopsis thaliana]

	•	•
	20265	gb AAD25552.1 AC005850_9 (AC005850)
. 60	20365_s_at	Highly Similar to Mlo proteins [Arabidopsis
60	(AC005850.19_S_AT	
61	13696_at (NIII3_AT)	No hits found less than or equal to 1e-15.
no cds	13697_at (NI16_AT)	
60	13751_at	gb AAF16751.1 AC010155_4 (AC010155)
62		F3M18.8 [Arabidopsis thaliana]
63	13764_at	gb AAD39641.1 AC007591_6 (AC007591)
. 03	(NOVARTIS22_AT)	• • •
	13818_s_at	gb AAD15433.1 (AC006218) putative
64	(AC000218.173_8_A T)	aspartate aminotransferase [Arabidopsis
	13880 s at	thaliana]
	(AL049480.183_S_A	emb CAB39611.1 (AL049480) possible
65	T)	apospory-associated like protein [Arabidopsis thaliana]
	13966 at	emb CAA17775.1 (AL022023) putative
66	(AL022023.172_AT)	protein [Arabidopsis thaliana]
,	(,02202011/2_111)	gb AAC78535.1 (AC005662) putative
•	14083 at	embryo-abundant protein [Arabidopsis
67	(AC005662.56_AT)	thaliana]
	14096 at	
68	(AC002291.12_AT)	No hits found.
	14110_i_at	emb CAB36854.1 (AL035528) putative
-	(AL035528.279_I_AT	disease resistance protein [Arabidopsis
69)	thaliana]
	14111_s_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_S_A	
70	T)	thaliana]
		gb AAC26243.1 (AF077407) contains
-	1/11/6 -4	similarity to sugar transporters (Pfam:
71	14116_at (AF077407.30_AT)	sugar_tr.hmm, score: 395.39) [Arabidopsis
/ 1	14141 at	thaliana]
72		No hits found less than or equal to 1e-15.
	(1.0 Michal Al)	dbj BAA22813.1 (D26015) CND41,
	14145 at	chloroplast nucleoid DNA binding protein
73	(NOVARTIS35_AT)	[Nicotiana tahacum]
	(= 10 11111)	[Triootiana tabacam]
	14146_at	gb AAD25550.1 AC005850_7 (AC005850)
74	(NOVARTIS36_AT)	Hypothetical protein [Arabidopsis thaliana]
٠,	14140 -4	
75	14148_at	gb AAF34713.1 AF224762_1 (AF224762)
13	(NOVAR11838_A1)	SigA binding protein [Arabidopsis thaliana]
76	14201_at	No Lite Court I and the second
70	14202 at	No hits found less than or equal to 1e-15.
	(NOVARTIS73 RC	
77	- , -	No hits found less than or equal to 1e-15.
	- ·	emb CAA19683.1 (AL024486) putative
78		protein [Arabidopsis thaliana]
	· · · · · · · · · · · · · · · · · · ·	E [- waotooboto manana]

79	14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
		gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027
80	14248_at (PAD3_AT) 14249 i at	come from this gene. emb CAB43438.1 (AL050300) putative
81	(PAD4 <u>I</u> AT) 14250 r at	protein [Arabidopsis thaliana]
82	(PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
83	14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis gb AAD18156.2 (AC006260) phenylalanine
84	14256_f_at (PAL1-INTRON_F_AT)	ammonia lyase (PAL1) [Arabidopsis thaliana]
85	14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana] gb AAD23719.1 AC005956_8 (AC005956)
86	14320_at (AC005956.54_AT)	putative RING zinc finger protein [Arabidopsis thaliana]
87	14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
88	14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
89	14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
90	14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana] gb AAA32835.1 (M96073)
91	14620_s_at (PAT1_S_AT)	phosphoribosylanthranilate transferase [Arabidopsis thaliana] gb AAA32835.1 (M96073)
92	14838_s_at (M96073.6_S_AT)	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
93	14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana] gb AAC69381.1 (AC005398) pathogenesis-
94	14635 s at (PR.1 S AT) 17128 s at (ATHERRIA S AT	related PR-1-like protein [Arabidopsis thaliana] gb[AAC69381.1] (AC005398) pathogenesis-
95)	related PR-1-like protein [Arabidopsis thaliana]
96	14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]

97	15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
98	14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
99	17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] gb AAA32879.1 (M81620) tryptophan
100	14673_s_at (TSB2_S_AT) 14682 i at	synthase beta-subunit [Arabidopsis thaliana] thaliana]
	(WT1012A_RC_I_A	r [·]
101) 14691_at	No hits found.
102	(WT1096_AT)	No hits found.
	14704 s at	gb AAD15461.1 (AC006067) unknown
103	$(WT768_RC_S_AT)$	protein [Arabidopsis thaliana]
	15846_at	gb AAD15461.1 (AC006067) unknown
104	(AC006067.63_AT)	protein [Arabidopsis thaliana]
	15847_g_at	· · · · · · · · · · · · · · · · · · ·
	(AC006067.63_G_AT	7 gb AAD15461.1 (AC006067) unknown
105)	protein [Arabidopsis thaliana]
100	14709_at	
106	(WT788_AT)	No hits found less than or equal to 1e-15.
	1.47.60	emb CAA60521.1 (X86958) protein kinase
107	14763_at	catalytic domain (fragment) [Arabidopsis
107	(X86958.1_AT)	thaliana]
108	14882_at (AL022605.63 AT)	emb CAA18753.1 (AL022605) putative
100	(AL022003.03_A1)	protein [Arabidopsis thaliana]
	15042 at	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein
109	(AL021961.3 AT)	[Arabidopsis thaliana]
	(111011701.5_111)	[Anaoloopsis manana]
	15116_f_at	gb AAD28243.1 AF121356_1 (AF121356)
110	(AF121356_F_AT)	peroxiredoxin TPx2 [Arabidopsis thaliana]
		gb AAB53975.1 (U90522) lysine-
	15161_s_at	ketoglutarate reductase/saccharopine
111	(ATU90522_S_AT)	dehydrogenase [Arabidopsis thaliana]
110	15366_at	gb AAB63077.1 (U93215) unknown protein
112	(U93215.38_AT)	[Arabidopsis thaliana]
113	15415_at	gb AAB72169.1 (AF000657) hypothetical
113	(AF000657.28_AT)	protein [Arabidopsis thaliana]
114	15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative
417	15523 s at	protein [Arabidopsis thaliana]
		emb CAB45071.1 (AL078637) putative
115	T)	protein [Arabidopsis thaliana]
. = =	15532 r at	emb CAB45069.1 (AL078637) putative
116		protein [Arabidopsis thaliana]
		· · · · · · · · · · · · · · · · · · ·

•	1) .	
	15616_s at	· .
		cmb CAA08794.1 (AJ009696) wall-
117)	associated kinase 1 [Arabidopsis thaliana]
•		dbj BAA24440.1 (AB010407)
	15629 s at	phosphoglycerate dehydrogenase
118	(AB003280 S AT)	[Arabidopsis thaliana]
	· /	gb AAD10829.1 (AF117063) putative
	15641 s at	inositol polyphosphate 5-phosphatase At5P2
119	(AF117063_S_AT)	[Arabidopsis thaliana]
	` /	gb AAB80922.1 (AF022658) putative c2h2
•	15665 s at	zinc finger transcription factor [Arabidopsis
120; 682	$(AF02\overline{2}658 S AT)$	thaliana]
	15778 at	emb CAA67234.1 (X98676) zinc finger
121	(X98676.2 AT)	protein [Arabidopsis thaliana]
	15779_g_at	emb CAA67234.1 (X98676) zinc finger
122	(X98676.2 G AT)	protein [Arabidopsis thaliana]
٠	15859 at	gb AAD15461.1 (AC006067) unknown
123	(AC006587.164 AT)	protein [Arabidopsis thaliana]
	15978 at	gb AAD15461.1 (AC006067) unknown
124	$(X685\overline{9}2.6 \text{ AT})$	protein [Arabidopsis thaliana]
	16053_i_at	emb CAA74639.1 (Y14251) glutathione S-
125	(Y14251.4 I AT)	transferase [Arabidopsis thaliana]
	16061 s at	gb AAB97145.1 (AF000977) MEK1
126	(AB004796 S AT)	[Arabidopsis thaliana] thaliana]
		gb AAD34615.1 AF153283 1 (AF153283)
	16083_s_at	putative progesterone-binding protein
127	(AF153283 S AT)	homolog [Arabidopsis thaliana]
	16150_s at	emb CAB41718.1 (AL049730) pEARLI 1
128	(ATHPEAR S AT)	[Arabidopsis thaliana]
	16232_s at	emb CAB45796.1 (AL080252) putative
129	(AL080252.77_S_AT)	protein [Arabidopsis thaliana]
	—, — ,	gb AAC32915.1 (AC004138) putative
•	16257_at	nucleoside triphosphatase [Arabidopsis
130	(AC004138.105_AT)	thaliana]
	16298_at	emb CAA17152.1 (AL021890) putative
131	(AL021890.71_AT)	protein [Arabidopsis thaliana]
	16299_at	emb CAA19705.1 (AL024486) putative
132	(AL024486.185_AT)	protein [Arabidopsis thaliana]
		gb AAD40144.1 AF149413_25 (AF149413)
	•	contains similarity to protein kinase domains
		(Pfam F00069, Score=162.6, E=6.8e-45,
	16357 at	N=1) and leucien rich repeats (Pfam
133	(AF149413.38 AT)	PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
100	(11 1) 113 13 (1 A 1)	
	16360 at	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3
134	—	Arabidopsis thalianal
	\	

135	16365_at (AC003974.136_AT) 16578 s at	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
136		emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
137	16817_s_at (AL096882.91_S_AT) 16914_s at	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana] emb CAB39936.1 (AL049500) osmotin
138		precursor [Arabidopsis thaliana] gb AAB87114.1 (AC002391) unknown
139		protein [Arabidopsis thaliana] gb AAD23027.1 AC006585_22 (AC006585)
140	17008_at (AC006585.212_AT) 17014_s at	putative tyrosine aminotransferase [Arabidopsis thaliana] gb AAC48925.1 (U05206) ribonuclease
141	(ATU05206_S_AT) 17051 s at	[Arabidopsis thaliana] gb AAD09952.1 (AF098947) CTF2B
142	(AF098947_S_AT) 17068_s_at	[Arabidopsis thaliana] gb AAA32857.1 (M84658) receptor-like
143	(ATHRLPKA_S_AT)	protein kinase [Arabidopsis thaliana]
144	17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
145	17097_s_at (ATU66345_S_AT) 17278 at	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana] gb AAD36959.1 AC000107 5 (AC000107)
146	(AC000107.5_AT) 17413 s at	F17F8.5 [Arabidopsis thaliana] emb CAA67551.1 (X99097) peroxidase
147	(AJ006961.4_S_AT)	[Arabidopsis thaliana] gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase
148	17464_at (AC000132.72 AT)	(gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
		emb CAB10405.1 (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis
149	(Z97340.345_S_AT)	thaliana] gb AAD19610.1 (AF107726) cyclic
150	17499_s_at (AF107726_S_AT)	nucleotide gated channel [Arabidopsis thaliana] gb AAB71482.1 (AC002294) similar to S-
151	17511_s_at	linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
152	(D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
153	17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]

154	17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana] gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator
155	17775_at (AC004392.2_AT) 17840 s at	(GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
156	(AC002333.223_S_A T) 17843_s_at	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
157	T)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
158	17899_at (Z97339.197_AT) 17930 s at	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana] emb CAA07352.1 (AJ006960) peroxidase
159	(AJ006960.4_S_AT)	[Arabidopsis thaliana] emb CAB59428.1 (AJ002295) inositol-
160	18012_s_at (AJ002295_S_AT)	1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana] emb CAB52675.1 (AJ010971) glucose-6-
161	18022_at (AJ010971_AT)	phosphate 1-dehydrogenase [Arabidopsis thaliana]
162	18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
163	18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
164	18217_g_at (X95573.2_G_AT) 18551 at	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana] gb AAB87112.1 (AC002391) putative
165	(AC002391.163_AT)	cytochrome P450 [Arabidopsis thaliana] gb AAC34217.1 (AC004411) putative
166	18567_at (AC004411.25_AT) 18590 at	alcohol dehydrogenase [Arabidopsis thaliana] emb CAA10955.1 (AJ222713) unnamed
167	(AJ222713.4_AT) 18591_at	protein product [Arabidopsis thaliana] emb CAA52772.1 (X74756) ATAF2
168; 665	(X74756.2_AT)	[Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs
169	18625_at (AC005278.22_AT) 18716_at	gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana] gb AAF26754.1 AC007396_3 (AC007396)
170	(X91916_AT)	T4O12.6 [Arabidopsis thaliana] gb AAC33239.1 (AC005315) putative
171	18844_at (AC005315.131_AT) 18908 i at	ligand-gated ion channel protein [Arabidopsis thaliana] gb AAC62611.1 (AF055848) subtilisin-like
172	(AF055848.2_I_AT)	-

170	18909_s_at	gb AAC62611.1 (AF055848) subtilisin-like
173	(AF055848.2_S_AT)	protease [Arabidopsis thaliana]
174	18946_at	emb CAA72484.1 (Y11788) peroxidase
174	(Y11788.1_AT)	ATP24a [Arabidopsis thaliana]
	10000 -4	gb AAD45127.1 AF163823_1 (AF163823)
175	18968_at	endoxyloglucan transferase [Arabidopsis
175	(AF163823.4_AT)	thaliana]
	190604	gb AAD45127.1 AF163823_1 (AF163823)
176	18969_g_at (AF163823.4_G_AT)	endoxyloglucan transferase [Arabidopsis thaliana]
176	18983 s at	mananaj
	· · ·	emb CAB41722.1 (AL049730) pEARLI 1-
177	(AL049730.104_8_A)	like protein [Arabidopsis thaliana]
	19158 at	emb CAA65053.1 (X95738) proline
178	(X95738.2 AT)	transporter 2 [Arabidopsis thaliana]
1,0	19171 at	gb AAB64325.1 (AC002335) putative
179	(AC002335.160 AT)	trypsin inhibitor [Arabidopsis thaliana]
	19177 at	emb CAA68191.1 (X99923) male sterility 2-
180	(X99923.1 AT)	like protein [Arabidopsis thaliana]
	19182 at	emb CAA21214.1 (AL031804) putative
181	(AL031804.245 AT)	protein [Arabidopsis thaliana]
	` _ /	
	19229_at	gb AAD10694.1 (AC003027) lcl prt_seq No
182	(AC003027.39_AT)	definition line found [Arabidopsis thaliana]
	19247 at	gb AAD11587.1 AAD11587 (AF071527)
183	(AF071527.44 AT)	hypothetical protein [Arabidopsis thaliana]
	- · · · · ·	gb[AAC27173.1] (AC003028) putative
	19284_at	anthocyanidin synthase [Arabidopsis
184	(AC003028.196_AT)	thaliana]
	19415_at	emb CAB45805.1 (AL080253) putative
185	(AL080253.32_AT)	protein [Arabidopsis thaliana]
	19594_i_at	emb CAA66965.1 (X98321) peroxidase
186	(X98321.2_I_AT)	[Arabidopsis thaliana]
		gb AAC95192.1 (AC004561) putative
	19640_at	glutathione S-transferase [Arabidopsis
187	(AC004561.78_AT)	thaliana]
		emb CAB43638.1 (AL050351) NAD(P)H
100	19664_at	oxidoreductase, isoflavone reductase-like
188	(AL050351.172_AT)	protein [Arabidopsis thaliana]
100	19672_at	gb AAC36019.1 (AC005687) RAP2.6
189	(AC005687.19_AT)	[Arabidopsis thaliana]
	10762 -4	emb CAB36812.1 (AL035527) peptide
100	19762_at	transporter-like protein [Arabidopsis
190	(AL035527.204_AT)	- ,
101	19892_at	gb AAC79626.1 (AC005770) putative
191	(AC005770.30_AT)	protease inhibitor [Arabidopsis thaliana]
	19894 at	emb CAA05025.1 (AJ001809) succinate
192	(AJ001809.1 AT)	dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
172	(1200100311_WT)	[mauluopoio manana]

	19914_at	gb AAC79593.1 (AC005727) unknown
193	(AC005727.175_AT)	protein [Arabidopsis thaliana]
194	19951_at	gb AAC42241.1 (AC005395) unknown
194	(AC005395.47_AT)	protein [Arabidopsis thaliana]
	10001 **	gb AAD21459.1 (AC007017) similar to
195	19991_at (AC007017.124 AT)	harpin-induced protein hin1 from tobacco
193	20189 at	[Arabidopsis thaliana] gb AAD32864.1 AC005489_2 (AC005489)
196	(AC005489.2 AT)	F14N23.2 [Arabidopsis thaliana]
. 100	(1C003407.2_A1)	emb CAA18469.1 (AL022347)
	20232 s at	serine/threonine kinase-like protein
197	 ,	[Arabidopsis thaliana]
	20238 at	emb CAA52619.1 (X74514) beta-
198	(X74514.2 AT)	fructofuranosidase [Arabidopsis thaliana]
	20239 g at	emb CAA52619.1 (X74514) beta-
199	(X74514.2 G AT)	fructofuranosidase [Arabidopsis thaliana]
	20245_s at	emb CAA05625.1 (AJ002584) AtMRP4
200	(AC005309.97_S_AT)	[Arabidopsis thaliana] thaliana]
	20246_s_at	gb AAC95354.1 (AF084037) receptor-like
201	(AF084037.3_S_AT)	protein kinase [Arabidopsis thaliana]
		gb AAB82640.1 (AC002387) putative
202	(AC002387.237_AT)	pectinesterase [Arabidopsis thaliana]
	20287_at	emb CAA74930.1 (Y14590) class IV
203	(Y14590.5_AT)	chitinase [Arabidopsis thaliana]
204	20288_g_at	emb CAA74930.1 (Y14590) class IV
204	(Y14590.5_G_AT)	chitinase [Arabidopsis thaliana]
	20221	gb AAD23617.1 AC007168_8 (AC007168)
205	20331_at (AC007168.86 AT)	putative aspartate aminotransferase [Arabidopsis thaliana]
203	20368 at	gb AAC36163.1 (AC005314) putative serpin
206	(AC005314.38 AT)	[Arabidopsis thaliana]
200	20420 at	emb CAA19698.1 (AL024486) putative
207	(AL024486.131 AT)	chitinase [Arabidopsis thaliana]
	20429_s at	emb CAB10219.1 (Z97336) hypothetical
208		protei [Arabidopsis thaliana]
	20620 g at	gb AAC98070.1 (AC005896) putative
	(AC005896.161_G_A	C2H2-type zinc finger protein [Arabidopsis
209	T)	thaliana]
,	00605	
210	20625_at	emb CAB41131.1 (AL049658) hypothetical
210	(AL049658.102_AT)	protein [Arabidopsis thaliana]
		emb CAA63012.1 (X91919) LEA76
		homologue typel [Arabidopsis thaliana] Arabidopsis thaliana. ESTs gb N97082,
	20641 at	gb Z27056 and gb Z29902 come from this
211	(X91919.1_AT)	gene.
	18224 s at	emb CAA17152.1 (AL021890) putative
789		protein [Arabidopsis thaliana]
	16522_at	emb CAA54631.1 (X77500) amino acid
790	(X77500.2_AT)	transporter [Arabidopsis thaliana]

		gb AAC17040.1 (AC002986) Similarity to
		A. thaliana gene product F21M12.20,
	19982 at	gb AC000132. EST gb Z25651 comes from
791	(AC002986.28 AT)	this gene. [Arabidopsis thaliana]
	18920 at	gb AAC16927.1 (AC002338) putative
367	(AC002338.11 AT)	laccase [Arabidopsis thaliana]
212	12324 i at	AC007212
793	12345 at	L36246
213	12500_s_at	AF081067
214; 662	12505 s at	AC005309
215	12608 i at	S70188
216	12642_at	AC006920
217	12746_i_at	AL096882
218	12748_f_at	AL096882
219	12761_s_at	AC006577
220	12773_at	AC005727
221	12778_r_at	AC006577
222	12798_at	AC003028
223	12802_at	AL022373
	12842_s_at	No hits found less than or equal to 1e-15
224	12843_s_at	AC007195
	12845_s_at	AJ004810
225	12879_s_at	U40856
226	12891_at	U73786
227	12892_g_at	U73786
228; 658	12904_s_at	AB008103
229	12905_s_at	AB008104
230	12908_s_at	AB008107
231	12909_s_at	Z97343
232	12911_s_at	X84229
233	12916_s_at	AF021244
234	13138_at	AL096882
235	13177_at	AL049640
236	13178_at	U93215
237	13187_i_at	U35829
238	13189_s_at	U35829
239	13198_i_at	AL021749
240	13212_s_at	AL137080
241	13217_s_at	AL049862
242	13258_s_at	AC005309
243	13273_s_at	U68017
244	13284_s_at	AJ002551
245	13604_at	AC000104
246	13615_at	AC002332
247	13617_at	AC006592
248	13718_at	Z72152
249	13771_at	AC006593
250	13785_at	AC007087
251	14052_at	AC004122

252	14096_at	AC002291
253	14097_at	AC005309
254	14116_at	AF077407
255	14141_at	AC011437
256; 683	14148_at	AF224762
257	14196_at	AC012563
258	14201_at	AL163972
259	14219_at	AC068667
260	14223_at	AL024486
261	14248_at	AC007357
262	14250_r_at	AL050300
263	14595_at	AL022580
264	14608_at	AC007357
265	14614_at	AC004165
266	14621_at	AC004747
267	14627_i_at	X76609
268	14628 r at	X76609
269	14635 s at	AC005398
270	14636 s at	AC013258
271	14643 s at	AC006836
272	14672 s_at	U18993
273	14675_s_at	D85191
274	14691_at	AP002046
275	14704_s_at	AC006067
276	14706_r_at	AL137189
277	14709_at	AP002046
278	14711_s_at	AF085279
279	14731_s_at	AF014960
280	14784_at	AC005310
281	14951_at	AL049481
282	15057_at	AL035440
283	15085_s_at	AL031018
284	15105_s_at	Z14987
285	15116_f_at	AF121356
286	15125_f_at	D85190
287	15141_s_at	D85191
288	15145_s_at	D64155
289	15154_s_at	AL096860
290	15161_s_at	U90522
291	15178_s_at	U43489
292	15216_s_at	U75198
293	15431_at	AL030978
294	15496_at	AC006282
295	15523_s_at	AL078637
296	15593_s_at	U54561
297	15611_s_at	L22567
298	15616_s_at	AJ009696
299	15622_s_at	U43945

300	15629 s at	AB010407
301	15665 s at	AF022658
302	15680 s at	D42061
303	15846 at	AC006067
304	15847 g at	AC006067
305	15866 s at	AC005770
306	15950 at	AC006429
307	15954 at	U72155
308	15978 at	X68592
309	16038 s at	L04173
310	16063 s at	AB008103
311	16105 s at	U68017
312	16150 s at	AL049730
313	16153 s at	AC013258
314	16393 s at	AC006436
315	16412 s at	AL022603
316	16442 s at	AJ002551
317	16504 s at	Z97335
318	16510 at	AL034567
319	16536 s at	AB008107
320	16539 s at	Z97343
321	16569 s at	L23968
322	16578 s at	AL137080
323	16609 s at	AB008104
324	16620 s at	AF051338
325	16637 s at	Z97336
326	16817 s at	AL096882
327	16864 i at	AL133248
328	16951_i_at	AC005662
329	16952_s_at	AC005662
330	16981_s_at	U35829
331	17014_s_at	U05206
332	17033_s_at	U83179
333	17054_s_at	AF134128
334	17073_s_at	AC006836
335	17119_s_at	AF132212
336	17123_s_at	AF106087
337	17128 s_at	AC005398
338	17187_at	AF128396
339; 669	17303_s_at	AC005499
340; 663	17379_at	AC018721
341	17386_at	AC006264
342	17413_s_at	X99097
343	17499_s_at	AF107726
344	17500_s_at	AL049862
345	17544_s_at	U40856
346	17567_at	AL162751
347	17886_at	AC004484

348	17899 at	Z97339
349	17917 s at	AC004261
350	17961 at	AC007323
351	17963 at	AL049730
352	18003 at	AF188334
302	18064 r at	No hits found
	18069 at	No hits found
	18009_at	No hits found
252	18070_1_at	
353		AC012375
354	18217_g_at	AC012375
355	18235_at	AC000348
356	18252_at	AL096882
357	18255_at	AC005770
358	18272_at	AF002109
359	18533_at	AL021684
360	18556_at	AC006264
361	18590_at	AJ222713
362	18591_at	X74756
363	18607 s at	U78721
364	18635 at	AC004005
365	18716 at	AC007396
366	18876 at	AF002109
367	18920 at	AC002338
368	18928 at	AC002338
369	19034 at	AL021768
370	19171 at	AC002335
371	19171_at	AB035137
372	19176_at	AL031804
373	19162_at	AL035538
374	19231_at 19640 at	AC004561
375	19040_at	
	_	AL049659
376	20017_at	AC004521
377	20034_i_at	A71607
378	20201_at	AL078470
379	20227_s_at	AB027252
380	20269_at	AC002387
381	20297_at	AC007153
382	20314_s_at	AL096882
383	20335_s_at	Y14208
384	20429_s_at	Z97336
385	20585 s at	AC005309
386	20641 at	X91919
387	12333 at	AJ286345
388	14028 at	· · · · · ·
389	14295 s at	Z54356
390	14965 at	AC002329
391	15969 s a	AJ133036
392	15982 s a	X98190
J / L	12205-2-4	A70170

		•
393	16461 I at	AC004683
394	16462 <u>s</u> a	AC004683
395	16514 at	AL035538
396	17549 s a	L37126
397	18706 s a	X75782
398	19594 i at	X98321
399	20555 s a	AL080318
		gb AAD17366.1 (AF128396) similar to
		human phosphotyrosyl phosphatase activator
400	16212_at	PTPA (GB:X73478) [Arabidopsis thaliana]
		gb AAC32233.2 (AC005168) unknown
794	14985_s_at	protein [Arabidopsis thaliana]
		emb CAB71046.1 (AL137898) shaggy-like
401	16411_s_at	kinase beta [Arabidopsis thaliana]
		gb AAD39561.1 AC007067_1 (AC007067)
402	15920_i_at	T10O24.1 [Arabidopsis thaliana]
		emb CAA19705.1 (AL024486) putative
403	16299_at	protein [Arabidopsis thaliana]
		-1-1A A C00450 11 (A C005051)
404	18445 at	gb AAC98458.1 (AC005851) putative
404	10443_at	glucosyltransferase [Arabidopsis thaliana]
		gb AAC23400.1 (AC004005) putative
405	19215 at	methyl chloride transferase [Arabidopsis
1 03	19213_at	thaliana]
406	16439 at	emb CAA50905.1 (X72022) ORF1 [Arabidopsis thaliana]
400	10439_at	gb[AAD20710.1] (AC006300) unknown
407	16047 at	protein [Arabidopsis thaliana]
407	10047_at	gb AAF01328.1 AF188334 1 (AF188334)
		Toll/interleukin-1 receptor-like protein
408	18003 at	[Arabidopsis thaliana]
100	10005_at	emb CAB10219.1 (Z97336) hypothetical
409	20429 s at	protei [Arabidopsis thaliana]
	20127_5_4	gb AAD12002.1 (AC004261) calcium
		binding protein (CaBP-22) [Arabidopsis
410	17917 s at	thaliana]
110	17717_5_4	emb CAB41717.1 (AL049730) pEARLI 1-
411	17963 at	like protein [Arabidopsis thaliana]
122	17705_ut	emb CAB41718.1 (AL049730) pEARLI 1
412	16150 s at	[Arabidopsis thaliana]
•	10100_0_4	emb CAA52619.1 (X74514) beta-
413	20239 g at	fructofuranosidase [Arabidopsis thaliana]
		emb CAA52619.1 (X74514) beta-
414	20238 at	fructofuranosidase [Arabidopsis thaliana]
	· · <u>-</u>	
		emb CAA08794.1 (AJ009696) wall-
415	15616_s_at	associated kinase 1 [Arabidopsis thaliana]
		emb CAA52772.1 (X74756) ATAF2
416	18591_at	[Arabidopsis thaliana]

417	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
		gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb AI100071
418	12759_at	come from this gene. [Arabidopsis thaliana] gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces
419	19060_at	occidentalis. [Arabidopsis thaliana]
420	12998_at	emb CAB41863.1 (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
40.1	10150	gb AAD30608.1 AC007369_18 (AC007369)
421 422	13172_s_at	Sugar transporter [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
422	14709_at	gb AAD41420.1 AC007727_9 (AC007727)
423	15931 at	F8K7.9 [Arabidopsis thaliana]
	-	emb CAB41109.1 (AL049656) ammonium
		transport protein (AMT1) [Arabidopsis
424	20369_s_at	thaliana]
425	14201_at	No hits found less than or equal to 1e-15.
426	14691_at	No hits found.
		gb AAF34713.1 AF224762_1 (AF224762)
75	14148_at	SigA binding protein [Arabidopsis thaliana]
	·	emb CAB42872.1 (AJ012423) wall-
426	16140_s_at	associated kinase 2 [Arabidopsis thaliana]
		emb CAB42924.1 (AL049862) putative
427	13625 s at	disease resistance protein [Arabidopsis thaliana]
721	13023_s_at	emb CAA19683.1 (AL024486) putative
428	13702 s_at	protein [Arabidopsis thaliana]
		gb AAC14530.1 (AC004484) unknown
429	17886_at	protein [Arabidopsis thaliana]
		gb AAC23641.1 (AC004684) putative
430	12354 g at	receptor-like protein kinase [Arabidopsis thaliana]
.50	12337_5_ui	gb AAC23641.1 (AC004684) putative
		receptor-like protein kinase [Arabidopsis
431	12353_at	thaliana]
	1,000	emb CAB10339.1 (Z97339) hypothetical
432	17899_at	protein [Arabidopsis thaliana]

		emb CAB43665.1 (AL050352) Ca2+-
		transporting ATPase-like protein
433	18894_at	[Arabidopsis thaliana]
		gb AAB64024.1 (AC002333) putative
434	14978 at	glucosyltransferase [Arabidopsis thaliana]
757	14270_at	emb CAA19683.1 (AL024486) putative
435	14223 at	protein [Arabidopsis thaliana]
.55	1 1225_dt	gb[AAC05342.1] (AC002521) putative
436	16109 s at	protein kinase [Arabidopsis thaliana]
		gb AAD28055.1 AC007166 3 (AC007166)
		putative protein kinase [Arabidopsis
437	18820 at	thaliana]
	-	gb AAC72865.1 (AF104919) similar to class
		I chitinases (Pfam: PF00182, E=1.2e-142,
438	20345_at	N=1) [Arabidopsis thaliana]
		gb AAF29406.1 AC022354_5 (AC022354)
439	14170_at	unknown protein [Arabidopsis thaliana]
		gb AAD38519.1 AF138281_1 (AF138281)
	.•	phospholipase D-gamma-2 [Arabidopsis
440	15143_s_at	thaliana]
		gb AAD19610.1 (AF107726) cyclic
441	17400	nucleotide gated channel [Arabidopsis
441	17499_s_at	thaliana]
		emb CAB37511.1 (AL035540)
	•	Phospholipase like protein [Arabidopsis
442	20500 at	
442	20590_at	thaliana]
442	20590_at	thaliana] gb AAD31074.1 AC007357_23 (AC007357)
442	20590_at	thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from
442	20590_at	thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the
442	20590_at	thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs
		thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this
442	20590_at	thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
		thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347)
	14608_at	thaliana] gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein
443		gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
443	14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative
443	14608_at 13550_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana]
443	14608_at 13550_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative
443	14608_at 13550_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative
443 444 445	14608_at 13550_at 13355_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis
443 444 445 446	14608_at 13550_at 13355_at 13564_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana] emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis
443 444 445	14608_at 13550_at 13355_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana] emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
443 444 445 446	14608_at 13550_at 13355_at 13564_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana] emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana] gb AAC32912.1 (AC004138) putative
443 444 445 446 447	14608_at 13550_at 13355_at 13564_at 19845_g_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana] emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana] gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis
443 444 445 446	14608_at 13550_at 13355_at 13564_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana] emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana] gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis thaliana]
443 444 445 446 447	14608_at 13550_at 13355_at 13564_at 19845_g_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana] emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana] emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana] gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana] emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana] gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis

		emb CAA66863.1 (X98190) peroxidase
450	15982_s_at	ATP2a [Arabidopsis thaliana]
•	•	gb AAD39285.1 AC007576_8 (AC007576)
451	12227_at	Unknown protein [Arabidopsis thaliana]
		emb CAB45975.1 (AL080318) copper amine
		oxidase like protein (fragment2)
452	20555_s_at	[Arabidopsis thaliana]
		emb CAB37510.1 (AL035540)
,		monooxygenase 2 (MO2) [Arabidopsis
453	19844_at	thaliana]
		gb AAC31242.1 (AC004747) unknown
454	13985_s_at	protein [Arabidopsis thaliana]
		gb AAD41421.1 AC007727 10 (AC007727)
		ESTs gb[N96028, gb]F14286, gb]T20680,
		gb F14443, gb AA657300 and gb N65244
455	13548 at	come from this gene. [Arabidopsis thaliana]
		gb AAA32775.1 (L22567) cor78
456	15611_s_at	[Arabidopsis thaliana]
		gb AAD25759.1 AC007060 17 (AC007060)
	•	Strong similarity to F19I3.2 gi 3033375
		putative berberine bridge enzyme from
		Arabidopsis thaliana BAC gb AC004238.
457	19840 s at	EST gb R90518 comes from this gene.
		emb CAA67340.1 (X98808) peroxidase
458	15985 at	ATP3a [Arabidopsis thaliana]
		gb AAD32844.1 AC007658 3 (AC007658)
459	14584_at	unknown protein [Arabidopsis thaliana]
		gb AAD36948.1 AF069441_8 (AF069441)
460	15422 at	hypothetical protein [Arabidopsis thaliana]
700	13422_at	gb AAB61076.1 (AF00727.1)
		A TM021B04.14 gene product [Arabidopsis
461	20150 at	thaliana]
101	20130_4	gb AAC33239.1 (AC005315) putative
		ligand-gated ion channel protein
462	18844 at	[Arabidopsis thaliana]
		emb CAA20203.1 (AL031187) receptor-like
		serine/threonine protein kinase ARK3
463	16360 at	[Arabidopsis thaliana]
	-	gb AAB87113.1 (AC002391) putative
464	20292_at	protein kinase [Arabidopsis thaliana]
	_	gb AAC18798.1 (AC003671) F1707.4
465	14554_at	[Arabidopsis thaliana]
		gb AAC19273.1 (AF069298) similar to
		several small proteins (~100 aa) that are
		induced by heat, auxin, ethylene and
		wounding such as Phaseolus aureus indole-3-
		acetic acid induced protein ARG
466	18604_at	(SW:32292) [Arabidopsis thaliana]

467	16061_s_at	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana]
	·	dbj BAA22813.1 (D26015) CND41,
468	14145 at	chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
	11115_dt	dbj BAA04870.1 (D21843) MAP kinase
469	16144_s_at	[Arabidopsis thaliana]
		gb AAC49697.1 (U66345) calreticulin
470	17097_s_at	[Arabidopsis thaliana]
		gb AAB71447.1 (AC000098) Similar to Arabidopsis Fe(II) transport protein
471	19718 at	(gb U27590). [Arabidopsis thaliana]
		gb[AAC25507.1] (AC003979) T22J18.6
472	14298_g_at	[Arabidopsis thaliana]
		gb AAD12037.1 (AC002392) putative
473	12307 at	receptor-like protein kinase [Arabidopsis thaliana]
413	12507_at	emb CAA18460.1 (AL022347) protein
474	20232 s at	kinase-like protein [Arabidopsis thaliana]
475	19322 at	gb AAF19738.1 AC012463_12 (AC012463)
4/3	19322_at	T2E6.14 [Arabidopsis thaliana] gb AAF07386.1 AC010675_9 (AC010675)
		putative peptide transporter [Arabidopsis
476	14224_at	thaliana]
	•	gb AAD39269.1 AC007203 1 (AC007203)
		Putative UDP-glucose:sterol
477	14270_at	glucosyltransferase [Arabidopsis thaliana]
400	1.7.4	emb CAB39671.1 (AL049483) putative
478	15479_at	protein [Arabidopsis thaliana]
		gb AAD41981.1 AC006438 13 (AC006438)
479	14090_i_at	unknown protein [Arabidopsis thaliana]
400	16160	gb AAB05099.1 (U39944) BELL1
480	16162_s_at	[Arabidopsis thaliana]
	•	gb AAB70415.1 (AC000106) Similar to Beta integral membrane protein (gb U43629).
481	20149_at	[Arabidopsis thaliana]
	-	gb AAD15574.1 (AC006340) unknown
482	12765_at	protein [Arabidopsis thaliana]
		gb AAC63643.1 (AC005309) putative
214	12505_s_at	CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana]
- •		gb AAC79588.1 (AC005727) putative RING
		zinc finger ankyrin protein [Arabidopsis
483	13140_at	thaliana]
		gb AAC72124.1 (AC005278) ESTs
484	15022_at	gb H37641 and gb AA651422 come from this gene. [Arabidopsis thaliana]
•		Parra francohara munumal

			emb CAB41935.1 (AL049751) putative
	485	16306_at	protein [Arabidopsis thaliana]
•			gb AAC26246.1 (AF077407) contains
			similarity to phosphoenolpyruvate synthase
			(ppsA) (GB:AE001056) [Arabidopsis
	486	18611_at	thaliana]
		- .	emb CAB43428.1 (AL050300) putative
	487	20199 at	protein [Arabidopsis thaliana]
		_	emb CAA18626.1 (AL022580) putative
	488	14595_at	protein [Arabidopsis thaliana]
		_	114 4 70 10 20 114 50 00 54 10 (4 50 0 70 5)
			gb AAD31337.1 AC007354_10 (AC007354)
			Strong similarity to gb Y09533 involved in
			starch metabolism from Solanum tuberosum
			and contains a PF 01326 Pyruvate phosphate
		•	dikinase, PEP/pyruvate binding domain. EST
	400	10520 -4	gb N96757 comes from this gene.
	489	12532_at	[Arabidopsis thaliana]
	400	10077	emb CAB41162.1 (AL049659) putative
	490	19977_at	protein [Arabidopsis thaliana]
			gb AAC79594.1 (AC005727) putative
	401	10772	membrane channel protein [Arabidopsis
	491	12773_at	thaliana]
	400	10.000	gb AAD32870.1 AC005489_8 (AC005489)
	492	19632_at	F14N23.8 [Arabidopsis thaliana]
	400	10050	emb CAA16957.1 (AL021811) putative
	493	19359_s_at	protein [Arabidopsis thaliana]
	40.4		emb CAA78712.1 (Z14988) glycine rich
	494	14716_f_at	protein [Arabidopsis thaliana] thaliana]
	40.5	10640	gb AAC19269.1 (AF069298) T14P8.18 gene
	495	13648_at	product [Arabidopsis thaliana]
	40.4	10760	gb AAD41977.1 AC006438_9 (AC006438)
	496	12768_at	unknown protein [Arabidopsis thaliana]
	40.5	16100	gb AAC69134.1 (U78721) putative auxin-
	497	16422_at	regulated protein [Arabidopsis thaliana]
			gb AAC26203.1 (AF053747) dormancy-
	498	15131_s_at	associated protein [Arabidopsis thaliana]
			emb CAB38829.1 (AL035679) drought-
	400	4.4680	inducible cysteine proteinase RD19A
	499	14659_s_at	precursor
		•	emb CAB38829.1 (AL035679) drought-
			inducible cysteine proteinase RD19A
	500	14658_s_at	precursor [Arabidopsis thaliana]
			emb CAB36513.1 (AL035440) putative
	501	1'5057_at	protein [Arabidopsis thaliana]
			emb CAB56039.1 (AJ133786) gigantea
	502	17581_g_at	protein [Arabidopsis thaliana]
			gb AAC34217.1 (AC004411) putative
			alcohol dehydrogenase [Arabidopsis
	503	18567_at	thaliana]

504 505	17047_s_at 15105_s_at	gb AAC68674.1 (AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana] emb CAA78711.1 (Z14987) glycine rich protein [Arabidopsis thaliana]
506	14196_at	gb AAF16557.1 AC012563_10 (AC012563) unknown protein [Arabidopsis thaliana] gb AAD50976.1 AF170494_1 (AF170494) ionotropic glutamate receptor ortholog GLR6
507	17599_s_at	[Arabidopsis thaliana]
508	18556_at	gb AAD29803.1 AC006264_11 (AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
509	16486_at	gb AAB04606.1 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] gb AAB95293.1 (AF002109) unknown
510	18272_at	protein [Arabidopsis thaliana]
795	12219_at	gb AAD31373.1 AC006053_15 (AC006053) unknown protein [Arabidopsis thaliana]
511	20446_s_at	gb AAC80600.1 (AC005106) T25N20.21 [Arabidopsis thaliana]
512	12561_at	emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
		gb AAD46000.1 AC005916_12 (AC005916) Contains similarity to gb AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb AF109179 cyclin T1 from Mus musculus. ESTs gb N95317, gb Z29139 and gb Z30853 come
513	12060_at	from this gene. [Arabidopsis thaliana] gb AAB61480.1 (AC000348) T7N9.4
514	18235_at	[Arabidopsis thaliana]
515	14021_r_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
516	14020_i_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana] emb CAA44630.1 (X62818) Metallothionein-like protein [Arabidopsis
517	16011_s_at	thaliana]
		gb AAD09232.1 (U83179) unknown
518	17033_s_at	[Arabidopsis thaliana]
518519	17033_s_at 16050_at	[Arabidopsis thaliana] gb AAD24630.1 AC006919_10 (AC006919) putative fructose bisphosphate aldolase [Arabidopsis thaliana]

	520	19692_at	gb AAC14039.1 (AC003981) F22O13.13 [Arabidopsis thaliana] gb AAC39464.1 (AF053065) late
	521	19181_s_at	embryogenesis abundant protein homolog [Arabidopsis thaliana]
			gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis
	792	13435_at	thaliana]
	522	17128_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis gb AAC69381.1 (AC005398) pathogenesis-
	523	14635_s_at	related PR-1-like protein [Arabidopsis thaliana]
	524	15846 at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
			gb AAD15461.1 (AC006067) unknown
	525	15847_g_at	protein [Arabidopsis thaliana]
			gb AAD15461.1 (AC006067) unknown
	526	14704_s_at	protein [Arabidopsis thaliana]
			gb AAB80678.1 (AC002332) putative
	527	17456_at	steroid dehydrogenase [Arabidopsis thaliana]
			emb CAB10562.1 (Z97344) acetylornithine
	528.	14895_s_at	deacetylase [Arabidopsis thaliana]
			gb AAB95235.1 (AC002130) F1N21.7
	529	19979_at	[Arabidopsis thaliana]
	520	20225	emb CAA78152.1 (Z12162) protein
	530	20325_s_at	phosphatase 1A [Arabidopsis thaliana] gb AAB61479.1 (AC000348) T7N9.3
	531	18234_at	[Arabidopsis thaliana]
	331	10254_at	emb CAA35838.1 (X51474) kin1
	532	16474 s at	[Arabidopsis thaliana]
			emb CAA38894.1 (X55053) cold regulated
	533	18701_s_at	[Arabidopsis thaliana]
			gb AAD23000.1 AC007087_19 (AC007087)
			cold-regulated protein corl 5b precursor
	534	13785_at	[Arabidopsis thaliana]
		•	gb AAC23422.1 (AC004005) putative
	535	20387 at	methionine aminopeptidase [Arabidopsis thaliana]
	333	_20367_at	gb AAB63086.1 (U93215) unknown protein
	536	13178_at	[Arabidopsis thaliana]
			gb AAD30603.1 AC007369 13 (AC007369)
•	537	12103_at	Unknown protein [Arabidopsis thaliana]
			emb CAA42483.1 (X59814) Cold and ABA
	538	13225 s at	regulated gene [Arabidopsis thaliana]
			O O F

		gb AAB95275.1 (AF002109) putative LIM-
539	17003_at	domain protein [Arabidopsis thaliana]
	,	emb CAA19880.1 (AL031032) putative
540	15878_at	protein [Arabidopsis thaliana]
		gb AAD03574.1 (AC003952) putative
		senescence-related protein [Arabidopsis
541	13004_at	thaliana]
		gb AAC34333.1 (AC004122) Highly Similar
		to branched-chain amino acid
542	14052_at	aminotransferase [Arabidopsis thaliana]
		gb AAC05351.1 (AC002521) putative
		receptor-like protein kinase [Arabidopsis
543	15798_at	thaliana]
	,	gb AAB67985.1 (L36246) anoxia-induced
793	12345_at	protein [Arabidopsis thaliana]
	•	emb CAA20206.1 (AL031187)
		serine/threonine kinase-like protein
544	16818_s_at	[Arabidopsis
		gb AAC62136.1 (AC005169) unknown
545	13916_at	protein [Arabidopsis thaliana]
		emb CAB41311.1 (AL049711) putative heat
	000.40	shock transcription factor [Arabidopsis
666	20342_at	thaliana]
		emb CAB10242.1 (Z97336) germin
546	20421 -4	precursor oxalate oxidase [Arabidopsis
340	20421_at	thaliana]
547	14250 r at	emb CAB43438.1 (AL050300) putative
J -1 1	14230_1_at	protein [Arabidopsis thaliana]
548	14249 i at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
. 540	17277_1_at	gb[AAC49282.1] (U40856) AIG1
549	17544 s at	[Arabidopsis thaliana]
5.15	17377_5_6	gb AAC49282.1 (U40856) AIG1
550	12879 s at	[Arabidopsis thaliana]
	12075_0_40	gb AAC16079.1 (AC004521) unknown
551	20017 at	protein [Arabidopsis thaliana]
		emb CAB40989.1 (AL049640) growth factor
552	13177 at	like protein [Arabidopsis thaliana]
		gb AAF18611.1 AC005170_1 (AC005170)
		similar to senescence-associated protein
553	19946 at	[Arabidopsis thaliana]
	. -	gb AAD08938.1 (AC005724) unknown
554	17894 at	protein [Arabidopsis thaliana]
	<u></u>	gb AAD15572.1 (AC006340) unknown
555	15855_at	protein [Arabidopsis thaliana]
		emb CAB45807.1 (AL080253) putative
556	15558_r_at	protein [Arabidopsis thaliana]
557	15208_s_at	No hits found less than or equal to 1e-15.
		

·	•	gb AAF21072.1 AC013258_10 (AC013258)
558	16153_s_at	thaumatin-like protein [Arabidopsis thaliana]
		gb AAF21072.1 AC013258_10 (AC013258)
559	14636_s_at	thaumatin-like protein [Arabidopsis thaliana]
		dbj BAA86999.1 (AB035137) blue copper
560	19178_at	binding protein [Arabidopsis thaliana]
		emb CAB56039.1 (AJ133786) gigantea
561	17580_at	protein [Arabidopsis thaliana]
		gb AAD31062.1 AC007357_11 (AC007357)
		Strong similarity to gb X97864 cytochrome
		P450 from Arabidopsis thaliana and is a
		member of the PF 00067 Cytochrome P450
		family. ESTs gb N65665, gb T14112,
562	14248 at	gb T76255, gb T20906 and gb AI100027 come from this gene.
302	142,40_di	emb CAA72484.1 (Y11788) peroxidase
563	18946 at	ATP24a [Arabidopsis thaliana]
000	10, 10_4	emb CAA17138.1 (AL021889) putative
564	13009 i at	protein [Arabidopsis thaliana]
		gb AAA33709.1 (L16797) glutamate
565	18508_s_at	decarboxylase [Petunia x hybrida]
		emb CAB45330.1 (AL079344) nucleotide
		pyrophosphatase-like protein [Arabidopsis
566	12556_at	thaliana]
		gb AAB60774.1 (AC000375) ESTs
	•	gb U75592,gb T13956,gb T43869 come from
567	13115_at	from this gene. [Arabidopsis thaliana]
		gb AAB87120.1 (AC003000) unknown
568	15046_s_at	protein [Arabidopsis thaliana]
		gb AAC67339.2 (AC005499) putative
. 339	17202 a at	WRKY-type DNA binding protein [Arabidopsis thaliana]
. 339	17303_s_at	emb CAB45881.1 (AL080282) berberine
		bridge enzyme-like protein [Arabidopsis
569	18597_at	thaliana]
		emb CAB42588.1 (A71590) unnamed
570	13908_s_at	protein product [Arabidopsis thaliana]
		emb CAB41103.1 (AL049655) putative
571	14553_at	protein [Arabidopsis thaliana]
_		gb AAB64044.1 (AC002333) putative
572	18928_at	endochitinase [Arabidopsis thaliana]

		gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470,
573	12772_at	gb Z35182, gb H76373, gb Z34678 and gb Z35387> emb CAA18124.1 (AL022141) putative receptor protein kinase [Arabidopsis
574	16326_at	thaliana]
575	20479_i_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana] gb AAD28318.1 AC006436_9 (AC006436) putative receptor-like protein kinase
576	16393_s_at	[Arabidopsis thaliana] emb CAA67551.1 (X99097) peroxidase
577	17413_s_at	[Arabidopsis thaliana] gb AAA32835.1 (M96073)
578	14620_s_at	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
579	20480_s_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [Arabidopsis thaliana] gb AAC79625.1 (AC005770) unknown
580	15866_s_at	protein [Arabidopsis thaliana] emb[CAA21214.1] (AL031804) putative
581	19182_at	protein [Arabidopsis thaliana] gb AAC79625.1 (AC005770) unknown
582	18255_at	protein [Arabidopsis thaliana] emb CAA74639.1 (Y14251) glutathione S-
583	16054_s_at	transferase [Arabidopsis thaliana]
584	14672_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
585	20291_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
586	16053_i_at	emb CAA74639.1 (Y14251) glutathione S- transferase [Arabidopsis thaliana]
587	17083_s_at	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
588	12889_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
589	12642_at	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
		•

590	17487_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] gb AAA32835.1 (M96073)
591	14838_s_at	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
592	17104_s_at	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana] gb AAC79626.1 (AC005770) putative
593	19892_at	protease inhibitor [Arabidopsis thaliana]
		gb AAC31756.1 (U68017) heat shock
594	16105_s_at	transcription factor 4 [Arabidopsis thaliana]
	12072	gb AAC31756.1 (U68017) heat shock
664	13273_s_at	transcription factor 4 [Arabidopsis thaliana] gb AAC63850.1 (U73786) ACC synthase
595	12892 g at	[Arabidopsis thaliana]
		dbj BAA22096.1 (D85191) vegetative
596	15141 s at	storage protein [Arabidopsis thaliana]
		emb CAA55322.1 (X78585) Di21
597	18231_at	[Arabidopsis thaliana]
•		dbj BAA24440.1 (AB010407)
	•	phosphoglycerate dehydrogenase
598	15629_s_at	[Arabidopsis thaliana]
	•	emb CAA48579.1 (X68592) adenosine
	1.5050	nucleotide translocator [Arabidopsis
599	15978_at	thaliana]
600	00000	gb AAB82640.1 (AC002387) putative
600	20269_at	pectinesterase [Arabidopsis thaliana]
		gb AAC16958.1 (AC004165) putative
601	14614_at	glucosyltransferase [Arabidopsis thaliana]
		emb CAA07352.1 (AJ006960) peroxidase
602	17930_s_at	[Arabidopsis thaliana]
602	16050	gb AAC78532.1 (AC005662) calmodulin-
603	16952_s_at	like protein [Arabidopsis thaliana]
604	12930 s at	gb AAC49679.1 (U77347) lethal leaf-spot 1
004	12842_s_at	homolog [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
	12072_5_at	dbj BAA32418.1 (AB008103) ethylene
		responsive element binding factor 1
605	16063 s at	[Arabidopsis thaliana]
		dbj BAA32418.1 (AB008103) ethylene
		responsive element binding factor 1
228	12904_s_at	[Arabidopsis thaliana]
		dbj BAA32422.1 (AB008107) ethylene
		responsive element binding factor 5
606	12908_s_at	[Arabidopsis thaliana]
		•

		•	emb CAA17127.1 (AL021889) hypothetical
	607	15937 at	protein [Arabidopsis thaliana]
		_	gb AAB87109.1 (AC002391) putative
	608	17843 s at	cytochrome P450 [Arabidopsis thaliana]
			gb AAC95196.1 (AC004561) putative
			glutathione S-transferase [Arabidopsis
	609	18966_at	thaliana]
		_	gb AAC80599.1 (AC005106) T25N20.20
	610	20519_at	[Arabidopsis thaliana]
		_	gb AAC95189.1 (AC004561) putative
		•	glutathione S-transferase [Arabidopsis
	611	19641_at	thaliana]
			gb AAD32297.1 AC006533 21 (AC006533)
			putative glucosyltransferase [Arabidopsis
	612	17408_at	thaliana]
			gb AAC37474.1 (L42212) serine
	613	15646_s_at	acetyltransferase [Arabidopsis thaliana]
	•		gb AAC49988.1 (AF014960) multidrug
•			resistance-associated protein 2; AtMRP2
	614	14731_s_at	[Arabidopsis thaliana]
			emb CAB41928.1 (AL049751) short-chain
			alcohol dehydrogenase like protein
	615	20685_at	[Arabidopsis thaliana]
			emb CAA17559.1 (AL021961)
		16060	glucosyltransferase -like protein [Arabidopsis
	616	16968_at	thaliana]
			gb AAC78440.1 (U92460) 12-
	617	10050	oxophytodienoate reductase OPR1
	017	18253_s_at	[Arabidopsis thaliana] thaliana]
		•	gb AAD20156.1 (AC006282) putative
	618	15496 at	glucosyl transferase [Arabidopsis thaliana]
			emb CAA52771.1 (X74755) ATAF1
	619	19137 at	[Arabidopsis thaliana]
•		-	emb CAA18722.1 (AL022603) putative
			NADPH quinone oxidoreductase
	620	19132_s_at	[Arabidopsis thaliana]
			gb AAD22649.1 AC007138_13 (AC007138)
			predicted protein of unknown function
	621	13656_at	[Arabidopsis thaliana]
			gb AAB67854.1 (U61231) cytochrome P450
	622	17024_s_at	[Arabidopsis thaliana]
•			emb CAB69849.1 (AL137189) anthranilate
			N-benzoyltransferase-like protein
	623	14705_i_at	[Arabidopsis thaliana]
	624	17500 s at	emb CAB42906.1 (AL049862) calmodulin-
	U24	11200 2 at	like protein [Arabidopsis thaliana]

	•	
625	13217_s_at	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana] gb AAC49573.1 (U43412) 3'-
626	15196_s_at	phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana] emb CAA10955.1 (AJ222713) unnamed
627	18590 at	protein product [Arabidopsis thaliana]
628	14700 at	No hits found less than or equal to 1e-15.
020	14700_at	ivo mis round less than of equal to 1e-13.
		emb CAA69879.1 (Y08568) trehalose-6-
629	14665 r at	phosphate synthase [Arabidopsis thaliana]
		gb AAF18681.1 AF024504_11 (AF024504)
630	12630_at	unknown protein [Arabidopsis thaliana]
		gb AAC69851.1 (AF077955) branched-
		chain alpha keto-acid dehydrogenase E1
631	18953_at	alpha subunit [Arabidopsis thaliana]
		emb CAA16793.1 (AL021713) putative
632	13514_s_at	protein [Arabidopsis thaliana]
		gb AAF02787.1 AF195115_7 (AF195115)
		weak similarity to receptor protein kinase
633	12490_at	[Arabidopsis thaliana]
	•	emb CAB10404.1 (Z97340) phytochrome D
634	12246_s_at	[Arabidopsis thaliana]
		emb CAB37488.1 (AL035539) putative
635	20536_s_at	protein [Arabidopsis thaliana]
		gb AAC72122.1 (AC005278) F15K9.14
636	18409_at	[Arabidopsis thaliana]
		gb AAD21475.1 (AC007017) unknown
637	19387_at	protein [Arabidopsis thaliana]
		gb AAB70244.1 (AF016848) WD-40 repeat
638	16117_s_at	protein [Arabidopsis thaliana]
	100.4	emb CAA21480.1 (AL031986) putative
639	18347_s_at	protein [Arabidopsis thaliana]
	15000	emb CAB38906.1 (AL035708) putative
640	15880_at	protein [Arabidopsis thaliana]
		gb AAC49767.1 (AF003094) AP2 domain
((2	00451	containing protein RAP2.1 [Arabidopsis
667	20471_at	thaliana]
		gb AAB58497.1 (U81293) UDP-
		glucose: indole-3-acetate beta-D-
641	16603 s at	glucosyltransferase [Arabidopsis thaliana]
	- -	gb AAC13598.1 (AF058914) F21E10.13
642	12049 at	gene product [Arabidopsis thaliana]
	-	• • •
		gb AAC78704.1 (AF001308) predicted
643	12048_at	glycosyl transferase [Arabidopsis thaliana]

٠		gb AAB61117.1 (AC002062) ESTs
644	14064 at	gb N38288,gb T43486,gb AA395242 come from this gene. [Arabidopsis thaliana]
077	14004_at	gb AAC04492.1 (AC003974) unknown
645	12149 at	protein [Arabidopsis thaliana]
0.5	12147_at	emb CAA91183.1 (Z54356) HD-ZIP
646	14295 s at	[Arabidopsis thaliana]
0.0	1 1255_5_d_at	emb CAA16930.1 (AL021768) TMV
		resistance protein N-like [Arabidopsis
647	19034 at	thaliana]
		gb AAC27848.1 (AC004218) unknown
648	18624 at	protein [Arabidopsis thaliana]
	-	gb AAC97218.1 (AC005936) unknown
649	13181 at	protein [Arabidopsis thaliana]
	· -	gb AAD10163.1 (AC005917) putative Tal 1-
		like non-LTR retroelement protein
650	18866_at	[Arabidopsis thaliana]
		emb CAB44686.1 (AL078620) cytochrome
651	19502_at	P450-like protein [Arabidopsis thaliana]
		emb CAA19807.1 (AL031018) hypothetical
652	16301_s_at	protein [Arabidopsis thaliana]
		gb AAD32774.1 AC007661_11 (AC007661)
653	19411_at	unknown protein [Arabidopsis thaliana]
		emb CAA71588.1 (Y10556) CONSTANS
654	20300_g_at	[Arabidopsis thaliana]
		emb CAA71588.1 (Y10556) CONSTANS
655	20299_at	[Arabidopsis thaliana]
		gb AAB57688.1 (U96045) APS reductase
656	18696_s_at	[Arabidopsis thaliana]
	•	gb AAC26980.1 (AF016283) 5'-
657	16106	adenylylsulfate reductase [Arabidopsis
657	15186_s_at	thaliana] [Arabidopsis thaliana]
659	16609_s_at	AtERF2 (, BAA32419.1; AB008104)
660	12909_s_at	EREBP4-like, AtERF6 (, CAB10530.1;
661	16536 s at	Z97343)
001	10330_s_at	AtERF5 (, BAA32422.1; AB008107) put. C2H2 zinc finger transcription factor (,
301	15665_s_at	AAB80922.1; AF022658)
201	15005_3_at	Myb-like (, emb CAA20567.1 (AL031394)
668	13176 at	putative protein
670	15778 at	X98676.2 at
671	20619 at	AC005896.161 at
672	_	AL023094.197 s at
673		Y14208.2 s at
674		Z54136.1 at
675	-	X98673.2 s at emb CAB41311.1
	<u>-</u> <u></u> -	225007512 6 at omojoriD41511.11

	•	(AL049711) putative heat shock transcription
		factor [Arabidopsis thaliana]
676	19646_s_at	AC005819.55 s at
677	19855_at	AC007260.16_at
		AC007047.101_at-gb AAC49767.1
		(AF003094) AP2 domain containing protein
. 678	18475_at	RAP2.1 [Arabidopsis thaliana]
		unspecified t-factor gb AAC49775.1
		(AF003102) AP2 domain containing protein
679	13001_at	RAP2.9 [Arabidopsis thaliana]
		AC004665.101_at emb CAA67234.1
		(X98676) zinc finger protein [Arabidopsis
680	15219_at	thaliana]
		ATTHIRED4_s_at gb AAC98070.1
		(AC005896) putative C2H2-type zinc finger
681	13189_s_at	protein [Arabidopsis thaliana]
•		hsp70_s_at emb CAA18838.1 (AL023094)
		bZIP transcription factor ATB2 [Arabidopsis
684	13284_s_at	thaliana]

Table 10

	<u>Set</u>	Content	Number of unique genes
	2	7 or 8 not edm1 not	55 genes
5		rps2 not pad4 or NahG	•
	3	edm1 not rps2 not pad4 or NahG	44 genes
	4	rps2 not edm1 not pad4 or NahG	12 genes
	5	pad4 or NahG not edm1 not rps2	20 genes
	6	edm1 and rps2 not pad4 or NahG	17 genes
10	7	edm1 and pad4 or NahG not rps2	18 genes
	8	rps2 and pad4 or NahG not edm1	7 genes
	9	edm1 and rps2 and pad4 or NahG	11 genes
		Total	184 genes

15 For engineering resistance to pathogens whose growth is restricted by RPP7 or RPP8 dependent responses, such as oomycete pathogens, all 184 genes are potentially useful. The 128 genes in sets 2, 3, 4, and 6 are more likely to be useful, as pad4 and NahG do not interfere with resistance mediated by RPP7 or RPP8, so genes under their control should not be important for this type of resistance. The 99 genes in sets 2 and 3 are even more likely to be useful, because they not affected by rps2, and RPP7 and RPP8 trigger a different kind of resistance response than the one triggered by RPS2. The 44 genes in set 3 are

most likely to be useful, as they require *EDM1*, and *EDM1* is required for resistance.

Example 3

Transcriptional Responses Triggered by the RPP7 Defense Signaling Pathway

The RPP7 defense-signaling pathway (Figure 1) mediates resistance of
the Arabidopsis ecotype Col-0 against the Peronospora isolate Hiks1. In
contrast to conventional R-gene dependent defense signaling pathways in
Arabidopsis, such as the RPP4 pathway, the RPP7 pathway does not essentially
require salicylic acid accumulation or previously described defense regulators,
such as EDS1, NDR1, NPR1, PAD4 and others.

15

20

25

30 ·

A comparative analysis of transcriptional responses triggered by the RPP7 and RPP8 pathways was performed by gene expression profiling using Affymetrix oligonucleotide chips with roughly 8,200 different Arabidopsis genes, representing roughly a third of the genome. For the analysis, 2 week old seedlings were harvested 0, 12 or 48 hours post infection with a particular Peronospora isolate (Table 11). To examine RPP8 triggered transcriptional responses, a transgenic line Col-0 line carrying the RPP8 resistance gene from the Arabidopsis ecotype Landsberg erecta was infected with the Peronospora isolate Emco5. This interaction is incompatible. The interaction between Emco5 and Col-0 wild type plants served as compatible control. Responses triggered by the RPP7 pathway were analyzed using the incompatible interaction between the *Peronospora* isolate Hiks1 and Col-0 wild type plants, as well as compatible interactions between Hiks1 and the susceptible mutants rpp7, edm1, edm2 and edm3. To compare transcriptional responses triggered by the unconventional RPP7 and RPP8 pathways with those triggered by the more conventional RPP4 pathway, Col-0 wild type plants were infected with the Peronospora isolate Emoy2, which is avirulent on this ecotype. The interactions between Emoy2 and NahG plants, as well as the mutants pad4, ndr1 and npr1, served as compatible controls. Whereas pad4 and NahG plants are fully Emoy2 susceptible, ndr1 and npr1 plants are only partly compromised in Emoy2 resistance.

	Table 11 Plant	Peronospora isolate	Interaction type
	Col-0 (tgRPP8)	Emco5	incompatible ·
	Col-0 (rpp8)	Emco5	compatible
5	Col-0 (RPP7)	Hiksl	incompatible (2x)
	Col-0 (rpp7; 3929)	Hiks1	compatible
	Col-0 (edm1)	Hiks1	compatible
	Col-0 (edm2)	Hiks1	compatible
	Col-0 (edm3)	Hiks1	compatible
10	Col-0 (RPP4)	Emoy2	incompatible
	Col-0 (ndr-1-1)	Emoy2	intermediate
	Col-0 (pad4-1)	Emoy2	compatible
	Col-0 (NahG)	Emoy2	compatible
•	Col-0 (npr1-1)	Emoy2	intermediate
		•	•

15

35

Results

<u>Identification of Genes Potentially Required for RPP7 Mediated Peronospora</u> Resistance

Genes that play a role in the establishment of resistance may show 20 differences in their regulation or their expression levels between compatible and incompatible interactions (e.g., genes may show lower expression levels in "loss of Hiks-resistance mutants" as compared to Col-0 wild type plants). Thus, for each gene expression, ratios were calculated between Col-0 and each of the four Hiks response mutants (rpp7, edm1, edm2 or edm3) at each time point (0, 12 and 48 hours). The resulting data set, consisting of 12 expression ratios for each of the 8,775 probe sets on the chip, was first analyzed with "CLUSTER" and "TREE VIEW", two commonly used programs for chip and micro-array data analysis (Eisen et al., 1998). Genes that demonstrated only minor or less significant expression differences between Col-0 wild type and the mutants were 30 excluded from analysis. Genes that showed at least one 3-fold expression difference over all 12 calculated expression ratios were first considered for further analysis.

Table 12 shows 194 probe sets corresponding to genes having SEQ ID NOs: 301-494, the expression of which is altered after infection of *Arabidopsis* with *P. parasitica* (wild-type relative to *rpp7*, *edm1*, *edm2*, or *edm3*). Table 13

depicts about 100 genes (genes comprising SEQ ID NOs: 373, 385, 242, 369, 306, 232, 346, 367, 212, 221, 307, 322, 240, 313, 270, 252, 383, 245, 377, 212, 327, 297, 375, 263, 250, 282, 358, 257, 332, 560, 284, 220, 259, 355, 248, 281, 215, 236, 309, 386, 253, 333, 336, 296, 319, 414, 354, 353, 293, 278, 324, 339, 5 345, 225, 249, 264, 310, 228, 214, 311, 343, 298, 384, 277, 314, 372, 331, 338, 370, 352, 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 223, 348, 318, 251, 291, 289, 361, 285, 368, 342, 290, 351, 312, 286, 287, 273, 239, 326, 226, 227, 350, 280, 317, 359, 294, 279, 382, 356, 234, 218, 217, 347, 379, 401, 378, 363, 341, 208, 268, 267, 364, 266, 337, 269, 269, 325, 10 793 and 224) represented by 137 probe sets that show at least one 3-foldexpression difference in comparisons between wild type Arabidopsis Col-0 and mutants rrp7 or edm1, edm2, or edm3 infected with P. parasitica Hiks1 (i.e., probe sets that show at least one 3-fold difference in expression levels over all 12 expression ratios calculated between Col-0 wild type and each of the 4 Hiks response mutants at each of the time points). Genes were grouped together 15 according to similarities of their expression characteristics. Expression ratios were color encoded. Positive expression ratios were red and negative ratios were green. Black indicated no expression difference. Genes were represented in rows and infection treatments in columns. Red generally indicated that a gene at 20 a given time point is more strongly expressed in Col-0 wild type plants as compared to the respective mutant. One cluster represented genes that are upregulated in response to Hiks1 infection by the RPP7 pathway (Table 14; genes comprising SEQ ID NOs: 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 310, 228, 214, 347 and 225, which are 25 induced by Hiks1-infection and which are RPP7, EDM1, EDM2, EDM3dependent genes and so may encode regulators acting downstream of those genes; see probe sets 12505, 13217 and 12904 which correspond to genes that encode potential regulators of Hiks response pathway). Genes in this cluster represent genes that are more strongly expressed in Col-0 wild type than in all 30 four mutants predominantly at the 12 hour time-point in each comparison. The expression difference is less pronounced in the case of edm2 and edm3, but it is consistent over all four comparisons.

Table 12

Affy ID (Probe Set)	Reference No
12324_i_at	AC007212
12333_at	AJ286345
12345_at	L36246
12500 s_at	AF081067
12505 s at	AC005309
12608 i at	S70188
12642 at	AC006920
12746 i at	AL096882
12748 f at	AL096882
12761 s at	AC006577
12773 at	AC005727
12778 r at	AC006577
12798_at	AC003028
12802 at	AL022373
12842_s_at	
12843 s at	AC007195
12845 s at	AJ004810
12879 s at	U40856
12891 at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12905_s_at	AB008104
12908 s at	AB008107
12909_s_at	Z97343
12911_s_at	X84229
12916_s_at	AF021244
13138_at	AL096882
13177_at	AL049640
13178_at	U93215
13187_i_at	U35829
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13273_s_at	U68017
13284_s_at	AJ002551
13604_at	AC000104
13615_at	AC002332
13617_at	AC006592
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14028_at	AF075597
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309

14116	_
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14223_at	AL024486
14248 at	AC007357
14250 r at	AL050300
14295 s at	Z54356
14595 at	AL022580
14608 at	AC007357
14614 at	AC004165
14621 at	AC004747
14627 i at	X76609
14628 r at	X76609
14635 s at	AC005398
14636 s at	AC013258
14643 s at	AC006836
14672 s at	U18993
14675 s at	D85191
14691 at	AP002046
14704 s at	AC006067
14706 r at	AL137189
14709 at	AP002046
14711 s at	AF085279
14731 s at	AF014960
14784 at	AC005310
14951 at	AL049481
14965 at	AC002329
15057 at	AL035440
15085 s at	AL031018
15105_s_at	Z14987
15116 t at	AF121356
15116_f_at	AF121356
15125_f_at	D85190
15125_f_at 15141_s_at	D85190 D85191
15125_f_at 15141_s_at 15145_s_at	D85190 D85191 D64155
15125_f_at 15141_s_at 15145_s_at 15154_s_at	D85190 D85191 D64155 AL096860
15125_f_at 15141_s_at 15145_s_at 15154_s_at 15161_s_at	D85190 D85191 D64155 AL096860 U90522
15125_f_at 15141_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at	D85190 D85191 D64155 AL096860 U90522 U43489
15125_f_at 15141_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198
15125_f_at 15141_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at 15431_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198 AL030978
15125_f_at 15141_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at 15431_at 15496_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198 AL030978 AC006282
15125_f_at 15141_s_at 15145_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at 15431_at 15496_at 15523_s_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198 AL030978 AC006282 AL078637
15125_f_at 15141_s_at 15145_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at 15431_at 15496_at 15523_s_at 15593_s_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198 AL030978 AC006282 AL078637 U54561
15125_f_at 15141_s_at 15145_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at 15431_at 15496_at 15523_s_at 15593_s_at 15611_s_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198 AL030978 AC006282 AL078637 U54561 L22567
15125_f_at 15141_s_at 15145_s_at 15145_s_at 15154_s_at 15161_s_at 15178_s_at 15216_s_at 15431_at 15496_at 15523_s_at 15593_s_at	D85190 D85191 D64155 AL096860 U90522 U43489 U75198 AL030978 AC006282 AL078637 U54561

15000	10010407
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15950_at	AC006429
15954_at	U72155
15969_s_a	AJ133036
15978_at	X68592
15982_s_a	X98190
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153 s at	AC013258
16393 s at	AC006436
16412 s at	AL022603
16442 s at	AJ002551
16461 I at	AC004683
16462 s a	AC004683
16504 s at	Z97335
16510 at	AL034567
16514 at	AL035538
16536 s at	AB008107
16539 s at	Z97343
16569 s at	L23968
16578 s at	AL137080
16609 s at	AB008104
16620 s at	AF051338
16637 s at	Z97336
16817 s at	AL096882
16864 i at	AL133248
16951 i at	AC005662
16952 s at	AC005662
16981 s at	U35829
17014 s at	U05206
17033 s at	U83179
17055_s_at 17054 s at	AF134128
17073 s at	AC006836
17075_s_at	AF132212
	AF106087
17128_s_at 17187 at	AC005398
-	AF128396
17303_s_at	AC005499
17379_at	AC018721
17386_at	AC006264
17413_s_at	X99097

17499_s_at	AF107726
17500_s_at	AL049862
17544 s at	U40856
17549_s_a	L37126
17567 at	AL162751
17886 at	AC004484
17899 at	Z97339
17917 s at	AC004261
17961 at	AC007323
17963 at	AL049730
18003 at	AF188334
18064 r at	
18069 at	
18070 r at	
18216 at	AC012375
18217_g_at	AC012375
18235 at	AC000348
18252 at	AL096882
18255 at	AC005770
18272 at	AF002109
18533 at	AL021684
18556 at	AC006264
18590_at	AJ222713
18591 at	X74756
18607 s at	U78721
18635 at	AC004005
<u>-</u>	X75782
18706_s_a 18716 at	AC007396
18876 at	AF002109
18920 at	AC002338
18928 at	AC002338
19034 at	AL021768
19034_at	
19171_at	AC002335
	AB035137
19182_at 19251 at	AL031804
_	AL035538
19594_i_at	X98321
19640_at	AC004561
19977_at	AL049659
20017_at	AC004521
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20297_at	AC007153
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336

20555_s_a	AL080318
20585_s_at	AC005309
20641_at	X91919

Table 13

Probe Set	Description
12324_i_at	AC007212
12345_at	L36246
12505_s_at	AC005309
12608_i_at	S70188
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843 s at	AC007195
12845 s at	AJ004810
12879 s at	U40856
12891 at	U73786
12892 g at	U73786
12904 s at	AB008103
12908 s at	AB008107
12911_s_at	X84229
13138_at	AL096882
13178_at	U93215
13189_s_at	U35829
13198 i at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13604_at	AC000104
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309
14116_at	AF077407
14148 at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14248_at	AC007357
14250_r_at	AL050300
14595_at	AL022580
- ,	

14608_at	AC007357
14621 at	AC004747
14627 i at	X76609
14628 r at	X76609
14635 s at	AC005398
14636 s at	AC013258
14675 s at	D85191
14691 at	AP002046
14704 s at	AC006067
14709 at	AP002046
14711 s at	AF085279
14731 s at	AF014960
14784 at	AC005310
14951 at	AL049481
15057 at	AL035440
15105 s at	Z14987
15116 f at	AF121356
15110_1_at 15125 f at	D85190
15141 s at	D85190 D85191
15141_s_at	D63131
15154 s at	AL096860
· ·	U90522
	U43489
	AL030978
15431_at	
15496_at	AC006282
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15846_at	AC006067
15847_g_at	AC006067
15950_at	AC006429
15954_at	U72155
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16504_s_at	Z97335
16510_at	AL034567
16536_s_at	AB008107
16578_s_at	AL137080
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
17014_s_at	U05206
17033_s_at	U83179

WO 02/22675

17054 s at	AF134128
17123 s at	AF106087
17128 s at	AC005398
17187 at	AF128396
_	
17303_s_at	AC005499
17386_at	AC006264
17413_s_at	X99097
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17567 at	AL162751
17886 at	AC004484
17899 at	Z97339
17961 at	AC007323
17963 at	AL049730
18003 at	AF188334
18064 r at	AI 100554
	
·	A C010275
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590 at	AJ222713
18607_s at	U78721
18635 at	AC004005
18716 at	AC007396
18920 at	AC002338
18928 at	AC002338
19034 at	AL021768
_	
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19640_at	AC004561
19977_at	AL049659
20034_i_at	A71607
20201 at	AL078470
20227 s at	AB027252
20269 at	AC002387
20314 s at	AL096882
20335 s at	Y14208
20429 s at	Z97336
	
20585_s_at	AC005309
20641_at	X91919

Table 14

5

10

15

20

Probe Set	Description
12505_s_at	AC005309
12879_s_at	U40856
12904_s_at	AB008103
13189_s_at	U35829
13217_s_at	AL049862
14116_at	AF077407
14148_at	AF224762
14201_at	AL163972
14248_at	AC007357
14250_r_at	AL050300
14691_at	AP002046
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16063_s_at	AB008103
17500_s_at	AL049862
17544_s_at	U40856
18716_at	AC007396
19178_at	AB035137
19640_at	AC004561
20269_at	AC002387
_	

Thus, Hiks1 induced upregulation is compromised in all four tested "loss of Hiks1 resistance mutants" and there is a correlation between breakdown of resistance and deregulation of these genes. This may indicate that these genes play important roles in mediating Hiks1 resistance. Furthermore, these genes appear to act downstream of all four genetically defined RPP7 pathway components, RPP7, EDM1, EDM2 and EDM3. Some genes of this set may encode important regulators; whereas others may indicate metabolic processes required for Hiks1 resistance.

Seventy-eight genes (Table 15; genes comprising SEQ ID NOs:330, 292, 311, 243, 237, 302, 315, 283, 300, 372, 308, 335, 272, 305, 357, 213, 362, 331, 254, 384, 277, 343, 298, 349, 314, 265, 262, 258, 256, 303, 321, 304, 275, 274, 323, 238, 374, 241, 344, 244, 365, 261, 380, 371, 295, 255, 316, 233, 345, 225, 260, 229, 324, 301, 235, 340, 278, 320, 231, 319, 230, 354, 353, 293, 376, 247, 246, 366, 216, 214, 276, 299, 310, 334, 271, 381 and 228) that show the same, but less pronounced, expression characteristics were selected using relaxed selection criterion (at least one 2-fold expression difference over all 12 calculated expression ratios). With a lower cutoff criterion of at least one 2-fold-expression difference across all twelve expression ratios, this cluster is larger

than that shown in Table 14. Genes that are part of this less stringently defined cluster were included in further analyses so as to not exclude potentially important genes. Potential regulators in this cluster are listed in Table 16 (genes comprising SEQ ID NOs: 220, 323, 231, 319, 214, 301, 340, 243, 227, 321, 235, 315, 298, 314, 328, 344 and 349). Four different ERF transcription factors genes are upregulated by the *RPP7*-pathway. Genes encoding ERFs are known to be upregulated in response to several stress-related stimuli, such as wounding, pathogens or ethylene. Moreover, ERF transcription factors bind to GCC boxes, which are ethylene, wounding and pathogen-responsive *cis*-elements. This cluster also contains a gene encoding an ACC synthase, a component of the ethylene biosynthetic pathway. Therefore, ethylene may play a role in the Hiks response pathway.

Table 15

5

10

Probe Set	Description
12500_s_at	AF081067
12505_s_at	AC005309
12642_at	AC006920
12879_s_at	U40856
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12916_s_at	AF021244
13177_at	AL049640
13187_i_at	U35829
13189_s_at	U35829
13217_s_at	AL049862
13273_s_at	U68017
13284_s_at	AJ002551
13615_at	AC002332
13617_at	AC006592
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14201_at	AL163972
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14614_at	AC004165
14643_s_at	AC006836
14672_s_at	U18993

14691 at	AP002046
14704 s at	AC006067
14706 r at	AL137189
14709 at	AP002046
14711 s at	AF085279
15085_s_at	AL031018
15216 s at	U75198
15431 at	AL030978
15523_s_at	AL078637
15616_s_at	AL078637
15622_s_at	U43945
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15978_at	X68592
16063_s_at	AB008103
16105_s_at	U68017
16393_s_at	AB008103
16412_s_at	U68017
16442_s_at	AJ002551
	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16609_s_at	AB008104
16620_s_at	AF051338
16952_s_at	AC005662
16981_s_at	U35829
17073_s_at 17119 s at	AC006836 AF132212
_ _	AC018721
17379_at 17499 s at	AF107726
17499_s_at 17500 s at	AL049862
17544 s at	U40856
17917 s at	AC004261
18070 r at	AC004201
18216 at	AC012375
18217 g at	AC012375
18255 at	AC005770
18591 at	X74756
18716 at	AC007396
18876 at	AF002109
19178 at	AB035137
19182 at	AL031804
19640 at	AC004561
20017 at	AC004521
_	,

20269_at AC002387 20297_at AC007153 20429_s_at Z97336

Additionally, a gene encoding a lipoxygenase, a component of the jasmonic acid biosynthetic pathway, is upregulated. Other regulators potentially acting downstream of RPP7, EDM1, EDM2 and EDM3 include some putative

zinc finger transcription factors and protein kinases as well as two calmodulinlike proteins and a calcium binding protein, which may point to a role of calcium in the RPP7-pathway.

Table 16

- 10 <u>I. Transcriptional regulators:</u>
 - 1.) AtERF1 (12904 s at, BAA32418.1; AB008103)
 - 2.) AtERF2 (16609_s_at, BAA32419.1; AB008104)
 - 3.) EREBP4-like (12909_s_at, CAB10530.1; Z97343)
 - 4.) AtERF5 (16536_s_at, BAA32422.1; AB008107)
- 5.) putative CONSTANS-like zinc finger (12505_s_at, AAC63643.1; AC005309)
 - 6.) putative C2H2 zinc finger transcription factor (15665_s_at, AAB80922.1; AF022658)
 - 7.) putative C3H zinc finger protein (17379_at, AAF18728.1; AC018721)
- 20 8.) heat shock transcription factor 4 (13273_s_at, AAC31756.1; U68017)
 - 9.) SigA binding protein (14148 s at, AAF34713.1; AF224762)
 - II. Other signaling proteins
 - 10.) AtACS-6 (12892 g at, CAB51412.1, AL096882, 35400..37154)
 - 11.) lipoxygenase (16569 s at, AAA32749.1; L23968)
- 25 12.) growth factor like protein (13177_at, CAB40989.1; AL049640)
 - 13.) serine/threonine protein kinase (16412 s at, CAA18704.1; AL022603)
 - 14.) wall associated kinase 1 (15616_s_at, CAB08794.1; AJ009696)
 - 15.) putative receptor-like protein kinase (16393_s_at, AAD28318.1; AC006436)
- 30 16.) calmodulin-like (16951 i at, AAC78532.1; AC005662)
 - 17.) calmodulin-like (17500 s at; CAB42906.1; AL049862)
 - 18.) calcium binding protein (17917 s at, AAD12002.1; AC004261)

Twenty-six genes (genes comprising SEQ ID NOs: 300, 308, 272, 213, 362, 265, 374, 241, 261, 380, 310, 228, 233, 330, 311, 243, 237, 254, 230, 244, 365, 216, 316, 345, 225, 301, 278, 354, 353, 293, 335, 271 and 321, also shown in Table 15), represented by 33 probe sets, were found to be commonly upregulated in response to both *Peronospora* isolates, Hiks1 and Emco5, in an *RPP7*- or *RPP8*-dependent (and *EDM1*, *EDM2* and *EDM3*-dependent) manner (Table 17). Elevated expression of these genes may be required for resistance against both *Peronospora* isolates or against *Peronospora parasitica* in general. Among these 26 genes are those encoding ERF1, putative zinc finger

transcription factors, two proteins potentially involved in calcium signaling, a lipoxygenase, and a cysteine rich antifungal protein.

Table 17

5

15

26 Peronospora (Hiks1 and Emco5) induced RPP8, RPP7, EDM1,2,3-dependent genes

Transcription factors

AtERF1

Putative salt-tolerance zinc finger transcription factor (18217 g at)

20 (ZFPI) hypothetical Cys-3-His zinc finger protein Putative C2H2 zinc finger transcription factor Heat shock transcription factor 4

Other potential proteins

Calmodulin-like protein
 Similarity to centrin, Marsilea vestita contains EF-hand calcium-binding domain
 (15431_at)
 Lipoxygenase

30 Others

heat shock protein 70 putative steroid sulfotransferase putative glucosyltransferase

 phosphoglycerate dehydrogenase ATAF2
 OPDA-reductase homolog coronatine-induced protein I thioredoxin h

40 IAA-amino acid hydrolase

tryptophan synthase alpha chain similar to xyloglucan fucosyltransferase (12642_at)
Pad3 (Cytochrome P450)
putative pectinesterase
AIG1
putative glutathione S-transferase
adenosine nucleotide translocator
contains similarity to sugar transporters
CYSTEINE-RICH ANTIFUNGAL
PROTEIN 1 PRECURSOR (AFP1)
(18716 at)

Thirteen of these 26 genes (genes comprising SEQ ID NOs: 308, 300, 272, 362, 265, 242, 261, 380, 228, 243, 254, 216 and 225, Peronospora (Hiks1, Emco5 and Emoy2) induced and RPP4, RPP8 and RPP7 dependent) were also found to be more strongly expressed during the incompatible interaction between the Peronospora isolate Emoy2 and Col-0 plants as compared to Emoy2 infections of the compatible or intermediate type (see Table 18). These 13 genes may play an important role in defense against Peronospora parasitica in general. Among these genes is PAD3, which was previously demonstrated to be required for pathogen-induced phytoalexin production. Strikingly, Hiks1 resistance is partially compromised in the pad1-1/pad3-1 double mutant, whereas Emoy2 resistance is reduced in the pad3-1 single mutant (Glazebrook et al. 1997).

Table 18

-AIG1 (12879 s at)

```
13 Peronospora (Hiks1, Emco5 and Emoy2) induced
15
                RRP4-pathway, RPP7-pathway, and RPP8-dependent genes
     -adenosine nucleotide translocator (15978 at)
     -phosphoglycerate dehydrogenase (15629 s at)
20
      -tryptophan synthase alpha chain (14672 s at)
     -ATAF2 (18591 at)
25
     -putative glucosyltransferase (14614 at)
      -calmodulin-like protein (13217 s at)
     -pad3 (cytochrome P450)(14248 at)
30
     -putative pectinesterase (20269 at)
     -ethylene responsive element binding factor 1 (12904 s at)
35
     -heat shock transcription factor 4 (13273 s at)
     -sugar transporter-like (14116 at)
     -similar to xyloglucan fucosyltransferase (12642 at)
40
```

Identification of promoter motifs common to RPP7 and RPP8 controlled genes

Sequence motifs conserved in the promoters of genes co-regulated by the RPP7 or RPP8 pathways may lead to information about the types of transcription factors controlling expression of these genes and may serve as starting points for isolating and/or cloning of such factors. Sub-categorization of RPP7-

upregulated genes by K-means clustering, based on the absolute expression levels of the genes, revealed the existence of only a few basic expression profiles. K-means clustering into five gene sets gave the most consistent and tight clusters. For each of the five gene sets (Table 19), the expression changes in two repetitions of the Col-0 wild type/Hiks1 interaction are shown as well as in the rpp7 mutant and edm1, edm2 and edm3.

The first set comprises genes (genes comprising SEQ ID NOs: 292, 302, 315, 300, 308, 213, 265, 374, 241, 344, 261, 299, 365 and 276) that show early and transient upregulation. The genes peak at 12 hours and return to their ground-states at approximately the 48 hours post infection. Genes of the second set (genes comprising SEQ ID NOs: 267, 305, 357, 362, 380, 310, 228, 295, 233, 329, 312, 243, 237, 283, 372, 254, 314, 323, 216, 260, 229 and 235) are also rapidly upregulated, but show a less pronounced or no decline after the peak. In both sets, the response is weaker in the mutants. Only a few genes in the first set respond almost as strongly in *edm2* and *edm3* plants as in wild type plants.

- Genes of the third (genes comprising SEQ ID NOs: 258, 256, 303, 304, 275, 244, 316, 354 and 225) and fifth (genes comprising SEQ ID NOs: 330, 384, 277, 343, 298, 349, 262, 274, 238 and 301) set show an almost linear increase of transcript level in wild type. In the mutants, this increase is delayed and in some cases less steep. In the fourth set (genes comprising SEQ ID NOs: 432, 347,
- 370, 412, 323, 411, 322, 449, 448, 385, 471, and 339) the expression levels rise in the first repetition of the Col-0 wild type/Hiks interaction, but respond very little in the second one. In *edm3*, the transcript levels drop from a high ground state. The probe sets and genes corresponding to each of these K-means cluster sets are shown in Table 19.

30

5

10

15

20

Table 19

K-means set 1	Description	K-means set2	Description
12500_s_at	AF081067	12642_at	AC006920
13217_s_at	AL049862	12904_s_at	AB008103
14248_at	AC007357	12905_s_at	AB008104

14614_at	AC004165	12916_s_at	AF021244
14706_r_at	AL137189	13177_at	AL049640
15216_s_at	U75198	13187_i_at	U35829
15622_s_at	U43945	13273_s_at	U68017
15629_s_at	AB010407	14116_at	AF077407
15680_s_at	D42061	14223_at	AL024486
15978_at	X68592	14672_s_at	X76609
16412_s_at	U68017	15085_s_at	AL031018
17500_s_at	AL049862	15523 s at	AL078637
18070 r at		15866 s at	AC005770
18716_at	AC007396	16063 s at	AB008103
19640_at	AC004561	16105 s at	AL049730
	•	16393 s at	AC006436
		16609 s at	AB008104
	•	16952 s at	AC005662
K-means set 3	Description	18255 at	AC005770
12879 s at	U40856	18591 at	X74756
13284 s at	AJ002551	19182 at	AL031804
14148 at	AF224762	20269 at	AC002387
14201 at	AC068667	_	
14704 s at	AC006067		
15846 at	AC006067	K-means set 5	Description
15847 g at	AC006067	13189 s at	U35829
16442 s at	AJ002551	14250 r at	AL050300
17544 s at	U40856	14691 at	AP002046
_`-		14709 at	AP002046
K-means set4	Description	15616 s at	AJ009696
12908 s at	AB008107	15665 s at	AF022658
	Z97343	16981 s at	U35829
13617 at		17499 s at	AF107726
14141_at	AC011437	17917 s at	AC004261
14711 s at	AF085279	20429 s at	Z97336
15431_at	AL030978		
16536 s at	AB008107		•
16539 s at	Z97343	•	
17379 at	AC018721		
18216 at	AC012375		•
18217 g at	AC012375		
20017 at	AC004521		
		• •	

Recently, the plant specific family of WRKY transcription factors has been implicated in the regulation of defense-associated genes. Promoters of genes upregulated during systemic acquired resistance were found to be strongly enriched in potential WRKY binding sites. WRKY factors comprise a large family of 72 different members in *Arabidopsis*. Generally these factors appear to bind to sequence motifs containing the core T G A C (W box). It has not yet

5

been determined whether individual WRKY family members differ in their preferences for distinct W box variations. However, it is probable that a given WRKY protein has a binding preference for a certain variation of the W box motif.

5 Using the program AlignACE, three variations of potential WRKY binding sites were found to be conserved in sub-sets of RPP7 controlled genes. Two of these motifs are highly enriched in promoters of genes from K-means cluster 3, representing genes that show a linear increase in transcript level after Peronospora infection (Table 20; genes comprising SEQ ID NOs: 384, 298, 349, 10 262 and 238 for W box I and genes comprising SEQ ID NOs: 384, 349, 262, 238 and 301 for W box II). These motifs are also present in promoters of K-means cluster 5, which represents a similar expression profile. Focusing on sustained up-regulated genes, that show a particularly pronounced expression difference between Col-0 wild type plants and the Hiks1 response mutants, a third variation 15 of potential WRKY binding sites was found to be significantly enriched (Table 21; genes comprising SEQ ID NOs: 397, 371, 238, 262, 256, 275, 254, 214 and 225). In all three cases, sequence conservation clearly exceeds the core motif of WRKY binding sites that appears to be recognized by all members of this family. These additionally conserved positions may confer specificity for certain WRKY family members. They may provide a highly defined binding site 20 preferentially recognized by a distinct WRKY factor or may serve as binding sites for another transcription factor binding closely adjacent to and specifically interacting with a distinct WRKY factor. In any case, the high conservation of extended potential WRKY binding motifs strongly suggests that specific 25 members of this family participate in the regulation of certain sub-sets of RPP7controlled genes.

Table 20

```
W box I MAP Score: 8.98114

GTCATCTTTTAATCTCTGG 0 638 1

GTCATCTTTTAATCGCCGG 0 932 1

GCCTTTGCTTATTTATAGG 0 1036 1

GTCATTTGTTACAAAGAGG 1 318 1

GTCATTGATCATAAACTGT 1 389 0

GCCACTGCTGAATTGTCGG 1 494 1

GTCCATTGTCAATAAATGG 2 689 1

GTCCATTGTAAAATGG 2 949 1
```

```
GTCATCTTTTAATCTCTGT 3 475 0
              GTCACGTATGAATGGAAGG 4 73 1
              GTCAACGTTTAGTTCATGT 4 226 0
              GTCAAGTTTTAAATTGTGG 4 352 1
 5
              GTCAACGTTTAGTTCATGT 4 401 0
                     * * * *
              GTCANNTNTNANTNNNNGG
                     G
                           A
    Expected frequency by chance: 0.02/1kb
10
    Observed frequency:
                                   1.2/1kb
    Enrichment: ~60 fold
    W box II MAP Score: 15.2966
              ATTAAAAGATGAC 0 638 0
              ATTAAAAGATGAC 0 932 0
15
              ATTAAATGCTGTC 2 752 0
              ATTAAATGCTGTC 2 1011 0
              AGCAAAAGCTGAC 2 1092 1
              ATTAAAAGATGAC 3 481 1
              ATCAAAAGTTGTC 3 829 1
20
              ACTAAACGTTGAC 4 232 1
              ACTAAACGTTGAC 4 407 1
              ACTAAAAAGTGAC 5 755 1
               * **** * ***
25
    W II
              ANTAAANGNTGAC
                C
                     A
                          T
              CCNNNNANTNANCNNTGAC
    W I:
30
    Expected frequency by chance: 0.04/1kb
    Observed frequency:
                                   1.35/1kb
    Enrichment: ~30 fold
    Table 21
    ATAGGTGGTCAAGT 1 106 0
35
    AATTGTGGTCATTT 1 823 0
    ACTTGTGGTCAATT 2 804 0
    AAAAGGGGTCATTT 2 970 1
    ATATGTCGTCTCTT 2 994 0
    AGTTGTGGTCTACC 3 502 0
40
    AAAAGTTGTCAATT 3 732 1
    AGACGTCGTAATTT 4 400 0
    ACGTGGCGTCATAT 5 179 0
    ATGTGGCGTCTCCT 6 249 1
    AGTTGGTGTCACGT 6 925 1
45
    ATTCGTGGTCAACT 7 582 1
    ATATGTCGTCACTT 7 875 1
       *****
    ANNNGTNGTCANNT
         G
```

50

expected: 0.05/1kb; in random set: 0/1kb; this set: 1/1kb; enrichment: 10-20 fold;

5

10

Novel, conserved promoter motifs were also found. Genes of K-means set 1, which are early and transient *RPP7*-pathway specific genes, share two similar highly conserved promoter motifs, G G T/C C C A (SEQ ID NO:714; genes comprising SEQ ID NOs: 302, 315, 308, 265, 374, 241, 261, 299 and 365) and G N C C A A A (SEQ ID NO:715; genes comprising SEQ ID NOs: 292, 302, 308, 265, 374, 241, 261, 299, 365 and 276) (Table 22). Both motifs are almost perfectly conserved and are represented in nearly all promoters of this gene set. They are compact six- or seven-mers, which is typical for transcription factor binding sites. For the second motif, the permutations G A C C A A A and G T C C A A A are strongly represented. These permutations may constitute the preferred binding site of a so far unknown transcription factor.

Table 22

Two related novel motifs are highly enriched in all 11 promoters of K-means set1

```
20
```

15

```
GGTCCA 1 232 0
    GGCCCA 1 289 1
    GGTCCA 1 597 1
25
    GGTCCA 2 517 0
    GGTCCA 3 211 1
    GGCCCA 3 360 1
    GGTCCA 4 597 1
    GGCCCA 4 681 1
30
    GGTCCA 5 352 0
    GGTCCA 5 1060 1
    GGTCCA 6 358 0
    GGCCCA 7 776 0
    GGCCCA 7 816 0
35
    GGTCCA 8 285 0
    GGTCCA 9 888 1
    *****
    GGTCCA
           C
    Expected frequency by chance: 0.22/1kb
    Observed frequency:
                                   1.2/1kb
    Enrichment: 5.4 fold
    GCCCAAA 0 601 1
    GTCCAAA 10 1186 1
    GTCCAAA 9 562 1
```

```
GACCAAA 8 640 0
    GCCCAAA 7 774 0
    GTCCAAA 7 717 1
    GTCCAAA 6 712 1
5
    GACCAAA 5 970 1
    GTCCAAA 5 350 0
    GACCAAA 4 1164 1
    GACCAAA 4 1072 1
    GTCCAAA 4 784 0
10
    GACCAAA 4 714 0
    GGCCAAA 4 698 0
    GCCCAAA 3 361 1
    GACCAAA 1 920 0
    GTCCAAA 1 230 0
15
    • * * * * *
    GNCCAAA
    Expected frequency by chance: 0.32/1kb
    Observed frequency:
                                    1.3/1kb
    Enrichment: 4 fold
```

20

25

30

35

Following a similar approach as for the Hiks1-induced RPP7 pathway controlled genes, a cluster of early and transiently Emco5-induced RPP8dependent genes were defined (Table 23). In Col-0-RPP8 plants these genes (genes comprising SEQ ID NOs: 364, 341, 288, 378, 363, 379 and 219) show a very pronounced upregulation 12 hours post Emco5 infection, after which they return to expression ground states. Using AlignACE, two different motifs (see Example 2) were found to be strongly enriched in the promoters of this cluster. The first motif strongly resembles the type I consensus binding site of Myb transcription factors. This motif is also almost identical to a recently identified cis-element conferring rapid elicitor responsive gene expression in parley cell culture (Kirsch et al., 2001). Interestingly, a gene encoding a Myb-like transcription factor (highlighted in yellow) is co-regulated with other genes of this cluster. The Myb-like transcription factor gene is the only gene of this cluster that does not contain this conserved motif in its promoter. This MYBlike factor could be a regulator of this cluster. The second motif does not resemble any known stress responsive plant cis element or transcription factor binding site. However, the second motif was found to be strongly represented in promoters from other defense related genes, such as SAR genes. As is typical of many transcription factor binding sites, certain permutations of its consensus

sequence may constitute palindromes. This motif was also found to be conserved by the program MEME.

Table 23

5 Glutathinone-conjugate transporter AtMRP4 putative GST putative cytochrome P450 (AC002340) PAD3 (similar to cytochrome P450) CTF2B (similarity to proteins involved in

10 Hydroxylation and oxidation of aromatic rings) Ribonuclease RNS1

Putative Myb-like protein

AlignACE Motif 1: CAACTTTGAC

AA TT

15 type I Myb binding site:

CAACTG T G

Frequency by chance: 0.05/1kb

Observed frequency in control cluster: 0.13/1kb Observed frequency in this cluster: 1.10/1kb

20 Observed frequency in th AlignACE Motif2:

TTGGGNCNAA

A A

MEME motif:

GTCTNTTGGGNCAAAA

TT AGC

25 Frequency by chance: 0.13/1kb

Observed frequency in control cluster: 0/1kb Observed frequency in this cluster: 1.2/1kb

Different types of transcription factors may participate in the control of 30 distinct RPP7-pathway dependent expression profiles. Promoters of genes showing a linear sustained increase of transcript are enriched in different variations of WRKY binding sites. However, no WRKY-pathway gene was found to be upregulated by the RPP7 pathway. Therefore, WRKY factors involved in RPP7 mediated up-regulation of K-means cluster 3 and 5 genes may 35 already be pre-formed when the pathogen signal is perceived. However, only 21 WRKY genes out of 72 members of this family in Arabidopsis are represented on the oligonucleotide chip. Upregulated WRKY factors participating in RPP7 mediated gene regulation may not be present on the chip. A novel type of transcription factor may be involved in regulation of early and transient RPP7-40 controlled genes (K-means cluster 1). Promoter stretches containing this motif may be used in yeast one hybrid screenings for novel factors. In addition, transgenic plants carrying appropriate promoter-reporter constructs could be used

as a basis for mutant screenings with the aim of identifying regulators acting on this motif.

A Myb-like transcription factor appears to be involved in the regulation of early and transient *RPP8*-controlled genes. A gene showing a similar pattern of regulation may encode a candidate factor controlling this cluster. The potential role of this factor in regulating *RPP8*-controlled genes may be examined using T-DNA insertion mutants.

Potential constitutive effects of the RPP7-pathway

In order to focus on genes showing multiple expression differences between Col-0 wild type plants and Hiks response mutants, all genes that showed at least four 1.8-fold expression differences across all comparisons were selected. The resulting clustergram contains the majority of RPP7 pathwaydependent Hiks1-induced genes. Two more clusters of genes behaving consistently in all four tested Hiks1-response mutants were found. The first cluster comprises genes that show at all tested time points (including the 0 hpi time point) elevated transcript levels in Col-0 wild type plants as compared to all four mutants (Table 24; genes comprising SEQ ID NOs: 364, 288, 378, 363, 379, 219, 399, 389 and 390). In most cases, expression levels are not affected by Hiks1 infection. These elevated expression levels may be directed by constitutive (non Hiks1-triggered) signal flow via the RPP7 pathway. This signal flow is disrupted in the rpp7, edm1, edm2 and edm3 mutants. Constitutive expression of these genes may be required for effective disease resistance and may be a prerequisite for induction of subsequent defense responses. A HD-ZIP transcription factor, which is included in this cluster, may act as a pre-formed regulator controlling genes responding to Hiks1-recognition. Its potential role in regulating RPP7 pathway-dependent genes may be examined using T-DNA insertion mutants.

Table 24

5

10

15

20

25

30

The RPP7 pathway constitutively activates a cluster of genes including a HD-ZIP transcription factor

PROBE SET	DESCRIPTION
14965_at	AC002329
18635 at	AC004005
14295 s at	Z54356
17386 at	AC006264

15145 s at	D64155
20201_at	AL078470
18607_s_at	U78721
20227 s at	AC007153
12761 s at	AC006577
20555 s a	AL080318

Genes of the second cluster show the opposite behavior (Table 25). Their transcript levels are elevated in all four Hiks1 response mutants as compared to Col-0 wild type plants. Hiks1-infection does also not affect their expression levels. Surprisingly, this cluster contains six genes encoding peroxidases. Since peroxidases are believed to play roles in conferring disease resistance, the biological significance of this phenomenon is obscure. Perhaps the mutant plants "realize" disruption of the RPP7-defense pathway and compensate for their reduced defense capacity by constitutively up-regulating some defense mechanisms. Alternatively, elevated expression of these peroxidases may be advantageous for invading Peronospora hyphae. Therefore, expression of these genes could be constitutively reduced by the RPP7 pathway.

Table 25

5

Probe Set	Description
15982_s_at	X98190
15954_at	U72155
12333_at	AJ286345
19594_i_at	X98321
15969_s_at	AJ133036
16462_s_at	.AC004683
16461_i_at	AC004683
12324_i_at	AC007212
12778_r_at	AC006577
16514_at	AL035538
17549_s_at	L37126
14028 at	AF075597
17054_s_at	AF134128

15

20

Predictions about RPP7-pathway hierarchy

Clustering of the Hiks1-infection data in the "treatment" dimension, instead of the "gene" dimension, revealed that at all three infection time points, gene expression profiles of the rpp7 mutant resemble most those of the edm1 mutant. Similarly, expression profiles of the edm2 mutant resemble those of the

edm3 mutant. This may indicate that RPP7 and EDM1 closely act together at a certain level in the RPP7 signalling cascade, whereas EDM2 and EDM3 may act closely together at a different level of the pathway. Close interaction of RPP7 and EDM1 is also suggested by a T-DNA tagged rpp7 mutant that phenotypically resembles the edm1 mutant. In contrast to rpp7, edm2 and edm3, which appear only to be compromised in resistance against the Peronospora isolate Hiks1, edm1 is also compromised in resistance to other Peronospora isolates that are avirulent on Col-0 plants. Like edm1, the putatively T-DNA tagged rpp7 mutant is also susceptible to a variety of normally Col-0 incompatible Peronospora isolates. This observation may indicate that the EDM1 protein requires a portion of the RPP7 protein for proper function, which is disrupted in the T-DNA tagged rpp7 mutant. Assuming that RPP7, which appears to constitute an NBS-LRR receptor, acts at the top of the Hiks1 recognition pathway hierarchy, EDM1 could act at a high level as well and EDM2 and EDM3 may act more downstream in the cascade.

Table 26

20

15

5

10

Hiks1
↑↓

RPP7 / EDM1
↓

EDM2 / EDM3
↓

RESISTANCE

25

Table 27 shows the plant and fungal orthologs of the *Arabidopsis* sequences identified herein.

Table 27

Query= AIG1 s at 12879 s at /id source genbank/description gb|aac49282.1| (u40856) aig1 [arabidopsis thaliana] /blast_score 1.00e-150

5 (1381 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10 Searching.....done

> Score Ε

Sequences producing significant alignments:

(bits) Value

15 gb[U64925]NTU64925 Nicotiana tabacum geranylgeranylated protein ... 260 1e-68 emb|AW625701|AW625701 EST319608 tomato radicle, 5 d post-imbibit... 228 6e-59 emb|AW720227|AW720227 LjNEST17c4r Lotus japonicus nodule library... 219 4e-56 emb|AW220184|AW220184 EST302667 tomato root during/after fruit s... 208 7e-53 emb[AI774580]AI774580 EST255680 tomato resistant, Cornell Lycope... 173 2e-42 20 -emb|AW685484|AW685484 NF030E02NR1F1000 Nodulated root Medicago t... 171 2e-41 emb|AI443867|AI443867 sa44d09.yl Gm-c1004 Glycine max cDNA clone... 170 3e-41 emb|AW397252|AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone... 168 1e-40 emb|AW033368|AW033368 EST276939 tomato callus, TAMU Lycopersicon... 162 5e-39 emb|AV417858|AV417858 AV417858 Lotus japonicus young plants (two... 153 4e-36 emblAI780050|AI780050 EST260929 tomato susceptible, Cornell Lyco... 138 9e-32 25 emb|AW039095|AW039095 EST281068 tomato mixed elicitor, BTI Lycop... 111 2e-23 emb|AI780139|AI780139 EST261018 tomato susceptible, Cornell Lyco... 86 7e-16 emb|AW164180|AW164180 Ljimpest21-672-c8 Ljimp Lambda HybriZap ... 84 2e-15 emb|AI781596|AI781596 EST262475 tomato susceptible, Cornell Lyco... 75 1e-12 30 emb|AW774764|AW774764 EST333915 KV3 Medicago truncatula cDNA clo... 62 7e-09 emb|AW348781|AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ... 54 2e-06 emblAI491210IAI491210 EST241919 tomato shoot, Cornell Lycopersic... 29 0.010 emb|AW651526|AW651526 EST329980 tomato germinating seedlings, TA... 29 0.011 emb|AW220594|AW220594 EST296979 tomato fruit mature green, TAMU ... 29 0.011 35 emb|AW926585|AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis... 29 0.025 emb|AW032321|AW032321 EST275775 tomato callus, TAMU Lycopersicon... 28 0.026 emb|AW736598|AW736598 EST333090 KV3 Medicago truncatula cDNA clo... 37 0.39 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 37 0.39 emb|AW713727|AW713727 h1f12ne.fl Neurospora crassa evening cDNA ... 35 1.0 40 emb|AW711542|AW711542 f3g07ne.f1 Neurospora crassa evening cDNA ... 35 1.0 emb|AB009972|AB009972 Aspergillus oryzae gene for beta-1,4-xylos... 35 1.0 emb|AW713709|AW713709 h1e09ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb|AW712721|AW712721 g3a07ne.f1 Neurospora crassa evening cDNA ... 35 1.0 emb|AW709185|AW709185 d3e02ne.f1 Neurospora crassa evening cDNA ... 35 1.0 45 emb[Y09354|SPABC1 S.pombe ABC1 gene. emb|Z99262|SPAC9E9 S.pombe chromosome I cosmid c9E9. 35 1.4 emb|AJ225108|STA225108 Solanum tuberosum (cultivar Bintje) mitoc... 35 1.4 emb|AW933326|AW933326 EST359169 tomato fruit mature green, TAMU ... 26 1.5 emb|Z25870|CACDC10G C.albicans CDC10 gene for cell division cycl... 31 1.5 50 emb[AC008368]AC008368 Trypanosoma brucei chromosome II clone RPC... 35 1.9 emb|AQ942780|AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso... 35 1.9 emb|AQ953508|AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom... 35 1.9 emb|AC009463|AC009463 Trypanosoma brucei chromosome II clone RPC... 35 1.9 emb|AQ950237|AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso... 35 1.9 55 emblAQ643883|AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano... 35 1.9 emblAQ948491|AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom... 35 1.9 emb|AW727289|AW727289 GA_Ea0011H24 Gossypium arboreum 7-10 dpa ... 35 1.9 emb|AW729536|AW729536 GA __Ea0025E24 Gossypium arboreum 7-10 dpa ... 35 1.9 gb|L36856|PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR... 28 2.1

emb|Z28341|PSCLOEP P.sativum (miranda) mRNA for chloroplast oute... 28 2.1

	emb AW776020 AW776020 EST335085 DSIL Medicago truncatula cDNA cl 28 2.2 emb AW685649 AW685649 NF032G04NR1F1000 Nodulated root Medicago truncatula cDNA cl 28 2.2 emb AW690755 AW690755 NF037H10ST1F1000 Developing stem Medicago 28 2.2
	emb AW256896 AW256896 EST305033 KV2 Medicago truncatula cDNA clo : 28 2.3
5	emb AV422565 AV422565 AV422565 Lotus japonicus young plants (two 28 2.3
	emb AW832303 AW832303 sm07c04.yl Gm-c1027 Glycine max cDNA clone 27 2.3
	emb AL136538 SPAC30 S.pombe chromosome I cosmid c30. 34 2.6
	emb AI724721 AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale 34 2.6
• •	emb AW256609 AW256609 EST304746 KV2 Medicago truncatula cDNA clo 34 2.6
10	emb AI775696 AI775696 EST256796 tomato resistant, Cornell Lycope 28 3.1
	emb Z71682 SCYNR067C S.cerevisiae chromosome XIV reading frame O 34 3.6
	emb AI776315 AI776315 EST257415 tomato resistant, Cornell Lycope 34 3.6
	emb AF230371 AF230371 Lycopersicon esculentum allene oxide synth 34 3.6
1.5	emb AA741645 AA741645 LmLv39p3/255A Leishmania major promastigot 34 3.6
15	gb U08843 PPU08843 Porphyra purpurea putative polysaccharide bin 34 3.6
	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK 29 4.7
	emb AQ399149 AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P 33 5.0
	emb AW615911 AW615911 EST325409 tomato flower buds 0-3 mm, Corne 33 5.0
20	emb AW035453 AW035453 EST281191 tomato callus, TAMU Lycopersicon 33 5.0
20	emb AF051695 AF051695 Trypanosoma cruzi sialidase homolog (P85.1 33 5.0 -emb Z37538 L-TGRR4-L-tarentolae mRNA encoding putative NADH subun 28 5.5
	-emb Z37538 LTGRR4-Ltarentolae mRNA encoding putative NADH subun 28 5.5 emb X85021 SCXLTORFS S.cerevisiae DNA from left arm of chromosom 33 6.8
	gb L25088 YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi 33 6.8
	emb AQ443826 AQ443826 GSSTc01287 Trypanosoma cruzi random genomi 33 6.8
25	emb AQ502942 AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc 33 6.8
	emb Z85962 MSZ85962 Musa sp. DNA for sequence tagged microsatell 33 6.8
	emb Z49377 SCYJL102W S.cerevisiae chromosome X reading frame ORF 33 6.8
	emb AW224537 AW224537 EST302980 tomato root, plants pre-anthesis 31 7.5
	emb AW257183 AW257183 EST305320 KV2 Medicago truncatula cDNA clo 32 9.4
30	emb AQ642922 AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos 32 9.4
	emb AW738509 AW738509 EST339936 tomato flower buds, anthesis, Co 32 9.4
	emb AW217351 AW217351 EST296174 tomato flower buds 0-3 mm, Corne 32 9.4
	emb AW219255 AW219255 EST301737 tomato root during/after fruit s 32 9.4
٠.	emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC 32 9.4
35	emb AW684118 AW684118 NF012F02NR1F1000 Nodulated root Medicago t 32 9.4
	emb AW622239 AW622239 EST313037 tomato root during/after fruit s 32 9.4
	emb AQ651543 AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom 32 9.4
	emb[Y11565]NC11565 N.crassa acu-15 gene. 32 9.4
40	emb AW775944 AW775944 EST335009 DSIL Medicago truncatula cDNA cl 32 9.4
40	emb AB014493 AB014493 Gibberella zeae gene for reductase, partia 32 9.4
	Query= ASA1_s_at 12889_s_at /id_source genbank /description
	gb aaa32738.1 (m92353) anthranilate synthase alpha subunit
45	[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
•••	/gb_link /ncgi
	(1788 letters)
	(1700 1011010)
	Database: plantfungal
50	661,018 sequences, 426,114,510 total letters
	,
	Searchingdone
	Score E
55	Sequences producing significant alignments: (bits) Value
	gb L34344 RTAANTSYNB Ruta graveolens anthranilate synthase alpha 772 0.0
	gb L34343 RTAANTSYNA Ruta graveolens anthranilate synthase alpha 467 0.0
60	emb AF079168 AF079168 Nicotiana tabacum feedback-insensitive ant 365 0.0
60	emb AW931942 AW931942 EST357785 tomato fruit mature green, TAMU 356 3e-97
	emb AW218352 AW218352 EST303535 tomato radicle, 5 d post-imbibit 210 1e-73

```
emb|AL031966|SPCC1442 S.pombe chromosome III cosmid c1442.
                                                                      209 6e-69
      emb|AW651095|AW651095 EST329549 tomato germinating seedlings, TA... 222 2e-64
      dbj|D89256|D89256 Schizosaccharomyces pombe mRNA, partial cds, c... 205 5e-64
      emb|AW982499|AW982499 HVSMEg0003G22f Hordeum vulgare pre-anthesi... 215 2e-58
 5
      emb|AW460005|AW460005 si07d11.y1 Gm-c1029 Glycine max cDNA clone... 116 1e-57
      gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 123 4e-48
      emb|X68327|SCTRP2 S.cerevisiae TRP2 gene for anthranilate syntha... 123 4e-48
      emb|AW719463|AW719463 LjNEST5b1r Lotus japonicus nodule library.... 184 1e-45
      emb|AI736775|AI736775 sb33d01.yl Gm-c1012 Glycine max cDNA clone... 104 2e-40
10
      gb|K01388|YSCTRP2 Yeast (S.cerevisiae) TRP2 gene coding for anth... 122 4e-38
      emb|AL032684|SPBP8B7 S.pombe chromosome II p1 p8B7.
      emb[AW509018]AW509018 si39b01.yl Gm-r1030 Glycine max cDNA clone... 113 5e-24
      gb|T14852|T14852 crs299 lambdaZAPST Ricinus communis cDNA clone ... 107 2e-22
      emb|AW223881|AW223881 EST300692 formato fruit red ripe, TAMU Lyco... 103 4e-21
15
      emb|AF119554|AF119554 Plasmodium falciparum para-aminobenzoic ac... 67 6e-10
      emb|AL111470|CNS019CM Botrytis cinerea strain T4 cDNA library un... 45 2e-05
      emb|AI329873|AI329873 b9g02ne.rl Neurospora crassa evening cDNA ... 48 3e-04
      emb|AW224247|AW224247 EST300974 tomato fruit red ripe, TAMU Lyco... 46 7e-04
      emb|AF149719|AF149719 Aspergillus fumigatus para aminobenzoic ac... 42 0.012
20
      emb|AQ448372|AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P... 39 0.15
      emb|AQ324360|AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P... 39 0.15
      emb|AQ160089|AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P... 39 0.15
      emb|AW599019|AW599019 gb01b03.y1 Moss EST library PPN Physcomitr... 37 0.38
      emb|AW599000|AW599000 ga99h03.y1 Moss EST library PPN Physcomitr... 37 0.38
25
      emb|AW678847|AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S... 35 0.88
      emb|AW680390|AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ... 35 0.89
      emb|AW678385|AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ... 35_0.89
      emb|AW747146|AW747146 WS1 66 E07.b1 A002 Water-stressed 1 (WS1) ... 35 0.89
      emb|AW678361|AW678361 WS1 15 H06.b1 A002 Water-stressed 1 (WS1) ... 35 0.90
30
      emb|AW745749|AW745749 WS1 37 D12.b1 A002 Water-stressed 1 (WS1) ... 35 0.90
      emb|AW747427|AW747427 WS1 68 B09.b1 A002 Water-stressed 1 (WS1) ... 35 0.90
      emb|AW678071|AW678071 WS1 13 E01.b1 A002 Water-stressed 1 (WS1) ... 35 0.90
      emb|AW747468|AW747468 WS1 68 B09.g1 A002 Water-stressed 1 (WS1) ... 35 0.90
      emb|AW672427|AW672427 LG1 359 A06.g1 A002 Light Grown 1 (LG1) So... 35 0.90
35
      emb|AW744836|AW744836 LG1 384 E07.g1 A002 Light Grown 1 (LG1) So... 35 0.90
      emb|AW746170|AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
      emb|AW922317|AW922317 DG1 17 E06.g1 A002 Dark Grown 1 (DG1) Sorg... 35 0.91
      emb|AQ648582|AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos... 36 0.99
      emb|AQ643551|AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos... 36 0.99
40
      emb|AI443370|AI443370 sa31b05.x1 Gm-c1004 Glycine max cDNA clone... 35 1.4
      emb|AW101313|AW101313 sd77d08.y1 Gm-c1009 Glycine max cDNA clone... 35 1.4
      emb|AW678030|AW678030 WS1_12 B10.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
      emb|AW349006|AW349006 GM210004A12H10R Gm-r1021 Glycine max cDNA ... 35 1.4
      emb|AW309961|AW309961 sf27b12.x1 Gm-c1028 Glycine max cDNA clone... 35 1.4
45
      emb|AW678582|AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
      emb|AW317198|AW317198 sf38f03.x1 Gm-c1028 Glycine max cDNA clone... 35 1.4
      emb|AW678305|AW678305 WS1 14 G05.g1 A002 Water-stressed 1 (WS1) ... 35 1.4
      emb|AW680905|AW680905 WS1_8 A08.b1 A002 Water-stressed 1 (WS1) S... 35 1.4
      emb|AW679666|AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
50
      emb|AL031746|PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq... 35 1.9
      emb|AI959816|AI959816 sc94f02.yl Gm-c1019 Glycine max cDNA clone... 35 1.9
      emb|AW924277|AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ... 35 1.9
      gb|J03998|PFAGAR Plasmodium falciparum glutamic acid-rich protei... 35 1.9
      emb|AW696796|AW696796 NF109A07ST1F1052 Developing stem Medicago ... 35 1.9
55
      emb|AW396753|AW396753 sf37c11.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
      gb[M98871|SOYCHS7A Glycine max chalcone synthase (chs7) gene, co... 35 2.6
      emb|AI460797|AI460797 sa69d02.yl Gm-c1004 Glycine max cDNA clone... 35 2.6
      emb|AW348617|AW348617 GM210002B22G1R Gm-r1021 Glycine max cDNA 3... 35 2.6
      emb|AW310362|AW310362 sf35a09.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
60
      emb|AI437832|AI437832 sa40c07.yl Gm-c1004 Glycine max cDNA clone... 35 2.6
      gb|BE023927|BE023927 sm94c05.yl Gm-c1015 Glycine max cDNA clone ... 35 2.6
```

	emb AW424189 AW424189 sh62b04.y1 Gm-c1015 Glycine max cDNA clone 35 2.6 emb AW101907 AW101907 sd72d01.y1 Gm-c1008 Glycine max cDNA clone 35 2.6 emb AW102370 AW102370 sd86h01.y1 Gm-c1009 Glycine max cDNA clone 35 2.6
5	emb AW309356 AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone 35 2.6 emb AL355932 NCB5O22 Neurospora crassa DNA linkage group II BAC 34 3.5 emb AQ652663 AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom 34 3.5 emb Z98056 SPAC5D6 S.pombe chromosome I cosmid c5D6. 34 3.5 emb AW348286 AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3 34 4.
10	emb AB018422 AB018422 Pisum sativum mRNA for DNA binding zinc fi 34 4.9 emb AW734949 AW734949 sk93b10.y1 Gm-c1035 Glycine max cDNA clone 34 4.9 emb AW679089 AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) 34 4.9 emb AW306776 AW306776 sf48c12.y1 Gm-c1009 Glycine max cDNA clone 34 4.9 gb M36941 BLYHORDCA Hordeum vulgare C-hordein gene, complete cds. 29 5.3 gb BE034677 BE034677 ML01H08 ML Mesembryanthemum crystallinum cD 33 6.7
15	emb Z26877 SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro 33 6.7 emb AW267708 AW267708 EST305836 DSIR Medicago truncatula cDNA cl 33 6.7 emb Z28162 SCYKL162C S.cerevisiae chromosome XI reading frame OR 33 6.7 emb AW980990 AW980990 EST392143 GVN Medicago truncatula cDNA clo 33 6.7 gb BE037412 BE037412 MP20G03 MP Mesembryanthemum crystallinum cD 33 6.7
20	emb Z28161 SCYKL161C S.cerevisiae chromosome XI reading frame OR 33 6.7
25	emb AI726247 AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium 33 6.7 emb AE001401 AE001401 Plasmodium falciparum chromosome 2, sectio 33 6.7 emb AW573801 AW573801 EST316392 GVN Medicago truncatula cDNA clo 33 6.7 emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque 33 9.2 emb AQ659747 AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom 33 9.2
	gb BE021269 BE021269 sm56h04.y1 Gm-c1028 Glycine max cDNA clone 33 9.2 emb AW222457 AW222457 EST299268 tomato fruit red ripe, TAMU Lyco 33 9.2 emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl 33 9.2 emb AW725836 AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa 33 9.2
30	emb AQ324451 AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P 33 9.2 gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN 33 9.2 emb AW132634 AW132634 se06h07.yl Gm-c1013 Glycine max cDNA clone 33 9.2 emb AI166186 AI166186 a032p32u Hybrid aspen plasmid library Popu 33 9.2 gb BE053953 BE053953 GA Ea0031D23f Gossypium arboreum 7-10 dpa 33 9.2
35	8-p
40	Query= AtACS6_at 12891_at /id_source genbank /description gb aac63850.1 (u73786) acc synthase [arabidopsis thaliana] /blast_score 0 /ec_number /family synthase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb atacs6 /ncgi http://www.ncgr.org/cgi-bin/ff?atacs6 (1567 letters)
45	
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
50	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
55	emb X82273 BOACCS B.oleracea mRNA for ACC synthase. 944 0.0 emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo 833 0.0 emb AB034992 AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc 725 0.0 emb AF057563 AF057563 Nicotiana glutinosa 1-aminocyclopropane-1 729 0.0 emb AJ005002 NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro 726 0.0
60	emb AB034993 AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc 723 0.0 gb U72389 LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1 724 0.0 gb U72390 LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1 720 0.0

gb|U68216|CPU68216 Carica papaya ACC synthase mRNA, complete cds. 435 0.0 emb|AB033503|AB033503 Populus euramericana peacs-2 mRNA for 1-am... 713 0.0 emb|AF061605|AF061605 Nicotiana glutinosa ACC synthase mRNA, com... 712 0.0 emb|AJ012551|CSI012551 Citrus sinensis mRNA for ACC synthase. 5 emb|AB033502|AB033502 Populus euphratica peacs-1 mRNA for 1-amin... 591 0.0 emb|AB013100|AB013100 Lycopersicon esculentum LE-ACS6 mRNA for 1... 706 0.0 emb|AB013346|AB013346 Lycopersicon esculentum mRNA for 1-aminocy... 704 0.0 gb[U88971|PHU88971 Pelargonium hortorum 1-aminocyclopropane-1-ca... 423 0.0 emb|Z11613|VRACCSYNM V.radiata mRNA for ACC synthase. 10 emb|X98492|NTACCS Nicotiana tabacum mRNA for ACC-synthase (clone... 425 0.0 emb|X67100|GMCACCS1 G.max mRNA for ACC synthase. emb|AJ012696|CSI012696 Citrus sinensis mRNA for ACC synthase (AC... 422 0.0 emb|Z18953|PHAMCRBSY P.hybrida mRNA for 1-aminocyclopropane 1-ca... 424 0.0 emb|AJ011095|CSI011095 Citrus sinensis mRNA for ACC synthase (ac... 424 0.0 15 emb|Z18952|DCAMCRBSY D.caryophyllus mRNA for 1-aminocyclopropane... 686 0.0 emb|AB006804|AB006804 Cucumis sativus CS-ACS2 mRNA for ACC synth... 423 0.0 emb|AF080258|AF080258 Musa acuminata 1-aminocyclopropane-1-carbo... 680 0.0 emb|AF016459|AF016459 Pisum sativum 1-aminocyclopropane-1-carbox... 415 0.0 dbj|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 678 0.0 20 emb|X65982|NTXACCSYN N.tabacum mRNA for 1-aminocyclopropane-1-ca... 417 0.0 emb|AF109927|AF109927 Musa acuminata 1-aminocyclopropane-1-carbo... 676 0.0 emb|AB006803|AB006803 Cucumis sativus CS-ACS1 mRNA for ACC synth... 676 0.0 gb[U17231]PHU17231 Pelargonium hortorum clone pGAC-2 1-aminocycl... 423 0.0 emb|AB021906|AB021906 Musa acuminata MA-ACS1 mRNA for ACC syntha... 671 0.0 25 emb|AF129508|AF129508 Musa acuminata 1-aminocyclopropane-1-carbo... 671 0.0 emb|AB015625|AB015625 Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy... 393 0.0 emb|AB031026|AB031026 Prunus mume PM-ACS1 mRNA for ACC synthase,... 405 0.0 emb|Y11357|CP1A1CS C.papaya mRNA for 1-aminocyclopropane-1-carbo... 404 0.0 dbj|D01032|CUCACCW Cucurbita maxima mRNA for 1-aminocyclopropane... 666 0.0 30 dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 666 0.0 emb|X62536|LEACC L.esculentum mRNA for ACC synthase. 327 0.0 gb|L20634|POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb... 403 0.0 emb[X59145]LEACC2MR Lycopersicon esculentum LE-ASCC2 mRNA (ptACC... 326 0.0 gb[M58323|CUCACCSYN Cucurbita pepo 1-aminocyclopropane-1-carboxy... 663 0.0 35 emb|AF057562|AF057562 Nicotiana glutinosa 1-aminocyclopropane-1-... 412 0.0 emb|AF239987|AF239987 Prunus persica ACC synthase ACS1 mRNA, par... 662 0.0 gb|M34289|TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha... 327 0.0 gb|M63490|TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth... 657 0.0 emb[X59146]LEACC4MR Lycopersicon esculentum LE-ACC4 mRNA (ptACC4... 656 0.0 40 emb|Y15739|MAACSYNTH Musa acuminata mRNA for 1-aminocyclopropane... 655 0.0 gb[U79999]MAU79999 Musa acuminata ACC synthase (acs3) mRNA, comp... 655 0.0 emb|AF178076|AF178076 Carica papaya 1-aminocyclopropane-1-carbox... 395 0.0 gb[U17229]PHU17229 Pelargonium hortorum clone pGAC-1 1-aminocycl... 407 0.0 emb|X82265|CAACC1 C.anuum mRNA for 1-aminocylopropane-1-carboxyl... 639 0.0 45 gb|U70842|STU70842 Solanum tuberosum 1-aminocyclopropane-1-carbo... 637 0.0 emb|AF144746|AF144746 Solanum melongena 1-aminocyclopropane-1-ca... 636 0.0 emb|AJ276295|CSI276295 Citrus sinensis partial mRNA for ACC synt... 418 0.0 emb|AJ012577|CPA012577 Carica papaya mRNA for 1-aminocyclopropan... 387 e-180 emb|AF038945|AF038945 Rumex palustris 1-aminocyclopropane-1-carb... 372 e-179 50 gb[U73815]MDU73815 Malus domestica ACC synthase (MdACS-2) mRNA, ... 623 e-178 dbj|D37937|D37937 Cucumis melo mRNA for 1-aminocyclopropane-1-ca... 380 e-177 emb|Z11562|VRACCSYN V.radiata mRNA for 1-aminocyclopropane-1-car... 375 e-176 emb|AF177769|AF177769 Carica papaya 1-aminocyclopropane-1-carbox... 369 e-175 emb|AF083814|AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR... 605 e-172 55 emb|AF178077|AF178077 Carica papaya 1-aminocyclopropane-1-carbox... 316 e-171 emb|AF239989|AF239989 Prunus persica ACC synthase ACS25 mRNA, pa... 597 e-170 gb|U22523|MIU22523 Mangifera indica 1-aminocyclopropane-carboxyl... 359 e-169 emb|X66605|DCACCS D.caryophyllus mRNA for 1-aminocyclopropane-1-... 396 e-168 emb|AF049137|AF049137 Dianthus caryophyllus 1-aminocyclopropane-... 338 e-167 60 emb|AF170705|AF170705 Mangifera indica 1-aminocyclopropane-1-car... 290 e-167 emb|AJ277160|CPA277160 Carica papaya partial paccs1A gene for 1-... 266 e-165

emblAB015624|AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 359 e-163 gb|U03294|MSU03294 Malus sylvestris 1-aminocyclopropane-1-carbox... 359 e-163 gb|L31347|MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox... 357 e-162 emb|AB015495|AB015495 Passiflora edulis PE-ACS2 mRNA for ACC syn... 368 e-162 5 emb|Z77854|PSPACS1 Phalaenopsis species mRNA for 1-aminocyclopro... 514 e-161 dbj|D01033|CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane... 349 e-159 emb|X87112|PCPCACS1G P.communis mRNA for 1-aminocyclopropane-1-c... 346 e-159 emb|AB007449|AB007449 Actinidia deliciosa mRNA for 1-aminocyclop... 336 e-159 gb|U73816|MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ... 504 e-158 10 gb|U17972|LEU17972 Lycopersicon esculentum 1-aminocyclopropane-1... 343 e-157 emb|AB007639|AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 502 e-157 gb[M66619[DINCARACC D.caryophyllus 1-aminocyclopropane-1-carboxy... 495 e-156 emb|AB006805|AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth... 342 e-156 gb|U34987|VRU34987 Vigna radiata 1-aminocyclopropane-1-carboxyli... 305 e-151 15 emb|AB000679|AB000679 Vigna radiata mRNA for 1-aminocyclopropane... 340 e-151 gb[U34986|VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli... 340 e-149 gb[U64031|DCU64031 Dendrobium crumenatum ACC synthase gene, comp... 259 e-149 emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 336 e-148 emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 238 e-147 emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 234 e-146 gb[U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 235 e-145 emblAF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 237 e-145 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 376 e-145 gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 236 e-143 25 gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 236 e-143 emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142 emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141 emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 234 e-141 emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140 30 gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-139 emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138

Query= AtACS6_g_at 12892_g_at /id_source genbank /description gb|aac63850.1| (u73786) acc synthase [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1567 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching......done

45 Score E

Sequences producing significant alignments: (bits) Value

emb|X82273|BOACCS B.oleracea mRNA for ACC synthase. 944 0.0 emb[X72676]BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo... 833 0.0 50 emb|AB034992|AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc... 725 0.0 emb|AF057563|AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-... 729 0.0 emb|AJ005002|NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro... 726 0.0 emb|AB034993|AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc... 723 0.0 gb|U72389|LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1... 724 0.0 55 gb|U72390|LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1... 720 0.0 gb|U68216|CPU68216 Carica papaya ACC synthase mRNA, complete cds. 435 0.0 emb|AB033503|AB033503 Populus euramericana peacs-2 mRNA for 1-am... 713 0.0 emb|AF061605|AF061605 Nicotiana glutinosa ACC synthase mRNA, com... 712 0.0 emb|AJ012551|CSI012551 Citrus sinensis mRNA for ACC synthase. 60 emb|AB033502|AB033502 Populus euphratica peacs-1 mRNA for 1-amin... 591 0.0 emb|AB013100|AB013100 Lycopersicon esculentum LE-ACS6 mRNA for 1... 706 0.0

emblAB013346lAB013346 Lycopersicon esculentum mRNA for 1-aminocy... 704 0.0 gb|U88971|PHU88971 Pelargonium hortorum 1-aminocyclopropane-1-ca... 423 0.0 emb|Z11613|VRACCSYNM V.radiata mRNA for ACC synthase. emb|X98492|NTACCS Nicotiana tabacum mRNA for ACC-synthase (clone... 425 0.0 5 emb|X67100|GMCACCS1 G.max mRNA for ACC synthase. emb|AJ012696|CSI012696 Citrus sinensis mRNA for ACC synthase (AC... 422 0.0 emb|Z18953|PHAMCRBSY P.hybrida mRNA for 1-aminocyclopropane 1-ca... 424 0.0 emb|AJ011095|CSI011095 Citrus sinensis mRNA for ACC synthase (ac... 424 0.0 emb|Z18952|DCAMCRBSY D.caryophyllus mRNA for 1-aminocyclopropane... 686 0.0 10 emb|AB006804|AB006804 Cucumis sativus CS-ACS2 mRNA for ACC synth... 423 0.0 emb|AF080258|AF080258 Musa acuminata 1-aminocyclopropane-1-carbo... 680 0.0 emb|AF016459|AF016459 Pisum sativum 1-aminocyclopropane-1-carbox... 415 0.0 dbi|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 678 0.0 emb[X65982]NTXACCSYN N.tabacum mRNA for 1-aminocyclopropane-1-ca... 417 0.0 15 emb|AF109927|AF109927 Musa acuminata 1-aminocyclopropane-1-carbo... 676 0.0 emb|AB006803|AB006803 Cucumis sativus CS-ACS1 mRNA for ACC synth... 676 0.0 gb|U17231|PHU17231 Pelargonium hortorum clone pGAC-2 1-aminocycl... 423 0.0 emb|AB021906|AB021906 Musa acuminata MA-ACS1 mRNA for ACC syntha... 671 0.0 emb|AF129508|AF129508 Musa acuminata 1-aminocyclopropane-1-carbo... 671 0.0 20 emb|AB015625|AB015625 Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy... 393 0.0 emb|AB031026|AB031026 Prunus mume PM-ACS1 mRNA for ACC synthase,... 405 0.0 emb|Y11357|CP1A1CS C.papaya mRNA for 1-aminocyclopropane-1-carbo... 404 0.0 dbj|D01032|CUCACCW Cucurbita maxima mRNA for 1-aminocyclopropane... 666 0.0 dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 666 0.0 - 25 emb|X62536|LEACC L.esculentum mRNA for ACC synthase. 327 0.0 gb|L20634|POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb... 403 0.0 emb|X59145|LEACC2MR Lycopersicon esculentum LE-ASCC2 mRNA (ptACC... 326 0.0 gb|M58323|CUCACCSYN Cucurbita pepo 1-aminocyclopropane-1-carboxy... 663 0.0 emb|AF057562|AF057562 Nicotiana glutinosa 1-aminocyclopropane-1-... 412 0.0 30 emb|AF239987|AF239987 Prunus persica ACC synthase ACS1 mRNA, par... 662 0.0 gb|M34289|TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha... 327 0.0 gb[M63490]TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth... 657 0.0 emb|X59146|LEACC4MR Lycopersicon esculentum LE-ACC4 mRNA (ptACC4... 656 0.0 emb|Y15739|MAACSYNTH Musa acuminata mRNA for 1-aminocyclopropane... 655 0.0 35 gb|U79999|MAU79999 Musa acuminata ACC synthase (acs3) mRNA, comp... 655 0.0 emb|AF178076|AF178076 Carica papaya 1-aminocyclopropane-1-carbox... 395 0.0 gb|U17229|PHU17229 Pelargonium hortorum clone pGAC-1 1-aminocycl... 407 0.0 emb|X82265|CAACC1 C.anuum mRNA for 1-aminocylopropane-1-carboxyl... 639 0.0 gb|U70842|STU70842 Solanum tuberosum 1-aminocyclopropane-1-carbo... 637 0.0 40 emb|AF144746|AF144746 Solanum melongena 1-aminocyclopropane-1-ca... 636 0.0 emb|AJ276295|CSI276295 Citrus sinensis partial mRNA for ACC synt... 418 0.0 emb|AJ012577|CPA012577 Carica papaya mRNA for 1-aminocyclopropan... 387 e-180 emb|AF038945|AF038945 Rumex palustris 1-aminocyclopropane-1-carb... 372 e-179 gb[U73815[MDU73815 Malus domestica ACC synthase (MdACS-2) mRNA, ... 623 e-178 45 dbj|D37937|D37937 Cucumis melo mRNA for 1-aminocyclopropane-1-ca... 380 e-177 emb|Z11562|VRACCSYN V.radiata mRNA for 1-aminocyclopropane-1-car... 375 e-176 emb|AF177769|AF177769 Carica papaya 1-aminocyclopropane-1-carbox... 369 e-175 emb|AF083814|AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR... 605 e-172 emb|AF178077|AF178077 Carica papaya 1-aminocyclopropane-1-carbox... 316 e-171 50 emb|AF239989|AF239989 Prunus persica ACC synthase ACS25 mRNA, pa... 597 e-170 gb|U22523|MIU22523 Mangifera indica 1-aminocyclopropane-carboxyl... 359 e-169 emb|X66605|DCACCS D.caryophyllus mRNA for 1-aminocyclopropane-1-... 396 e-168 emb|AF049137|AF049137 Dianthus caryophyllus 1-aminocyclopropane-... 338 e-167 emb|AF170705|AF170705 Mangifera indica 1-aminocyclopropane-1-car... 290 e-167 emb|AJ277160|CPA277160 Carica papaya partial paccs1A gene for 1-... 266 e-165 emb|AB015624|AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 359 e-163 gb|U03294|MSU03294 Malus sylvestris 1-aminocyclopropane-1-carbox... 359 e-163 gb|L31347|MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox... 357 e-162 emb|AB015495|AB015495 Passiflora edulis PE-ACS2 mRNA for ACC syn... 368 e-162 60 emb|Z77854|PSPACS1 Phalaenopsis species mRNA for 1-aminocyclopro... 514 e-161 dbj|D01033|CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane... 349 e-159

emb|X87112|PCPCACS1G P.communis mRNA for 1-aminocyclopropane-1-c... 346 e-159 emb|AB007449|AB007449 Actinidia deliciosa mRNA for 1-aminocyclop... 336 e-159 gb|U73816|MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA. ... 504 e-158 gb|U17972|LEU17972 Lycopersicon esculentum 1-aminocyclopropane-1... 343 e-157 5 emb|AB007639|AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 502 e-157 gb|M66619|DINCARACC D.caryophyllus 1-aminocyclopropane-1-carboxy... 495 e-156 emb|AB006805|AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth... 342 e-156 gb|U34987|VRU34987 Vigna radiata 1-aminocyclopropane-1-carboxyli... 305 e-151 emb|AB000679|AB000679 Vigna radiata mRNA for 1-aminocyclopropane... 340 e-151 10 gb|U34986|VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli... 340 e-149 gb|U64031|DCU64031 Dendrobium crumenatum ACC synthase gene, comp... 259 e-149 emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 336 e-148 emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 238 e-147 emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 234 e-146 15 gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 235 e-145 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 237 e-145 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 236 e-143 gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 236 e-143 20 emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142 emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141 emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 234 e-141 emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140 gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-139 25 emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138

Query= AtERF2 s_at 12905 s_at /id_source genbank /description
dbj|baa32419.1| (ab008104) ethylene responsive element binding factor
2 [arabidopsis thaliana] /blast_score 1.00e-112 /ec_number /family
/chip nova /gb_link /ncgi
(921 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

60

Searching.....done

40 Score E
Sequences producing significant alignments: (bits) Value

dbj[D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 132 9e-43 dbj[D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 134 6e-41 emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 161 5e-39 emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 160 1e-38 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 155 5e-37 gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 138 3e-32 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 135 1e-31 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 134 1e-30

emb|AW729466|AW729466 GA__Ea0025B11 Gossypium arboreum 7-10 dpa ... 132 4e-30 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 125 4e-28 emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 124 8e-28 emb|AW396250|AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone... 116 2e-25 emb|AW233956|AW233956 sf32e02.y1 Gm-c1028 Glycine max cDNA clone... 115 5e-25 emb|AW185128|AW185128 se87b10.y1 Gm-c1023 Glycine max cDNA clone... 114 1e-24

emb|AW185128|AW185128 se87b10.yl Gm-c1023 Glycine max cDNA clone... 114 1e-24 emb|AI897834|AI897834 EST267277 tomato ovary, TAMU Lycopersicon ... 113 2e-24 emb|AW349516|AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ... 113 2e-

emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 111 6e-24

emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24 emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 89 6e-24 emb|AI899000|AI899000 EST268443 tomato ovary, TAMU Lycopersicon ... 110 2e-23 emb|AI965917|AI965917 sc79f12.yl Gm-c1018 Glycine max cDNA clone... 110 2e-23 5 emb|AI794657|AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone... 110 2e-23 emblAW200919|AW200919 se95c12.yl Gm-c1027 Glycine max cDNA clone... 109 3e-23 emb|AW507860|AW507860 si45h05.yl Gm-r1030 Glycine max cDNA clone... 109 3e-23 emb|AW507898|AW507898 si46f03.yl Gm-r1030 Glycine max cDNA clone... 97 3e-23 dbj|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 10 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 109 4eemb|AW278190|AW278190 sf40g11.yl Gm-c1009 Glycine max cDNA clone... 109 4e-23 emb|AI486689|AI486689 EST245011 tomato ovary, TAMU Lycopersicon ... 108 5e-23 emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 108 8e-23 15 emb|AW776671|AW776671 EST335736 DSIL Medicago truncatula cDNA cl... 108 8e-23 emb|AW759181|AW759181 sl38a09.yl Gm-c1027 Glycine max cDNA clone... 107 1e-22 emb|AW596384|AW596384 sj02f12.yl Gm-c1032 Glycine max cDNA clone... 107 1e-22 emb|AI897797|AI897797 EST267240 tomato ovary, TAMU Lycopersicon ... 107 1e-22 emb|AI973653|AI973653 sd07h05.yl Gm-c1020 Glycine max cDNA clone... 107 le-22 emb|AW620490|AW620490 sj05h02.yl Gm-c1032 Glycine max cDNA clone... 106 2e-22 20 emb|AI899889|AI899889 sb94g05.y1 Gm-c1017 Glycine max cDNA clone... 105 4e-22 emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 105 4e-22 emb|AI778693|AI778693 EST259572 tomato susceptible, Cornell Lyco... 105 4e-22 emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 105 4e-22 25 emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 105 4e-22 emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 103 2e-21 gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 103 2e-21 emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 103 2e-21 emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 103 2e-21 30 emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 100 1e-20 emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 100 2e-20 emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20 emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 100 3e-20 emb|AW781602|AW781602 sl82d06.yl Gm-c1037 Glycine max cDNA clone... 100 3e-20 35 emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 100 3e-20 emb|AI440657|AI440657 sa63d09.y1 Gm-c1004 Glycine max cDNA clone... 99 4e-20 gb[U81157]NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 98 8e-20 emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 98 8e-20 emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 1e-19 40 emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 97 2e-19 emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 97 2e-19 emb|AI966559|AI966559 sc52a04.y1 Gm-c1015 Glycine max cDNA clone... 97 2e-19 emb|AI495036|AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone... 95 5e-19 emb|AI442716|AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone... 95 5e-19 45 emb|AI055252|AI055252 coau0003H16 Cotton Boll Abscission Zone cD... 67 8e-19 emb|AI967551|AI967551 Ljirnpest05-400-d11 Ljirnp Lambda HybriZap... 95 1e-18 emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 94 1e-18 emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycope... 93 3e-18 emb[AW686013]AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 92 5e-18 50 emb|AW981323|AW981323 EST392476 DSIL Medicago truncatula cDNA cl... 92 5e-18 emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 92 5e-18 emb|AW618246|AW618246 EST314296 L. pennellii trichome, Cornell U... 92 5e-18 emb|AW685077|AW685077 NF024H04NR1F1000 Nodulated root Medicago t... 90 2e-17 emb|AW573782|AW573782 EST316373 GVN Medicago truncatula cDNA clo... 90 2e-17 55 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 88 1e-16 emb|AW782252|AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone... 59 1e-16 emb|AW980481|AW980481 EST391634 GVN Medicago truncatula cDNA clo... 87 2e-16 gb|BE023264|BE023264 sm80all.yl Gm-c1015 Glycine max cDNA clone ... 87 2e-16 emb|AW458901|AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone... 86 4e-16 emblAW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 85 8e-16 60 emb[AW685799]AW685799 NF030D09NR1F1000 Nodulated root Medicago t... 53 1e-15

	111777MMAGAGIATTIMAGAGAGAGAGAGAGAGAGATTAA
	emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 84 2e-15
	emb AI731242 AI731242 BNLGHi9002 Six-day Cotton fiber Gossypium 84 2e-15
	emb AI898992 AI898992 EST268435 tomato ovary, TAMU Lycopersicon 84 2e-15
	emb AI736796 AI736796 sb33f06.yl Gm-c1012 Glycine max cDNA clone 83 3e-15
5	
3	emb AW560968 AW560968 EST316016 DSIR Medicago truncatula cDNA cl 57 4e-15
	emb AW560196 AW560196 EST315244 DSIR Medicago truncatula cDNA cl 57 4e-15
	emb AI489709 AI489709 EST248048 tomato ovary, TAMU Lycopersicon 56 6e-15
	emb AW759236 AW759236 sl38f08.yl Gm-c1027 Glycine max cDNA clone 80 2e-14
	gb BE057468 BE057468 sm58e08.yl Gm-c1028 Glycine max cDNA clone 55 7e-14
10	EDIDLOS 7400 ELECTROS SILDECOS, Y CHIPCTUZE OTYCHIE HEA CENTA CHOIC 55 76-14
10	gb T14923 T14923 crs406 lambdaZAPST Ricinus communis cDNA clone 56 9e-14
	emb AI489199 AI489199 EST247538 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI486929 AI486929 EST245251 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI483636 AI483636 EST249507 tomato ovary, TAMU Lycopersicon 52 le-13
	emb AW033743 AW033743 EST277314 tomato callus, TAMU Lycopersicon 52 1e-13
15	emb AI483510 AI483510 EST249359 tomato ovary, TAMU Lycopersicon 52 1e-13
13	
	emb AI771755 AI771755 EST252855 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI485175 AI485175 EST243479 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI489919 AI489919 EST248258 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI897787 AI897787 EST267230 tomato ovary, TAMU Lycopersicon 52 1e-13
20	emb AI771834 AI771834 EST252934 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI485460 AI485460 EST243781 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI771795 AI771795 EST252895 tomato ovary, TAMU Lycopersicon 52 1e-13
25	Query= AtERF5_s_at 12908 s at /id source genbank /description
	dbj baa32422.1 (ab008107) ethylene responsive element binding factor
	5 [arabidopsis thaliana] /blast_score 1.00e-117 /ec_number /family
	/chip nova /gb_link /ncgi
	(1059 letters)
30	
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	001,010 004101000, 120,111,010 101111011010
	Carrobina
25	Searchingdone
35	
35	Score E
35	
35	Score E
35	Score E Sequences producing significant alignments: (bits) Value
	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37
35 40	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35
	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33
	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32
	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33
	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30
40	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 26
	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 26
40	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29
40	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29
40	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29
40 45	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29
40	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28
40 45	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28
40 45	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28
40 45	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27
40 45	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AI794657 AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AI794657 AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1030 Glycine max cDNA clone 123 2e-27
40 45	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AI794657 AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AI794657 AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone 123 2e-27 emb AW5775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone 123 2e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 93 8e-27 emb AW685077 AW685077 NF024H04NR1F1000 Nodulated root Medicago t 93 8e-27
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2c emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AW98900 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone 123 2e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27 emb AW685077 AW685077 NF024H04NR1F1000 Nodulated root Medicago t 93 8e-27 emb AW573782 AW573782 EST316373 GVN Medicago truncatula cDNA clo 93 9e-27
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA cl 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 123 2e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27 emb AW573782 AW573782 EST316373 GVN Medicago truncatula cDNA clone 121 1e-26 emb AW620490 AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone 121 1e-26
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA 130 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW75918 AW775819 EST334884 DSIL Medicago truncatula cDNA clone 123 2e-27 emb AW75787 AW685077 NF024H04NR1F1000 Nodulated root Medicago t 95 5e-27 emb AW65737 AW685077 NF024H04NR1F1000 Nodulated root Medicago t 93 8e-27 emb AW6573782 AW573782 EST316373 GVN Medicago truncatula cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26 emb AW759181 AW759181 sl38a09.y1 Gm-c1027 Glycine max cDNA clone 121 1e-26
40 45 50	Score E Sequences producing significant alignments: (bits) Value emb AW396250 AW396250 sh26c01.y1 Gm-c1016 Glycine max cDNA clone 141 4e-37 emb AW200919 AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone 149 5e-35 emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl 94 5e-33 emb AW776671 AW776671 EST335736 DSIL Medicago truncatula cDNA cl 111 2e-32 emb AI897834 AI897834 EST267277 tomato ovary, TAMU Lycopersicon 132 2e-30 emb AW349516 AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA cl 130 2e-29 emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl 125 2e-29 emb AI899000 AI899000 EST268443 tomato ovary, TAMU Lycopersicon 128 3e-29 emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 108 8e-29 dbj D38125 TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 127 1e-28 emb AI486689 AI486689 EST245011 tomato ovary, TAMU Lycopersicon 127 2e-28 gb BE023264 BE023264 sm80a11.y1 Gm-c1015 Glycine max cDNA clone 103 5e-28 emb AI897797 AI897797 EST267240 tomato ovary, TAMU Lycopersicon 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 124 1e-27 emb AW507860 AW507860 si45h05.y1 Gm-c1019 Glycine max cDNA clone 123 2e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27 emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 95 5e-27 emb AW573782 AW573782 EST316373 GVN Medicago truncatula cDNA clone 121 1e-26 emb AW620490 AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone 121 1e-26

emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 118 6e-26 emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 118 6e-26 emb|AI899889|AI899889 sb94g05.y1 Gm-c1017 Glycine max cDNA clone... 117 1e-25 emb|AW185128|AW185128 se87b10.y1 Gm-c1023 Glycine max cDNA clone... 116 2e-25 emb|AW688546|AW688546 NF008H02ST1F1000 Developing stem Medicago ... 89 2e-25 emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 115 5e-25 emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 115 5e-25 emb|AI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 115 8e-25 emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 114 1e-24 10 emb|AW781602|AW781602 sl82d06.yl Gm-c1037 Glycine max cDNA clone... 114 1e-24 emb[AW267820]AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 113 2e-24 emb|AI965917|AI965917 sc79f12.y1 Gm-c1018 Glycine max cDNA clone... 113 3e-24 emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 112 5e-24 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 111 1e-23 15 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 110 2e-23 emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 109 3e-23 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 109 3e-23 emb|AW101306|AW101306 sd77c11.yl Gm-c1009 Glycine max cDNA clone... 89 5e-23 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 107 2e-20 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 107 2e-22 gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 107 2e-22 emb|AW596384|AW596384 sj02f12.yl Gm-c1032 Glycine max cDNA clone... 107 2e-22 dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 105 8e-22 25 emblAV417552|AV417552 AV417552 Lotus japonicus young plants (two... 103 2e-21 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 103 2e-21 emb|AW278190|AW278190 sf40g11.yl Gm-c1009 Glycine max cDNA clone... 103 2e-21 emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 102 4e-21 emb|AI973653|AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone... 102 4e-21 30 emb|AW690929|AW690929 NF034G08ST1F1000 Developing stem Medicago ... 73 9e-21 emb|AW233956|AW233956 sf32e02.yl Gm-c1028 Glycine max cDNA clone... 101 1e-20 emb|AW736415|AW736415 EST332429 KV3 Medicago truncatula cDNA clo... 73 2e-20 emb|AI440657|AI440657 sa63d09.yl Gm-c1004 Glycine max cDNA clone... 100 2e-20 35 emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20 emb|AI967551|AI967551 Ljirnpest05-400-d11 Ljirnp Lambda HybriZap... 100 2e-20 emb|AI731242|AI731242 BNLGHi9002 Six-day Cotton fiber Gossypium ... 100 3e-20 gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 99 5e-20 40 emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 99 5e-20 emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 99 5e-20 emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 99 5e-20 emb|AW729466|AW729466 GA_Ea0025B11 Gossypium arboreum 7-10 dpa ... 98 1e-19 emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 98 1e-19 45 emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 98 1e-19 emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 2e-19 emb|AI736796|AI736796 sb33f06.y1 Gm-c1012 Glycine max cDNA clone... 97 2e-19 emb|AI966559|AI966559 sc52a04.y1 Gm-c1015 Glycine max cDNA clone... 97 2e-19 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 96 3e-19 50 emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 96 5e-19 emb|AI898992|AI898992 EST268435 tomato ovary, TAMU Lycopersicon ... 95 6e-19 emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 95 6e-19 emb|AI495036|AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone... 94 2e-18 gb|U81157|NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 94 2e-18 emb|AW706628|AW706628 sj62g05.y1 Gm-c1033 Glycine max cDNA clone... 70 3e-18 emb|AI442716|AI442716 sa85d10.yl Gm-c1004 Glycine max cDNA clone... 93 4e-18 emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 93 4e-18 emb|AW035119|AW035119 EST280381 tomato callus, TAMU Lycopersicon... 91 1e-17 emb|AI490591|AI490591 EST249145 tomato ovary, TAMU Lycopersicon ... 91 1e-17 60 emb|AI489147|AI489147 EST247486 tomato ovary, TAMU Lycopersicon ... 91 1e-17 emb|AW782252|AW782252 sm03d11.yl Gm-c1027 Glycine max cDNA clone... 63 1e-17

```
emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 90 2e-17
      emb|AW759236|AW759236 sl38f08.yl Gm-c1027 Glycine max cDNA clone... 90 2e-17
      emb|AW686013|AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 90 2e-17
      emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycope... 89 4e-17
 5
      emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycop... 89 5e-17
      emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 89 5e-17
      emb|AF211541|AF211541 AF211541 34.1B Nicotiana tabacum cDNA clon... 87 2e-16
      emb|AW621700|AW621700 EST312498 tomato root during/after fruit s... 87 2e-16
      emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 62 2e-16
10
      emb|AW560968|AW560968 EST316016 DSIR Medicago truncatula cDNA cl... 60 4e-16
      emb|AW560196|AW560196 EST315244 DSIR Medicago truncatula cDNA cl... 60 4e-16
      emb[AW185802]AW185802 se59h01.yl Gm-c1019 Glycine max cDNA clone... 71 5e-16
      emb|AW734757|AW734757 sk88d02.yl Gm-c1035 Glycine max cDNA clone... 85 le-15
      emblAV417624|AV417624 AV417624 Lotus japonicus young plants (two... 58 1e-15
15
      emb|AV407462|AV407462 AV407462 Lotus japonicus young plants (two... 58 le-15
      emb|AW256448|AW256448 EST304585 KV2 Medicago truncatula cDNA clo... 59 1e-15'
      emb|AW560135|AW560135 EST315183 DSIR Medicago truncatula cDNA cl... 59 2e-15
      emb[AW267756]AW267756 EST305884 DSIR Medicago truncatula cDNA cl... 59 2e-15
      emb|AW560134|AW560134 EST315182 DSIR Medicago truncatula cDNA cl... 59 2e-15
20
      emb|AW574073|AW574073 EST316664 GVN Medicago truncatula cDNA clo... 61 2e-15
      Query= AthCOR1_s_at 12916_s_at /id_source genbank /description
      gb|aac13947.1| (af021244) coronatine-induced protein 1 [arabidopsis
25
      thaliana] /blast score 0 /ec number /family /chip nova /gb link.
           (1188 letters)
      Database: plantfungal
30
            661,018 sequences; 426,114,510 total letters
      Searching......done
                                         Score
35
      Sequences producing significant alignments:
                                                         (bits) Value
      emb|AF134301|AF134301 Chenopodium album CaCLH (CaCLH) mRNA, comp... 89 4e-57
      emb|AB025025|AB025025 Chenopodium album mRNA for chlorophyllase.... 89 4e-57
      emb]AF160869]AF160869 Citrus sinensis chlorophyllase mRNA, compl... 84 4e-54
40
      emb|AW039135|AW039135 EST281108 tomato mixed elicitor, BTI Lycop... 127 2e-38
      gb|BE037470|BE037470 MP21E05 MP Mesembryanthemum crystallinum cD... 81 4e-35
      emb|AW093776|AW093776 EST286956 tomato mixed elicitor, BTI Lycop... 59 4e-34
      emb|AW616099|AW616099 EST296862 L. hirsutum trichome, Cornell Un... 67 1e-29
      emb|AW266073|AW266073 L30-2749T3 Ice plant Lambda Uni-Zap XR exp... 79 3e-29
45
      emb|AA887366|AA887366 L30-338T3 Ice plant Lambda Uni-Zap XR expr... 79 2e-26
      emb|AA556157|AA556157 12 Loblolly pine N Pinus taeda cDNA clone ... 120 3e-26
      emb|AW042994|AW042994 ST27H11 Pine TriplEx shoot tip library Pin... 106 7e-26
      emb|AW265807|AW265807 L30-2522 T3 Ice plant Lambda Uni-Zap XR ex... 84 2e-21
      emb|AW678075|AW678075 WS1_13_D09.b1_A002 Water-stressed 1 (WS1) ... 81 1e-19
50
      emb|AW133452|AW133452 se19b10.yl Gm-c1015 Glycine max cDNA clone... 62 1e-17
      emb|AI777679|AI777679 EST258474 tomato susceptible, Cornell Lyco... 53 7e-17
      emb|AW596770|AW596770 sj16e05.yl Gm-c1032 Glycine max cDNA clone... 89 9e-17
      emb|AW596245|AW596245 sj01a09.y1 Gm-c1032 Glycine max cDNA clone... 87 3e-16
      emb|AI771244|AI771244 EST252260 tomato ovary, TAMU Lycopersicon ... 67 3e-16
55
      emb|AW831810|AW831810 sm36f12.yl Gm-c1028 Glycine max cDNA clone... 85 8e-16
      emb|AW678155|AW678155 WS1_13_D09.g1_A002 Water-stressed 1 (WS1) ... 67 2e-10
      emblAI771428|AI771428 EST252528 tomato ovary, TAMU Lycopersicon ... 67 4e-10
      emb|AI822354|AI822354 L0-803T3 Ice plant Lambda Uni-Zap XR expre... 59 5e-09
      gb|BE058857|BE058857 sn21g11.y1 Gm-c1016 Glycine max cDNA clone ... 41 0.019
60
      gb|BE058853|BE058853 sn21g06.y1 Gm-c1016 Glycine max cDNA clone ... 41 0.019
```

emb|AW773701|AW773701 EST332687 KV3 Medicago truncatula cDNA clo... 39 0.094

	emb AV408460 AV408460 AV408460 Lotus japonicus young plants (two 37 0.33
	emb AV413861 AV413861 AV413861 Lotus japonicus young plants (two 37 0.33
	emb AV428585 AV428585 AV428585 Lotus japonicus young plants (two 37 0.33
	emb AV423848 AV423848 AV423848 Lotus japonicus young plants (two 37 0.33
5	emb AV412195 AV412195 AV412195 Lotus japonicus young plants (two 37 0.33
	411 664 44 611 614 615 64
	emb AQ646813 AQ646813 RPCI93-EcoRI-5A7.TJ RPCI93-EcoRI Trypanoso 36 0.4
	emb AZ216717 AZ216717 Sheared DNA-85A6.TF Sheared DNA Trypanosom 36 0.4
10	emb AW395857 AW395857 sh01b07.yl Gm-c1026 Glycine max cDNA clone 36 0.60
10	emb AV415537 AV415537 AV415537 Lotus japonicus young plants (two 35 0.86
	gb L33656 L33656 BNAESTF703 Mustard flower buds Brassica rapa cD 35 0.86
	emb AV417584 AV417584 AV417584 Lotus japonicus young plants (two 35 0.86
	gb L33647 L33647 BNAESTF649 Mustard flower buds Brassica rapa cD 35 0.86
1.5	emb AW455247 AW455247 EST311907 tomato root during/after fruit s 35 0.86
15	emb AQ909224 AQ909224 GSSTc07661 Trypanosome cruzi random genomi 35 0.86
	emb AQ909223 AQ909223 GSSTc07660 Trypanosome cruzi random genomi 35 0.86
•	emb AV421772 AV421772 AV421772 Lotus japonicus young plants (two 35 0.86
	emb AL114831 CNS01BXZ Botrytis cinerea strain T4 cDNA library un 35 0.86
	emb AW625056 AW625056 EST313873 tomato radicle, 5 d post-imbibit 35 0.86
20	emb AW719366 AW719366 LjNEST3d5r Lotus japonicus nodule library, 35 0.86
	emb AL023634 SPBC530 S.pombe chromosome II cosmid c530. 35 1.2
	emb AV420271 AV420271 AV420271 Lotus japonicus young plants (two 35 1.2
	emb AV414699 AV414699 AV414699 Lotus japonicus young plants (two 35 1.2
	emb AF154666 AF154666 Nicotiana tabacum clone PR58 mRNA sequence. 35 1.2
25 ·	emb AV424919 AV424919 AV424919 Lotus japonicus young plants (two 35 1.2
	emb AV428060 AV428060 AV428060 Lotus japonicus young plants (two 35 1.2
	emb AI612620 AI612620 TENG0402 T. Cruzi epimastigote normalised 35 1.2
	emb AW615881 AW615881 EST325379 tomato flower buds 0-3 mm, Corne 35 1.2
	emb AV410945 AV410945 AV410945 Lotus japonicus young plants (two 35 1.2
30	emb AW616956 AW616956 EST323367 L. hirsutum trichome, Cornell Un 35 1.6
	emb AW626060 AW626060 EST319967 tomato radicle, 5 d post-imbibit 35 1.6
	emb AI055068 AI055068 coau0002P04 Cotton Boll Abscission Zone cD 35 1.6
	emb AJ242531 TAE242531 Triticum aestivum rht-Dla gene for gibber 35 1.6
	emb AW926582 AW926582 HVSMEg0007J16 Hordeum vulgare pre-anthesis 27 1.9
35	emb AC067936 AC067936 Neurospora crassa chromosome 7, clone X3-B 34 2.2
-	emb AW649885 AW649885 EST328339 tomato germinating seedlings, TA 34 2.2
	emb AW092862 AW092862 EST286042 tomato mixed elicitor, BTI Lycop 34 2.2
	emb AW037417 AW037417 EST278919 tomato mixed elicitor, BTI Lycop 34 2.2
	emb AI771746 AI771746 EST252846 tomato ovary, TAMU Lycopersicon 34 2.2
40	emb AC023489 AC023489 Trypanosoma brucei chromosome IV clone RPC 34 2.2
	emb X78547 GMREPHYD G.max mRNA for epoxide hydrolase. 34 2.2
	emb AW507737 AW507737 si44e05.yl Gm-r1030 Glycine max cDNA clone 34 2.2
	gb[U02498]STU02498 Solanum tuberosum Lemhi Russet clone EH9.2 ep 34 2.2
	emb AV387727 AV387727 AV387727 Chlamydomonas reinhardtii C9 Chla 34 2.2
45	emb AW217951 AW217951 EST296665 tomato flower buds, anthesis, Co 34 2.2
	emb AW933299 AW933299 EST359142 tomato fruit mature green, TAMU 34 2.2
	emb AW164476 AW164476 se73b10.yl Gm-c1023 Glycine max cDNA clone 34 2.2
	dbj D63781 SOYEHA Soybean mRNA for epoxide hydrolase, complete cds. 34 2.2
	gb U02495 STU02495 Solanum tuberosum Lemhi Russet clone EH4.1 ep 34 2.2
50	emb AI485507 AI485507 EST243828 tomato ovary, TAMU Lycopersicon 34 2.2
J U	
	gb U02497 STU02497 Solanum tuberosum Lemhi Russet clone EH10.1 e 34 2.2
	emb X82454 SHSHST3 S.hamata mRNA for low affinity sulphate trans 34 2.2
55	emb AW930466 AW930466 EST340839 tomato fruit mature green, TAMU 34 2.2
33	emb AW308974 AW308974 sf92e06.yl Gm-c1019 Glycine max cDNA clone 34 2.2
	emb AI894653 AI894653 EST264096 tomato callus, TAMU Lycopersicon 34 2.2
	emb AI485258 AI485258 EST243562 tomato ovary, TAMU Lycopersicon 34 2.2
	emb AI485798 AI485798 EST244119 tomato ovary, TAMU Lycopersicon 34 2.2
6 0	emb AI461013 AI461013 sa77h01.y1 Gm-c1004 Glycine max cDNA clone 34 2.2
60	emb AW038692 AW038692 EST280553 tomato mixed elicitor, BTI Lycop 34 2.2
	emb AW706725 AW706725 sk02c03.yl Gm-c1023 Glycine max cDNA clone 34 2.2

emb|AW217942|AW217942 EST296656 tomato flower buds, anthesis, Co... 34 2.2 emb|AW568104|AW568104 si68e03.yl Gm-r1030 Glycine max cDNA clone... 34 2.2 gb|BE021125|BE021125 sm55g03.yl Gm-c1028 Glycine max cDNA clone ... 34 2.2 emb|AI748138|AI748138 sb48f09.yl Gm-c1011 Glycine max cDNA clone... 34 2.2 gb|BE037499|BE037499 MP02C04 MP Mesembryanthemum crystallinum cD... 34 2.2 emb|AW932296|AW932296 EST358139 tomato fruit mature green, TAMU ... 34 2.2 emb|AI900294|AI900294 sc03f01.yl Gm-c1012 Glycine max cDNA clone... 34 2.2 emb|AW694549|AW694549 NF077D06ST1F1057 Developing stem Medicago ... 27 2.5 emb|AW286854|AW286854 LG1_222_C10.b1_A002 Light Grown 1 (LG1) So... 34 3.1 10 emb|AQ943121|AQ943121 Sheared DNA-33N2.TF Sheared DNA Trypanosom... 34 3.1 dbj|D87065|D87065 Triticum aestivum gene for histone H1, complet... 34 3.1 gb|BE053401|BE053401 GA_Ea0033I09f Gossypium arboreum 7-10 dpa ... 34 3.1 emb|AW286874|AW286874 LG1 222 E10.b1 A002 Light Grown 1 (LG1) So... 34 3.1 emb|AA063702|AA063702 T3328 MVAT4 bloodstream form of serodeme W... 34 3.1 15 Query= ATPRITAN r at 12933 r at /id source genbank /description emb|caa65420.1| (x96600) pathogenesis-related protein 1 [arabidopsis thaliana] /blast score 1.00e-101 /ec number /family /chip nova 20 /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|atprltan|/ncgi http://www.ncgr.org/cgi-bin/ff?atprltan (2616 letters) 25 Database: plantfungal 661,018 sequences: 426,114,510 total letters Searching.....done 30 Score Е Sequences producing significant alignments: (bits) Value emb[X66942[NTPRB1B N.tabacum prb-1b gene. 247 3e-64 emb|AW040954|AW040954 EST283818 tomato mixed elicitor, BTI Lycop... 245 1e-63 35 emb]AW219480]AW219480 EST301878 tomato root during/after fruit s... 245 le-63 emb|AW092623|AW092623 EST285803 tomato mixed elicitor, BTI Lycop... 245 1e-63 emb|AI894650|AI894650 EST264093 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW041033|AW041033 EST283897 tomato mixed elicitor, BTI Lycop... 245 1e-63 emb|AW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 245 1e-63 40 emb[AW034330]AW034330 EST277901 tomato callus, TAMU Lycopersicon... 245 le-63 emb|AI894391|AI894391 EST263846 tomato callus, TAMU Lycopersicon... 245 le-63 emb|AW217013|AW217013 EST295727 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW040983|AW040983 EST283847 tomato mixed elicitor, BTI Lycop... 245 1e-63 emb|AW032139|AW032139 EST275593 tomato callus, TAMU Lycopersicon... 245 1e-63 45 emb|AW092403|AW092403 EST285583 tomato mixed elicitor, BTI Lycop... 245 1e-63 emb|AI896249|AI896249 EST265692 tomato callus, TAMU Lycopersicon... 245 1e-63 emb[AW219671]AW219671 EST302153 tomato root during/after fruit s... 245 1e-63 emb|AW034206|AW034206 EST277777 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW034724|AW034724 EST278526 tomato callus, TAMU Lycopersicon... 245 1e-63 50 emb[AW034260]AW034260 EST277831 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW625930|AW625930 EST319825 tomato radicle, 5 d post-imbibit... 245 1e-63 emblAW032514|AW032514 EST276073 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW034454|AW034454 EST278025 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW032723|AW032723 EST276282 tomato callus, TAMU Lycopersicon... 245 le-63 55 emb[AW033873]AW033873 EST277444 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AI895090|AI895090 EST264533 tomato callus, TAMU Lycopersicon... 245 1e-63 emb|AW033593|AW033593 EST277164 tomato callus, TAMU Lycopersicon... 243 4e-63 emb|AW032749|AW032749 EST276308 tomato callus, TAMU Lycopersicon... 243 5e-63 emb|Al782621|Al782621 EST263500 tomato susceptible, Cornell Lyco... 242 7e-63 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 240 5e-62 60 emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 237 3e-61

	emb AW033687 AW033687 EST277258 tomato callus, TAMU Lycopersicon 232 7e-60
	emb AW094536 AW094536 EST287716 tomato mixed elicitor, BTI Lycop 230 5e-59
	emb AW038553 AW038553 EST280236 tomato mixed elicitor, BTI Lycop 230 5e-59
_	emb AI896011 AI896011 EST265454 tomato callus, TAMU Lycopersicon 230 5e-59
5	emb AW218808 AW218808 EST301288 tomato root during/after fruit s 230 5e-59
	emb AW035735 AW035735 EST281889 tomato callus, TAMU Lycopersicon 228 2e-58
	emb AW622662 AW622662 EST313462 tomato root during/after fruit s 227 2e-58
	emb AW031086 AW031086 EST274393 tomato callus, TAMU Lycopersicon 227 2e-58
	emb AW981257 AW981257 EST392410 DSIL Medicago truncatula cDNA cl 227 2e-58
10	emb AW559894 AW559894 EST314942 DSIR Medicago truncatula cDNA cl 209 3e-58
	emb AW559895 AW559895 EST314943 DSIR Medicago truncatula cDNA cl 209 3e-58
	emb AW329241 AW329241 N200453e rootphos(-) Medicago truncatula c 209 3e-58
	emb AW035757 AW035757 EST281911 tomato callus, TAMU Lycopersicon 227 3e-58
	emb X14065 NTPRP1 Nicotiana tabacum gene for basic form of patho 149 7e-58
15	emb AW032727 AW032727 EST276286 tomato callus, TAMU Lycopersicon 226 9e-58
	emb AW033469 AW033469 EST277040 tomato callus, TAMU Lycopersicon 224 2e-57
	emb X71592 LEPR1A1A L.esculentum PR-1a1 mRNA. 224 2e-57
	emb AW034455 AW034455 EST278026 tomato callus, TAMU Lycopersicon 224 2e-57
•	emb X52555 NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat 129 6e-57
20	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P 154 2e-56
	gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds. 154 2e-56
	emb AW035158 AW035158 EST280420 tomato callus, TAMU Lycopersicon 221 2e-56
	emb AW035469 AW035469 EST281207 tomato callus, TAMU Lycopersicon 221 3e-56
	omble W13636314 W136363 N1004600 morbbook) Medicage transport is 200 32 56
25	emb AW126362 AW126362 N100469e rootphos(-) Medicago truncatula c 209 3e-56
23	emb AW040722 AW040722 EST283586 tomato mixed elicitor, BTI Lycop 220 4e-56
	emb AW559969 AW559969 EST315017 DSIR Medicago truncatula cDNA cl 194 4e-56
	emb X05959 NTPRIAG Tobacco PR-1a gene for pathogenesis-related p 134 2e-55
	emb X12737 NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p 134 2e-55
20	emb X06361 NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela 134 2e-55
30	emb X12485 NTPR1A Tobacco mRNA fragment for pathogenesis-related 134 2e-55
	emb X06930 NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related 133 3e-55
	emb X17681 NTPR1CA Tobacco gene for pathogenesis-related protein 128 3e-55
	emb X05454 NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 128 3e-55
25	emb X12487 NTPR1C Tobacco mRNA fragment for pathogenesis-related 128 3e-55
35	emb AJ011520 LES011520 Lycopersicon esculentum pr1a (P4) gene. 147 5e-55
	dbj D90196 TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu 133 5e-55
	gb[M69247]TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat 147 5e-55
	emb A22634 LEPI4GENE L.esculentum P14 gene. 147 5e-55
40	gb BE034214 BE034214 MH01C07 MH Mesembryanthemum crystallinum cD 116 8e-55
40	emb AW053720 AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp 116 8e-55
	gb U64806 BNU64806 Brassica napus pathogenesis-related protein P 149 1e-54
	emb AW034882 AW034882 EST279111 tomato callus, TAMU Lycopersicon 144 5e-54
	emb AI782416 AI782416 EST263295 tomato susceptible, Cornell Lyco 144 7e-54
4-	emb AW559392 AW559392 EST314440 DSIR Medicago truncatula cDNA cl 191 9e-54
45	emb X17680 NTPR1BA Tobacco gene for pathogenesis-related protein 133 2e-53
	emb X03465 NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate 133 2e-53
	dbj D90197 TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 133 2e-53
	emb AJ250136 STU250136 Solanum tuberosum mRNA for pathogenesis r 144 2e-53
	emb[AI352851]AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl 149 2e-53
50	emb X12486 NTPR1B Tobacco mRNA fragment for pathogenesis-related 133 2e-53
	emb Y08804 LEPR1B1 L.esculentum mRNA for PR protein. 139 1e-52
	gb M69248 TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat 139 1e-52
	emb X68738 LEP1P14A L.esculentum mRNA for ethylene-induced P1(p1 139 1e-52
	emb AI781499 AI781499 EST262378 tomato susceptible, Cornell Lyco 139 1e-52
55	emb AI779424 AI779424 EST260303 tomato susceptible, Cornell Lyco 139 1e-52
	emb AW031093 AW031093 EST274400 tomato callus, TAMU Lycopersicon 139 1e-52
	emb AI779425 AI779425 EST260304 tomato susceptible, Cornell Lyco 139 1e-52
	emb AW040587 AW040587 EST283367 tomato mixed elicitor, BTI Lycop 141 1e-52
	emb AI782545 AI782545 EST263424 tomato susceptible, Cornell Lyco 139 1e-52
60	emb AI782822 AI782822 EST263701 tomato susceptible, Cornell Lyco 139 1e-52
	embl 1778686 A 1778686 FST 250565 tomato susceptible Cornell Lyco 120 1e 52

emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 139 1e-52 emb|AW039236|AW039236 EST281471 tomato mixed elicitor, BTI Lycop... 141 1e-52 emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 139 1e-52 emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 139 1e-52 5 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 139 1e-52 emb|AI778790|AI778790 EST259669 tomato susceptible, Cornell Lyco... 139 1e-52 emb|AI778791|AI778791 EST259670 tomato susceptible, Cornell Lyco... 139 1e-52 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 139 1e-52 emb|AW032026|AW032026 EST275480 tomato callus, TAMU Lycopersicon... 139 1e-52 10 emb|AI782288|AI782288 EST263167 tomato susceptible, Cornell Lyco... 139 1e-52 Query= ATTHIRED4 i at 13187 i at /id source genbank /description gblaac49356.1 (u35829) thioredoxin h [arabidopsis thaliana] 15 /blast score 2.00e-63 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|atthired4|/ncgi http://www.ncgr.org/cgi-bin/ff?atthired4 (528 letters) 20 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 25 Score Ε Sequences producing significant alignments: (bits) Value gb[U59379]BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 4e-49 30 emb[X89759]BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 4e-49 emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 2e-48 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 191 4e-48 emb|AW569018|AW569018 si74e02.yl Gm-c1031 Glycine max cDNA clone... 186 1e-46 emb|AI988470|AI988470 sd02f07.yl Gm-c1020 Glycine max cDNA clone... 186 le-46 35 emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 184 3e-46 emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. gb|BE053835|BE053835 GA Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 2e-45 emb|AW565750|AW565750 LG1 349 G02.g1 A002 Light Grown 1 (LG1) So... 181 3e-45 emb|AW677651|AW677651 WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45 40 emb|AW671668|AW671668 LG1 349 G02.b1 A002 Light Grown 1 (LG1) So... 181 3e-45 emb|AW924685|AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45 emb[AW677726]AW677726 WS1_10 F03.g1 A002 Water-stressed 1 (WS1) ... 181 3e-45 emb|AW349345|AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 180 6e-45 emb|AI461219|AI461219 sa76f11.yl Gm-c1004 Glycine max cDNA clone... 180 6e-45 emb|AI938238|AI938238 sc41e05.y1 Gm-c1014 Glycine max cDNA clone... 180 6e-45 emb|AW164730|AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone... 180 8e-45 emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. emb|AW255195|AW255195 ML185 peppermint glandular trichome Mentha... 178 2e-44 50 emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 177 5e-44 gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 5e-44 dbi|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 8e-44 gb|BE054543|BE054543 GA_Ea0026K15f Gossypium arboreum 7-10 dpa ... 177 8e-44 emb|AW983331|AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi... 177 8e-44 55 emb|AW329521|AW329521 N200767e rootphos(-) Medicago truncatula c... 176 1e-43 gb|BE053246|BE053246 GA_Ea0021K08f Gossypium arboreum 7-10 dpa ... 176 1e-43 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 175 2e-43 emb|AW781479|AW781479 s179e04.y1 Gm-c1037 Glycine max cDNA clone... 175 3e-43 emb|A48516|A48516 Sequence 4 from Patent WO9603505. 175 3e-43 60 emb|AW705063|AW705063 sk57b09.yl Gm-c1019 Glycine max cDNA clone... 175 3e-43

emb[AW164347]AW164347 se71c11.yl Gm-c1023 Glycine max cDNA clone... 175 3e-43

```
emb|AJ001903|TDAJ1903 Triticum durum mRNA for thioredoxin H.
                                                                        175 3e-43
       emb|A48520|A48520 Sequence 8 from Patent WO9603505.
                                                                     175 3e-43
      emb|X69915|TATHIORDH T.aestivum mRNA for thioredoxine H.
                                                                        175 3e-43
      emb|A48514|A48514 Sequence 2 from Patent WO9603505.
                                                                     175 3e-43
 5
      emb|AW568753|AW568753 si72f07.yl Gm-c1031 Glycine max cDNA clone... 175 3e-43
      emb|A48519|A48519 Sequence 7 from Patent WO9603505.
                                                                     175 3e-43
      emb|AW329764|AW329764 N201033e rootphos(-) Medicago truncatula c... 174 4e-43
      emb|AW982237|AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi... 174 Se-43
      emb|AW983305|AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi... 174 5e-43
10
      emb|AW626018|AW626018 EST319925 tomato radicle, 5 d post-imbibit... 174 5e-43
      emb|AW349509|AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ... 173 7e-
      gb|U59380|BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 8e-43
      emb|X58527|NTTRNA N.tabacum mRNA for thioredoxin.
                                                                     173 1e-42
15
      gb|C95504|C95504 C95504 Citrus unshiu Miyagawa-wase maturation s... 172 le-42
      emb|AI441505|AI441505 sa87c03.y1 Gm-c1004 Glycine max cDNA clone... 171 2e-42
      emb|AW277335|AW277335 sf80b02.y1 Gm-c1019 Glycine max cDNA clone... 171 2e-42
      emb|AW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 5e-42
      emb|AW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 5e-42
20
      emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 5e-42
      emblAW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emblAW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emblAW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 5e-42
25
      emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycope... 171 5e-42
      emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycope... 171 5e-42
      emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycope... 171 5e-42
30
      emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 5e-42
      emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 5e-42
35 .
      emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW597424|AW597424 si92g01.yl Gm-c1031 Glycine max cDNA clone... 169 2e-41
      emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 2e-41
      emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 2e-41
      emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 2e-41
40
      gb|BE057793|BE057793 sn07c11.yl Gm-c1016 Glycine max cDNA clone ... 168 2e-41
      emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 4e-40
      emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 1e-39
      emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 2e-39
45
      emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 2e-39
      emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 2e-39
50
      emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 3e-39
      emb|AW736931|AW736931 NXNV_081_G02_F Nsf Xylem Normal wood Verti... 161 3e-39
      emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161_4e-39
      emb|AW680877|AW680877 WS1 7 D07.g1 A002 Water-stressed 1 (WS1) S... 161 4e-39
      emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 5e-39
      emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 7e-39
      emb|AI736736|AI736736 sb32g12.yl Gm-c1012 Glycine max cDNA clone... 93 1e-38
      emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 1e-38
      emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 2e-38
      emb|AW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 3e-38
60
      emb|AA740038|AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'... 157 5e-38
      emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 5e-38
```

emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 1e-37 emb|AW706540|AW706540 sj57g11.y1 Gm-c1033 Glycine max cDNA clone... 156 1e-37 emb|AI461254|AI461254 sa60f10.y1 Gm-c1004 Glycine max cDNA clone... 155 2e-37 emb|AW924415|AW924415 WS1_69_D02.b1_A002 Water-stressed 1 (WS1) ... 154 4e-37 emb|AW679524|AW679524 WS1_29_F05.g1_A002 Water-stressed 1 (WS1) ... 154 4e-37 emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 4e-37 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37 emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

10

20

30

5

Query= ATTHIRED4_r_at 13188_r_at /id_source genbank /description gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana] /blast_score 2.00e-63 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|atthired4| /ncgi http://www.ncgr.org/cgi-bin/ff?atthired4 (528 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching......done

Score E

25 Sequences producing significant alignments:

(bits) Value

emb|X89759|BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 4e-49 emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 2e-48 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 191 4e-48 emb|AW569018|AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone... 186 1e-46 emb|AI988470|AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone... 186 1e-46 emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 184 3e-46 emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. 183 9e-46

gb|U59379|BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 4e-49

35 gb|BE053835|BE053835 GA_ Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 2e-45 emb|AW565750|AW565750 LG1_349_G02.gl_A002 Light Grown 1 (LG1) So... 181 3e-45 emb|AW677651|AW677651 WS1_10_F03.bl_A002 Water-stressed 1 (WS1) ... 181 3e-45 emb|AW671668|AW671668 LG1_349_G02.bl_A002 Light Grown 1 (LG1) So... 181 3e-45 emb|AW924685|AW924685 WS1_71_B11.bl_A002 Water-stressed 1 (WS1) ... 181 3e-45

40 emb|AW677726|AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ... 181 3e-45 emb|AW349345|AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 180 6e-45

emb|AI461219|AI461219 sa76f11.y1 Gm-c1004 Glycine max cDNA clone... 180 6e-45 emb|AI938238|AI938238 sc41e05.y1 Gm-c1014 Glycine max cDNA clone... 180 6e-45 emb|AW164730|AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone... 180 8e-45 emb|AJ009762|TAE9762 Triticum aestiyum mRNA for thioredoxin H 179 2e-44

emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. 179 2e-44 emb|AW255195|AW255195 ML185 peppermint glandular trichome Mentha... 178 2e-44 emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 177 5e-44 gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 5e-44

dbj|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 8e-44 gb|BE054543|BE054543 GA_Ea0026K15f Gossypium arboreum 7-10 dpa ... 177 8e-44 emb|AW983331|AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi... 177 8e-44 emb|AW329521|AW329521 N200767e rootphos(-) Medicago truncatula c... 176 1e-43 gb|BE053246|BE053246 GA Ea0021K08f Gossypium arboreum 7-10 dpa ... 176 1e-43

55 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 175 2e-43 emb|AW781479|AW781479 s179e04.y1 Gm-c1037 Glycine max cDNA clone... 175 3e-43 emb|A48516|A48516 Sequence 4 from Patent WO9603505. 175 3e-43 emb|AW705063|AW705063 sk57b09.y1 Gm-c1019 Glycine max cDNA clone... 175 3e-43 emb|AW164347|AW164347 se71c11.y1 Gm-c1023 Glycine max cDNA clone... 175 3e-43

60 emb|AJ001903|TDAJ1903 Triticum durum mRNA for thioredoxin H. 175 3e-43 emb|A48520|A48520 Sequence 8 from Patent WO9603505. 175 3e-43

```
emblX69915|TATHIORDH T.aestivum mRNA for thioredoxine H.
                                                                        175 3e-43
      emb|A48514|A48514 Sequence 2 from Patent WO9603505.
                                                                     175 3e-43
      emb|AW568753|AW568753 si72f07.yl Gm-c1031 Glycine max cDNA clone... 175 3e-43
      emb|A48519|A48519 Sequence 7 from Patent WO9603505.
                                                                     175 3e-43
 5
      emb|AW329764|AW329764 N201033e rootphos(-) Medicago truncatula c... 174 4e-43
      emb[AW982237]AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi... 174 5e-43
      emblAW983305|AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi... 174 5e-43
      emb|AW626018|AW626018 EST319925 tomato radicle, 5 d post-imbibit... 174 5e-43
      emb|AW349509|AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ... 173 7e-
10
      gb|U59380|BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 8e-43
      emb[X58527]NTTRNA N.tabacum mRNA for thioredoxin.
                                                                     173 1e-42
      gb|C95504|C95504 C95504 Citrus unshiu Miyagawa-wase maturation s... 172 1e-42
      emb|AI441505|AI441505 sa87c03.yl Gm-c1004 Glycine max cDNA clone... 171 2e-42
15
      emb|AW277335|AW277335 sf80b02.yl Gm-c1019 Glycine max cDNA clone... 171 2e-42
      emb|AW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 5e-42
      emblAW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 5e-42
      emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 5e-42
      emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
20
      emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycope... 171 5e-42
25
      emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycope... 171 5e-42
      emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycope... 171 5e-42
      emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 5e-42
30
      emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 5e-42
      emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW597424|AW597424 si92g01.yl Gm-c1031 Glycine max cDNA clone... 169 2e-41
35
      emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 2e-41
      emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 2e-41
      emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 2e-41
      gb|BE057793|BE057793 sn07c11.yl Gm-c1016 Glycine max cDNA clone ... 168 2e-41
      emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 4e-40
40
      emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 1e-39
      emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 2e-39
45
      emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 2e-39
      emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 3e-39
      emb|AW736931|AW736931 NXNV 081 G02 F Nsf Xylem Normal wood Verti... 161 3e-39
50
      emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 4e-39
      emb|AW680877|AW680877 WS1_7 D07.g1 A002 Water-stressed 1 (WS1) S... 161 4e-39
      emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 5e-39
      emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 7e-39
      emb|AI736736|AI736736 sb32g12.yl Gm-c1012 Glycine max cDNA clone... 93 1e-38
55
      emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 1e-38
      emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 2e-38
      emb|AW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 3e-38
      emb|AA740038|AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'... 157 5e-38
      emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 5e-38
60
      emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 1e-37
      emb|AW706540|AW706540 sj57g11.yl Gm-c1033 Glycine max cDNA clone... 156 1e-37
```

emb|AI461254|AI461254 sa60f10.yl Gm-c1004 Glycine max cDNA clone... 155 2e-37 emb|AW924415|AW924415 WS1_69_D02.b1_A002 Water-stressed 1 (WS1) ... 154 4e-37 emb|AW679524|AW679524 WS1 29 F05.g1 A002 Water-stressed 1 (WS1) ... 154 4e-37 emb|AW681036|AW681036 WS1 8 D05.b1 A002 Water-stressed 1 (WS1) S... 154 4e-37 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37 emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

Query= ATTHIRED4 s at 13189 s at /id source genbank /description 10 gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana] /blast score 2.00e-63 /ec number /family /chip nova /gb link /ncgi (528 letters)

Database: plantfungal

5

25

40

15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score

20 Sequences producing significant alignments:

(bits) Value

emb|X89759|BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 4e-49 emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 2e-48 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 191 4e-48 emb|AW569018|AW569018 si74e02.yl Gm-c1031 Glycine max cDNA clone... 186 1e-46 emb|AI988470|AI988470 sd02f07.yl Gm-c1020 Glycine max cDNA clone... 186 1e-46 emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 184 3e-46 emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. 183 9e-46

gb[U59379|BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 4e-49

30 gb|BE053835|BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 2e-45 emb|AW565750|AW565750 LG1_349 G02.g1 A002 Light Grown 1 (LG1) So... 181 3e-45 emb|AW677651|AW677651 WS1 10 F03.b1 A002 Water-stressed 1 (WS1) ... 181 3e-45 emb|AW671668|AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So... 181 3e-45 emb|AW924685|AW924685 WS1 71 B11.b1 A002 Water-stressed 1 (WS1) ... 181 3e-45

35 emb|AW677726|AW677726 WS1 10 F03.g1 A002 Water-stressed 1 (WS1) ... 181 3e-45 emb|AW349345|AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 180 6e-

emb|AI461219|AI461219 sa76f11.yl Gm-c1004 Glycine max cDNA clone... 180 6e-45 emb|AI938238|AI938238 sc41e05.yl Gm-c1014 Glycine max cDNA clone... 180 6e-45 emb|AW164730|AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone... 180 8e-45 emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. emb|AW255195|AW255195 ML185 peppermint glandular trichome Mentha... 178 2e-44 emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 177 5e-44

gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 5e-44 45 dbj|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 8e-44 emb|AW983331|AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi... 177 8e-44 emb|AW329521|AW329521 N200767e rootphos(-) Medicago truncatula c... 176 1e-43 gb|BE053246|BE053246 GA_Ea0021K08f Gossypium arboreum 7-10 dpa ... 176 1e-43

50 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 175 2e-43 emb|AW781479|AW781479 s179e04.y1 Gm-c1037 Glycine max cDNA clone... 175 3e-43 emb|A48516|A48516 Sequence 4 from Patent WO9603505. 175 3e-43 emb|AW705063|AW705063 sk57b09.y1 Gm-c1019 Glycine max cDNA clone... 175 3e-43 emb|AW164347|AW164347 se71c11.yl Gm-c1023 Glycine max cDNA clone... 175 3e-43

emb]AJ001903[TDAJ1903 Triticum durum mRNA for thioredoxin H. 175 3e-43 emb|A48520|A48520 Sequence 8 from Patent WO9603505. 175 3e-43 emb|X69915|TATHIORDH T.aestivum mRNA for thioredoxine H. 175 3e-43 emb|A48514|A48514 Sequence 2 from Patent WO9603505. 175 3e-43 emb|AW568753|AW568753 si72f07.yl Gm-c1031 Glycine max cDNA clone... 175 3e-43 60 emb|A48519|A48519 Sequence 7 from Patent WO9603505. 175 3e-43

emb|AW329764|AW329764 N201033e rootphos(-) Medicago truncatula c... 174 4e-43

```
emb|AW982237|AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi... 174 Se-43
      emb|AW983305|AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi... 174 5e-43
      emb|AW626018|AW626018 EST319925 tomato radicle, 5 d post-imbibit... 174 5e-43
      emb|AW349509|AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ... 173 7e-
 5
      gb|U59380|BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 8e-43
      emb[X58527]NTTRNA N.tabacum mRNA for thioredoxin.
      gb|C95504|C95504 C95504 Citrus unshiu Miyagawa-wase maturation s... 172 1e-42
      emb|AI441505|AI441505 sa87c03.yl Gm-c1004 Glycine max cDNA clone... 171 2e-42
10
      emb|AW277335|AW277335 sf80b02.yl Gm-c1019 Glycine max cDNA clone... 171 2e-42
      emb|AW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 5e-42
      emb|AW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 5e-42
      emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 5e-42
      emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
15
      emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycope... 171 5e-42
20
      emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycope... 171 5e-42
      emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycope... 171 5e-42
      emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 5e-42
25
      emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 5e-42
      emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 5e-42
      emb|AW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 5e-42
      emb|AW597424|AW597424 si92g01.yl Gm-c1031 Glycine max cDNA clone... 169 2e-41
30
      emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 2e-41
      emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 2e-41
      emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 2e-41
      gb|BE057793|BE057793 sn07c11.yl Gm-c1016 Glycine max cDNA clone ... 168 2e-41
      emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 4e-40
35
      emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 1e-39
      emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 2e-39
40
      emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 2e-39
      emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 2e-39
      emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 3e-39
      emb|AW736931|AW736931 NXNV 081 G02 F Nsf Xylem Normal wood Verti... 161 3e-39
45
      emb|AW680784|AW680784 WS1 7 D07.b1 A002 Water-stressed 1 (WS1) S... 161 4e-39
      emb|AW680877|AW680877 WS1 7 D07.g1 A002 Water-stressed 1 (WS1) S... 161 4e-39
      emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 5e-39
      emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 7e-39
      emb|AI736736|AI736736 sb32g12.yl Gm-c1012 Glycine max cDNA clone... 93 1e-38
50
      emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 1e-38
      emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 2e-38
      emb|AW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 3e-38
      emb|AA740038|AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'... 157 5e-38
      emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 5e-38
      emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 1e-37
      emb|AW706540|AW706540 sj57g11.yl Gm-c1033 Glycine max cDNA clone... 156 1e-37
      emb|AI461254|AI461254 sa60f10.yl Gm-c1004 Glycine max cDNA clone... 155 2e-37
      emb|AW924415|AW924415 WS1 69_D02.b1_A002 Water-stressed 1 (WS1) ... 154 4e-37
      emb|AW679524|AW679524 WS1 29 F05.g1 A002 Water-stressed 1 (WS1) ... 154 4e-37
60
      emb|AW681036|AW681036 WS1 8 D05.b1_A002 Water-stressed 1 (WS1) S... 154 4e-37
      emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37
```

emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

```
Query= ATTS0190 i at 13198 i at /id source genbank /description
 5
      emb|caa16892.1| (al021749) 12s cruciferin seed storage protein
       [arabidopsis thaliana] /blast_score 1.00e-46 /ec_number /family
      /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|atts0190| /ncgi
10
      http://www.ncgr.org/cgi-bin/ff?atts0190
           (433 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
15
      Searching......done
                                           Score
                                                   E
      Sequences producing significant alignments:
                                                           (bits) Value
20
      emb|X62120|BNCRU1 B.napus cru1 gene for cruciferin subunit.
                                                                     169 4e-48
      gb|J05233|BNACRUCA B.napus cruciferin mRNA, 3' end.
                                                                     169 9e-48
      emb|X59808|RSCRUG R.sativus pgCruRsE5 gene for cruciferin.
                                                                      168 4e-43
      emb|X59802|RSCRU1 R.sativus pAF7 mRNA for cruciferin.
                                                                     165 le-42
25
      emb|X59804|RSCRU3 R.sativus pAC2 mRNA for cruciferin.
                                                                      123 le-41
      emb|X57850|BNCRU4RN B.napus cru4 mRNA for cruciferin cru4 subunit. 138 2e-32
      emb|X57848|BNCRU4RNA B.napus cru4 mRNA for cruciferin cru4 subunit. 137 6e-32
      gb|M16860|BNACRUC Rapeseed cruciferin mRNA, complete cds.
                                                                         132 1e-30
      emblX59294|BNC1G B.napus BnC1 gene for cruciferin storage protein. 132 1e-30
30
      emb|X14555|BNCRUA Brassica napus cruA gene for cruciferin.
                                                                      132 1e-30
      emb|X57849|BNCRU23 B.napus cru2/3 mRNA for cruciferin cru2/3 sub... 132 1e-30
      emb|X59807|RSCRU6 R.sativus pAE10 mRNA for cruciferin.
                                                                      131 3e-30
      emb|X59806|RSCRU5 R.sativus pBB6 mRNA for cruciferin.
                                                                      131 3e-30
      emb|X59295|BNC2G B.napus BnC2 gene for cruciferin storage protein.
                                                                       130 5e-30
35
      emb|X82121|AHGLOBLN A.hypochondriacus mRNA for globulin.
                                                                          118 3e-26
      gb|U38914|CSU38914 Citrus sinensis seed storage protein citrin m... 108 3e-23
      emb|X59803|RSCRU2 R.sativus pAG4 mRNA for cruciferin.
                                                                      81 3e-22
      emb|AF262998|AF262998 Ricinus communis legumin-like protein mRNA... 104 4e-22
      gb|T14851|T14851 crs298 lambdaZAPST Ricinus communis cDNA clone ... 99 2e-20
40
      emb|X82464|MSLEGA2 M.salicifolia mRNA for legumin precursor (A2).
      emb|X78119|PABTPRU1 P.amygdalus, Batsch (Texas) pru1 mRNA.
                                                                          99 2e-20
      gb|T23274|T23274 crs1128 lambdaZAPST Ricinus communis cDNA clone... 98 3e-20
      emb|AF262999|AF262999 Ricinus communis seed storage protein mRNA... 98 3e-20
      gb|T15203|T15203 crs691 lambdaZAPST Ricinus communis cDNA clone ... 98 3e-20
45
      gb T14921 T14921 crs404 lambda ZAPST Ricinus communis cDNA clone ... 98 3e-20
      gb|T15096|T15096 crs739 lambdaZAPST Ricinus communis cDNA clone ... 98 4e-20
      emb|X78120|PABTPRU2 P.amygdalus, Batsch (Texas) pru2 mRNA.
                                                                          97 6e-20
      emb|X82463|MSLEGA11 M.salicifolia mRNA for legumin precursor (A1... 97 8e-20
      gb|T15159|T15159 crs641 lambdaZAPST Ricinus communis cDNA clone ... 95 4e-19
50
      gb|U64443|CAU64443 Coffea arabica 11S storage globulin mRNA, com... 94 5e-19
      gb T24329 T24329 crs1443 lambdaZAPST Ricinus communis cDNA clone... 93 le-18
      gb|U43727|GHU43727 Gossypium hirsutum legumin B (LegB-C134) gene... 92 2e-18
      gb|M16936|COTSPB G.hirsutum (cotton) storage protein (beta-globu... 92 2e-18
      emb|AF054895|AF054895 Coffea arabica 11S storage globulin mRNA, ... 92 2e-18
      emb|Y16976|CAR16976 Coffea arabica mRNA for 11S storage protein.
      gb|M28832|HNNHAG3D1S Sunflower 11S storage protein (G3-D1) DNA, ... 91 4e-18
      emb|AW036288|AW036288 EST278367 tomato seed, TAMU Lycopersicon e... 90 7e-18
      gb|T24192|T24192 crs605 lambdaZAPST Ricinus communis cDNA clone ... 90 9e-18
      gb|M36407|CUC11SGB Pumpkin 11-S globulin beta-subunit mRNA, comp... 89 2e-17
60
      emb|Y09116|SSPPLEGUM S.sagittifolia mRNA for pre-pro-legumin.
      emb|X82465|MSLEGB14 M.salicifolia mRNA for legumin precursor (B14). 89 2e-17
```

	emb AW395643 AW395643 sg73e07.yl Gm-c1007 Glycine max cDNA clone 88 4e-17 emb X74740 ASGLAV1G A.sativa GLAV l gene for 11S globulin. 88 4e-17 dbj D87982 D87982 Fagopyrum esculentum mRNA for legumin-like pro 88 4e-17
5	emb AF216801 AF216801 Fagopyrum esculentum allergenic protein ge 87 6e-17 emb AF152003 AF152003 Fagopyrum esculentum major allergenic stor 87 6e-17 emb AW036551 AW036551 EST283050 tomato seed, TAMU Lycopersicon e 87 6e-17
,	gb T24206 T24206 crs620 lambdaZAPST Ricinus communis cDNA clone 87 6e-17 gb T24336 T24336 crs1452 lambdaZAPST Ricinus communis cDNA clone 87 8e-17 dbj D87980 D87980 Fagopyrum esculentum mRNA for legumin-like pro 86 1e-16
10	emb X68648 AS12S A.sativa pseudogene for 12S seed globulin. 86 1e-16 gb M69188 COTDGALA Cotton legumin A D-genome alloallele gene, co 86 1e-16 gb M16905 COTSPD G.hirsutum (cotton) storage protein (beta-globu 86 1e-16
15	emb X74741 ASGLAV3G A.sativa GLAV 3 gene for 11S globulin. 86 1e-16 emb AF091842 AF091842 Sesamum indicum strain Tainan 1 11S globul 86 2e-16 gb J05485 ASTSSP12S A.sativa 12S globulin seed storage protein g 85 2e-16
	emb X17637 AS12SSP Oat gene for 12S seed storage protein. 85 2e-16 gb T24158 T24158 crs141 lambdaZAPST Ricinus communis cDNA clone 85 3e-16 emb X15121 GMGY1 Soybean Gyl gene for glycinin subunit G1. 84 4e-16 emb AI941002 AI941002 sb83b02.yl Gm-c1010 Glycine max cDNA clone 84 4e-16
20	gb M36686 SOYGLYBSU Soybean glycinin A-1a-B-x subunit mRNA, comp 84 4e-16 emb AW318204 AW318204 sg62d03.y1 Gm-c1007 Glycine max cDNA clone 84 4e-16 emb AW397452 AW397452 sg79a12.y1 Gm-c1007 Glycine max cDNA clone 84 4e-16 gb T14825 T14825 crs267 lambdaZAPST Ricinus communis cDNA clone 84 4e-16 emb AW433058 AW433058 si04a05.y1 Gm-c1029 Glycine max cDNA clone 84 4e-16
25	emb AI748751 AI748751 sb61e06.y1 Gm-c1010 Glycine max cDNA clone 84 4e-16 emb X02985 GMGLY1A Soybean mRNA for glycinin AlaBx precursor. 84 4e-16 emb AW317751 AW317751 sg56g11.y1 Gm-c1007 Glycine max cDNA clone 84 4e-16 emb AW317991 AW317991 sg59g07.y1 Gm-c1007 Glycine max cDNA clone 84 4e-16 emb AI735878 AI735878 sb20a12.y1 Gm-c1007 Glycine max cDNA clone 84 4e-16
30	emb AW397311 AW397311 sg77c11.yl Gm-c1007 Glycine max cDNA clone 84 4e-16 emb AW318315 AW318315 sg63f06.yl Gm-c1007 Glycine max cDNA clone 84 4e-16 emb X95509 AELEG18GN A.europaeum mRNA for legumin. 84 6e-16 dbj E08573 E08573 cDNA encoding 12S globulin A2B of oats. 84 6e-16 emb X76738 AS12SGLOB A.sativa (L) mRNA for 12S globulin (1685 bp). 84 6e-16
35	emb AW397302 AW397302 sg77c02.yl Gm-c1007 Glycine max cDNA clone 84 6e-16 emb Y09117 SSPPLTAND S.sagittifolia mRNA for pre-pro-legumin and 84 8e-16 emb AI941031 AI941031 sb83e04.yl Gm-c1010 Glycine max cDNA clone 83 1e-15 emb AI748075 AI748075 sb47h08.yl Gm-c1011 Glycine max cDNA clone 83 1e-15 emb AW036363 AW036363 EST278488 tomato seed, TAMU Lycopersicon e 83 1e-15
40	emb AI777374 AI777374 EST263782 tomato seed, TAMU Lycopersicon e 83 1e-15 emb AW036221 AW036221 EST278219 tomato seed, TAMU Lycopersicon e 83 1e-15 emb AW036121 AW036121 EST274497 tomato seed, TAMU Lycopersicon e 83 1e-15 emb AW036283 AW036283 EST278362 tomato seed, TAMU Lycopersicon e 83 1e-15 emb AF261691 AF261691 Elaeis guineensis glutelin mRNA, complete 82 2e-15
45	emb AW397866 AW397866 sg69c05.yl Gm-c1007 Glycine max cDNA clone 82 3e-15 gb T24371 T24371 crs1501 lambdaZAPST Ricinus communis cDNA clone 82 3e-15 gb T24377 T24377 crs1511 lambdaZAPST Ricinus communis cDNA clone 82 3e-15 gb T24370 T24370 crs1500 lambdaZAPST Ricinus communis cDNA clone 82 3e-15 emb X15123 GMGY3 Soybean Gy3 gene for glycinin subunit G3. 81 4e-15
50	emb AI748727 AI748727 sb61b06.yl Gm-c1010 Glycine max cDNA clone 81 4e-15 emb AF193433 AF193433 Elaeis guineensis glutelin (PKT9) mRNA, co 81 4e-15 emb X76737 AS12SGL1 A.sativa (L) mRNA for 12S globulin (1556 bp). 81 5e-15 gb M21405 ASTSPGLBA Oat seed storage globulin mRNA, complete cds. 81 5e-15 gb T23264 T23264 crs1114 lambdaZAPST Ricinus communis cDNA clone 81 5e-15
55	gb M16868 ASTGLOB Oat storage protein 12S globulin mRNA, partial 81 5e-15 emb AW397079 AW397079 sg66g02.yl Gm-c1007 Glycine max cDNA clone 81 5e-15 emb AF180392 AF180392 Perilla frutescens legumin-like protein mR 80 7e-15 emb AI941048 AI941048 sb83f11.yl Gm-c1010 Glycine max cDNA clone 80 7e-15
60	gb[T14967[T14967 crs454 lambdaZAPST Ricinus communis cDNA clone 80 7e-15

Query= cafferoylCoAmethyltrans s_at 13215_s_at /id_source genbank /description gb/aaf16576.1/ac012563 29 (ac012563) putative s-adenosyl-l-methionine:trans-caffeoyl-coenzyme a 3-o-methyltransferase [arabidopsis thaliana] /blast score 1.00e-121 /ec number /family /chip nova /gb_link /ncgi 5 (965 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching......done Score E Sequences producing significant alignments: (bits) Value 15 emb|AB000408|AB000408 Populus kitakamiensis mRNA for caffeoyl-Co... 215 3e-73 gb[U20736]MSU20736 Medicago sativa S-adenosyl-L-methionine:trans... 142 2e-68 emb|AW624860|AW624860 EST313689 tomato radicle, 5 d post-imbibit... 139 2e-67 emb|AF022775|AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methylt... 138 2e-67 20 emb|Z54233|VVCCOAOMT V.vinifera mRNA for caffeoyl-CoA O-methyltr... 136 9e-67 gb|M69184|PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl... 133 2e-66 gb|U27116|PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr... 135 3e-66 emb|AJ224894|PBTAJ4894 Populus balsamifera subsp. trichocarpa mR... 135 3e-66 gb|U13151|ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-... 136 4e-66 25 emb|AI489305|AI489305 EST247644 tomato ovary, TAMU Lycopersicon ... 139 4e-66 emb|AJ224895|PBTAJ4895 Populus balsamifera subsp. trichocarpa mR... 136 6e-66 emb|AJ224896|PBTAJ4896 Populus balsamifera subsp. trichocarpa mR... 136 6e-66 emb|AF168780|AF168780 Eucalyptus globulus caffeoyl-CoA O-methylt... 133 8e-66 emb|AF053553|AF053553 Mesembryanthemum crystallinum caffeoyl-CoA... 132 1e-65 30 emb|AF240466|AF240466 Populus tomentosa caffeoyl-CoA O-methyltra... 135 1e-65 emb|A22706|A22706 Caffeoyl-CoA-3-O-Methyltransferase gene. gb|U62734|NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 5e-65 emb|Z56282|NTCCOAOMT N.tabacum mRNA for caffeoyl-CoA O-methyltra... 132 5e-65 gb|U62736|NTU62736 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 136 5e-65 35 gb|U38612|NTU38612 Nicotiana tabacum caffeoyl-coenzymeA O-methyl... 136 5e-65 emb|Y12228|EG12228 E.gunnii mRNA for caffeoyl-CoA O-methyltransf... 133 7e-65 gb|L22203|SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr... 124 8e-65 emb|AF046122|AF046122 Eucalyptus globulus caffeoyl-CoA 3-O-methy... 133 9e-65 gb|U62735|NTU62735 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 3e-64 40 emb|AF036095|AF036095 Pinus taeda caffeoyl-CoA O-methyltransfera... 130 6e-64 emb|AF060180|AF060180 Nicotiana tabacum caffeoyl-coenzyme A trun... 90 9e-60 emb|AW102353|AW102353 sd86f04.yl Gm-c1009 Glycine max cDNA clone... 139 5e-58 emb|AJ130841|PBA130841 Populus balsamifera subsp. trichocarpa mR... 133 2e-57 emb|AJ001447|FVAJ1447 Fragaria vesca mRNA for putative caffeoyl-... 137 3e-57 gb|BE124003|BE124003 EST394128 DSIL Medicago truncatula cDNA clo... 127 9e-57 emb|AW775400|AW775400 EST334465 DSIL Medicago truncatula cDNA cl... 142 2e-56 emb|AW030189|AW030189 EST273444 tomato callus, TAMU Lycopersicon... 133 4e-56 emb|AW695080|AW695080 NF091D11ST1F1093 Developing stem Medicago ... 142 6e-56 emb|AW348485|AW348485 GM210002B12A10R Gm-r1021 Glycine max cDNA ... 131 2e-50 emb|AI486500|AI486500 EST244821 tomato ovary, TAMU Lycopersicon ... 139 2e-55 emb|AI166541|AI166541 xylem.est.363 Poplar xylem Lambda ZAPII li... 135 7e-55 gb|BE034896|BE034896 ML05H01 ML Mesembryanthemum crystallinum cD... 132 1e-54 emb|AW306951|AW306951 sf50h03.y1 Gm-c1009 Glycine max cDNA clone... 133 2e-54 emb|AW278810|AW278810 sf98g06.y1 Gm-c1019 Glycine max cDNA clone... 135 3e-54 emb|AI939180|AI939180 sc67h02.yl Gm-c1016 Glycine max cDNA clone... 125 3e-54 emb|AW102461|AW102461 sd88d11.yl Gm-c1009 Glycine max cDNA clone... 133 3e-54 emb|AW776700|AW776700 EST335765 DSIL Medicago truncatula cDNA cl... 127 4e-54 emb|AW757356|AW757356 sl32c10.yl Gm-c1027 Glycine max cDNA clone... 133 2e-53 60 emb|AW030736|AW030736 EST273991 tomato callus, TAMU Lycopersicon... 133 8e-53

emb|AI898029|AI898029 EST267472 tomato ovary, TAMU Lycopersicon ... 133 8e-53

emb|AW625527|AW625527 EST319434 tomato radicle, 5 d post-imbibit... 133 8e-53 emb|AW218547|AW218547 EST303730 tomato radicle, 5 d post-imbibit... 133 8e-53 emblAW733300|AW733300 sk71f10.yl Gm-c1016 Glycine max cDNA clone... 134 1e-52 emb|AW442463|AW442463 EST307393 tomato mixed elicitor, BTI Lycop... 133 1e-52 5 emb|AW094365|AW094365 EST287545 tomato mixed elicitor, BTI Lycop... 133 1e-52 gb|BE021597|BE021597 sm60a04.yl Gm-c1028 Glycine max cDNA clone ... 135 1e-52 emb|AW034347|AW034347 EST277918 tomato callus, TAMU Lycopersicon... 133 2e-52 emb|AI443130|AI443130 sa84g01.y1 Gm-c1004 Glycine max cDNA clone... 131 2e-51 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51 10 emb|AW424002|AW424002 sh59c10.yl Gm-c1015 Glycine max cDNA clone... 115 2e-51 emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50 emb|A1899227|A1899227 EST268670 tomato ovary, TAMU Lycopersicon ... 139 3e-50 emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50 15 emb|AW690185|AW690185 NF029D09ST1F1000 Developing stem Medicago ... 142 1e-49 emb|AI895091|AI895091 EST264534 tomato callus, TAMU Lycopersicon... 99 3e-49 emb|AW306980|AW306980 sf51c05.yl Gm-c1009 Glycine max cDNA clone... 135 8e-48 emb|AW695176|AW695176 NF092D12ST1F1101 Developing stem Medicago ... 142 1e-47 emb[AW684885]AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47 20 emb|AA660318|AA660318 00189 MtRHE Medicago truncatula cDNA 5' si... 144 2e-47 emb|AW703717|AW703717 sk23e07.yl Gm-c1028 Glycine max cDNA clone... 132 4e-47 emb|AW776435|AW776435 EST335500 DSIL Medicago truncatula cDNA cl... 142 5e-47 emb|AI486948|AI486948 EST245270 tomato ovary, TAMU Lycopersicon ... 100 1e-46 emb|AW620537|AW620537 sj06d09.yl Gm-c1032 Glycine max cDNA clone... 133 1e-46 25 emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycope... 139 2e-46 gb|BE124333|BE124333 EST393368 GVN Medicago truncatula cDNA clon... 125 3e-46 emb|AW704578|AW704578 sk38h08.y1 Gm-c1028 Glycine max cDNA clone... 140 3e-46 emb|AW350997|AW350997 GM210010A10C11R Gm-r1021 Glycine max cDNA ... 97 6e-46 emb|AW707224|AW707224 sk22c12.yl Gm-c1028 Glycine max cDNA clone... 140 9e-46 30 emb|AW625126|AW625126 EST313943 tomato radicle, 5 d post-imbibit... 133 6e-45 emb|AI974778|AI974778 T113251e KV2 Medicago truncatula cDNA clon... 142 6e-45 emb|AI898101|AI898101 EST267544 tomato ovary, TAMU Lycopersicon ... 98 8e-45 gb|BE124175|BE124175 EST394300 DSIL Medicago truncatula cDNA clo... 127 1e-44 emb|AW686370|AW686370 NF040G10NR1F1000 Nodulated root Medicago t... 127 4e-44 35 emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44 emb|AW256836|AW256836 EST304973 KV2 Medicago truncatula cDNA clo... 144 5e-44 emb|AW559274|AW559274 EST306110 DSIR Medicago truncatula cDNA cl... 142 5e-44 emb|AW278618|AW278618 sf46h04.y1 Gm-c1009 Glycine max cDNA clone... 139 1e-43 gb|BE059325|BE059325 sn31c09.yl Gm-c1016 Glycine max cDNA clone ... 140 3e-43 40 emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43 emb|AI938893|AI938893 sc62d08.y1 Gm-c1016.Glycine max cDNA clone... 134 2e-42 emb|AW257069|AW257069 EST305206 KV2 Medicago truncatula cDNA clo... 142 2e-42 emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42 45 emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41 emb|AW152892|AW152892 se32d04.y1 Gm-c1015 Glycine max cDNA clone... 82 2e-41 gb|BE125749|BE125749 DG1 55 H11.b1 A002 Dark Grown 1 (DG1) Sorgh... 127 2e-41 gb|BE022002|BE022002 sm65c10.yl Gm-c1028 Glycine max cDNA clone ... 137 3e-41 emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41 50 emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40 emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40 emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40 emb|Al960196|Al960196 sc80a08.yl Gm-c1018 Glycine max cDNA clone... 132 5e-40 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39 55 ... emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

Query= calmodulinlike_s_at 13217_s_at /id_source genbank /description emb|cab42906.1| (al049862) calmodulin-like protein [arabidopsis thaliana] /blast_score 6.00e-99 /ec_number /family /chip nova /gb link /ncgi

(827 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters 5 Searching.....done E Score Sequences producing significant alignments: (bits) Value 10 emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28 emb|AW350323|AW350323 GM210007B20E12R Gm-r1021 Glycine max cDNA ... 80 2e-27 emb|AW509006|AW509006 si38h07.yl Gm-r1030 Glycine max cDNA clone... 79 2e-26 emb|AW685404|AW685404 NF028H10NR1F1000 Nodulated root Medicago t... 74 2e-24 15 emb|AW781320|AW781320 sk68d07.y1 Gm-c1016 Glycine max cDNA clone... 86 2e-24 emb|AI897832|AI897832 EST267275 tomato ovary, TAMU Lycopersicon ... 78 1e-23 emb[AW102460]AW102460 sd88d10.y1 Gm-c1009 Glycine max cDNA clone... 70 2e-22 emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22 emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20 20 gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19 emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 le-18 emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18 dbi|D10521|TETCALW T.pyriformis mRNA for calmodulin. 73 7e-18 gb|M76407|SLECALMODU Stylonychia lemnae calmodulin gene, complet... 74 9e-18 25 emb|AF007889|AF007889 Symbiodinium microadriaticum calmodulin (S... 74 1e-17 emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17 emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17 emb|X52096|TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. emb|AF030033|AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 75 2e-17 30 emb|X90560|PPCAMPROT Physcomitrella patens mRNA for calmodulin. gb|U91642|POU91642 Pleurotus ostreatus calmodulin mRNA, complete... 75 2e-17 emblAF078680|AF078680 Olea europaea calcium-binding protein (PCA... 57 2e-17 emb|X85091|MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17 gb|M83535|PHTCALPIA P.infestans calmodulin (calA) gene, complete... 75 2e-17 35 emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17 gb|C96396|C96396 C96396 Marchantia polymorpha immature sex organ... 73 3e-17 emb|AL113315|CNS01ARV Botrytis cinerea strain T4 cDNA library un... 72 3e-17 emb|AB044286|AB044286 Chara corallina ccam mRNA for calmodulin, ... 75 4e-17 emb|AB041712|AB041712 Chara corallina cccam2 mRNA for calmodulin... 75 4e-17 40 emb|AB041711|AB041711 Chara corallina cccam1 mRNA for calmodulin... 75 4e-17 gbJ05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17 emb|X70923|NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17 emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17 emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17 45 gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17 gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. gb|S68025|S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic... 74 8e-17 emb|AW164773|AW164773 se77e12.yl Gm-c1023 Glycine max cDNA clone... 64 8e-17 emb|AW719875|AW719875 LjNEST11d4r Lotus japonicus nodule library... 57 8e-17 50 emb|AW830090|AW830090 sm22a12.yl Gm-c1028 Glycine max cDNA clone... 64 8e-17 emb|AW126204|AW126204 N100049e rootphos(-) Medicago truncatula c... 57 8e-17 emb|X52242|TTCALM T.thermophila mRNA for calmodulin. gb|L02963|NEUCLMDLN Neurospora crassa calmodulin mRNA, complete ... 74 1e-16 emb|AW625406|AW625406 EST319229 tomato radicle, 5 d post-imbibit... 62 1e-16 55 gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16 gblM88307|BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16 gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 73 2e-16 emb|X89890|BPCALMGEN B.pilosa mRNA for calmodulin. 73 2e-16 emb|AW099396|AW099396 sd39h01.yl Gm-c1016 Glycine max cDNA clone... 76 2e-16 60 emb|AW101324|AW101324 sd77e09.y1 Gm-c1009 Glycine max cDNA clone... 59 2e-16 emb|AL112713|CNS01AB5 Botrytis cinerea strain T4 cDNA library un... 73 2e-16

```
emb|AL114582|CNS01BR2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
       emb|AL112170|CNS019W2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
       emb|AL114124|CNS01BEC Botrytis cinerea strain T4 cDNA library un... 74 2e-16
       emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
 5
       emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16
       emb|AW573768|AW573768 EST316359 GVN Medicago truncatula cDNA clo... 72 2e-16
       emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin.
      emb|AI727960|AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium ...
      emb|AA660367|AA660367 00239 MtRHE Medicago truncatula cDNA 5' si... 71 3e-16
10
      emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16
      emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16
      emblAW738989|AW738989 gb23c06.yl Moss EST library PPN Physcomitr... 73 3e-16
      gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16
      gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16
15
      gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
      emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16
      gb|S81594|S81594 auxin-regulated calmodulin [Vigna radiata=mung ... 73 4e-16
      gb|L20691|VIRCALMOD Vigna radiata calmodulin mRNA, complete cds.
      emb|AW730911|AW730911 GA_Ea0029I11 Gossypium arboreum 7-10 dpa ... 73 4e-16
20
      gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16
      emb|AF030032|AF030032 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16
      gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16
      emb|Y09853|CACAM Cicer arietinum mRNA for CaM protein.
      gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16
25
      gb|U49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16
      gblU49105TAU49105 Triticum aestivum calmodulin TaCaM4-1 mRNA, c... 73 4e-16
      emb|AF030034|AF030034 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16
      emb|AW728030|AW728030 GA_Ea0029H21 Gossypium arboreum 7-10 dpa ... 73 4e-16
      gb|L20507|VIRCALMODU Vigna radiata (clone pMBCaM-1) calmodulin m... 73 4e-16
30
      gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16
      gb|M80836|PETCAM81 Petunia hybrida CAM81 mRNA,.
                                                                     73 4e-16
      gb|U49103|TAU49103 Triticum aestivum calmodulin TaCaM3-2 mRNA, c... 73 4e-16
      emb|X52398|MSCAL1 Alfalfa cal1 mRNA for calmodulin.
                                                                   73 4e-16
      gb|U48688|TAU48688 Triticum aestivum calmodulin TaCaM1-2 mRNA, c... 73 4e-16
35
      gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
      emb|AW927068|AW927068 HVSMEg0009G21 Hordeum vulgare pre-anthesis... 73 4e-16
      gb|U48689|TAU48689 Triticum aestivum calmodulin TaCaM1-3 mRNA, c... 73 4e-16
      gb[M80831]PETCALPRO Petunia hybrida CAM53 mRNA, complete cds.
      emblAW348582|AW348582 GM210002B22C3R Gm-r1021 Glycine max cDNA 3... 73 4e-16
40
      emb|X59751|DCCAM1G Carrot Ccam-1 gene for calmodulin.
      emb|AW775754|AW775754 EST334819 DSIL Medicago truncatula cDNA cl... 73 4e-16
      gb|BE052400|BE052400 GA_Ea0001L24f Gossypium arboreum 7-10 dpa ... 73 4e-16
      emb|AW666735|AW666735 GA Ea0005N08 Gossypium arboreum 7-10 dpa ... 73 4e-16
      gb|U13882|PSU13882 Pisum sativum Alaska calmodulin mRNA, complet... 73 4e-16
45
      gb|BE051931|BE051931 GA Ea0002G11f Gossypium arboreum 7-10 dpa ... 73 4e-16
      emb|AW666619|AW666619 GA Ea0005C16 Gossypium arboreum 7-10 dpa ... 73 4e-16
      emblAW108833|AW108833 gate0001L24f Gossypium arboreum 7-10 dpa f... 73 4e-16
      emb|Z12839|LLCALMOD L.longiflorum mRNA encoding calmodulin.
      gb|L18912|LILCALMODU Lilium longiflorum calmodulin mRNA, complet... 73 4e-16
50
      Query= HSF4_s_at 13273_s_at /id source genbank /description
      gb|aac31756.1| (u68017) heat shock transcription factor 4 [arabidopsis
      thaliana] /blast score 1.00e-113 /ec number /family /chip nova
      /gb link /ncgi
           (1408 letters)
55
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
      Searching......done
60
```

Score E

Sequences producing significant alignments:

(bits) Value

emb|AB014483|AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho... 213 2e-62 emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 210 2e-53 5 emb|AI900223|AI900223 sc02f05.yl Gm-c1012 Glycine max cDNA clone... 205 3e-53 emb|Z46953|GMHSF34 G.max mRNA for heat shock transcription facto... 203 6e-53 emb|AV408054|AV408054 AV408054 Lotus japonicus young plants (two... 203 3e-51 emb|AV415115|AV415115 AV415115 Lotus japonicus young plants (two... 197 2e-49 emb|AW774951|AW774951 EST334102 KV3 Medicago truncatula cDNA clo... 194 1e-48 10 emb|AW689532|AW689532 NF021G10ST1F1000 Developing stem Medicago ... 194 1e-48 emb|AI728175|AI728175 BNLGHi10028 Six-day Cotton fiber Gossypium... 192 5e-48 emb|AI055366|AI055366 coau0003M17 Cotton Boll Abscission Zone cD... 191 1e-47 emb|AW703969|AW703969 sk14g08.yl Gm-c1023 Glycine max cDNA clone... 191 1e-47 emb|AW428882|AW428882 Ljirnpest25-001-b9 Ljirnp Lambda HybriZap ... 190 2e-47 15 emb|AW931781|AW931781 EST357624 tomato fruit mature green, TAMU ... 189 3e-47 emb|AW686121|AW686121 NF033H01NR1F1000 Nodulated root Medicago t... 188 1e-46 emb|Z46956|GMHSF5 G.max mRNA for heat shock transcription factor 5. 185 6e-46 emb|AW109013|AW109013 gate0002O16f Gossypium arboreum 7-10 dpa f... 179 4e-44 20 gb|BE020791|BE020791 sm52h09.yl Gm-c1028 Glycine max cDNA clone ... 178 1e-43 emb|AW696868|AW696868 NF111F05ST1F1046 Developing stem Medicago ... 166 3e-43 emb|AW686271|AW686271 NF039H06NR1F1000 Nodulated root Medicago t... 171 5e-42 emb|AW931176|AW931176 EST357019 tomato fruit mature green, TAMU ... 168 8e-41 gb|C95479|C95479 C95479 Citrus unshiu Miyagawa-wase maturation s... 166 5e-40 25 emb|AW033421|AW033421 EST276992 tomato callus, TAMU Lycopersicon... 165 1e-39 emb|AW030725|AW030725 EST273980 tomato callus, TAMU Lycopersicon... 165 1e-39 emb|AW041695|AW041695 EST284559 tomato mixed elicitor, BTI Lycop... 165 1e-39 emb|AW217982|AW217982 EST296697 tomato flower buds, anthesis, Co... 165 1e-39 emb|X67600|LPHSF8 L.peruvianum Lp-hsf8 mRNA for heat stress tran... 161 1e-38 30 emb|AW774397|AW774397 EST333548 KV3 Medicago truncatula cDNA clo... 160 2e-38 emb|AW686582|AW686582 NF042H04NR1F1000 Nodulated root Medicago t... 155 6e-37 emb|AW776460|AW776460 EST335525 DSIL Medicago truncatula cDNA cl... 152 7e-36 emb|AW738023|AW738023 EST339450 tomato flower buds, anthesis, Co... 150 2e-35 emb|AW036683|AW036683 EST278726 tomato fruit mature green, TAMU ... 149 5e-35 35 emb|AI729182|AI729182 BNLGHi12855 Six-day Cotton fiber Gossypium... 149 5e-35 emb|AI489721|AI489721 EST248060 tomato ovary, TAMU Lycopersicon ... 149 5e-35 emb|AW034402|AW034402 EST277973 tomato callus, TAMU Lycopersicon... 148 7e-35 emb|X67601|LPHSF30 L.peruvianum Lp-hsf30 mRNA for heat stress tr... 148 9e-35 emb|AW906822|AW906822 EST342945 potato stolon, Cornell Universit... 147 2e-34 40 emb[AW164509]AW164509 se74f12.yl Gm-c1023 Glycine max cDNA clone... 147 2e-34 emb|AW034874|AW034874 EST279103 tomato callus, TAMU Lycopersicon... 147 2e-34 emb|AF235958|AF235958 Medicago sativa heat shock transcription f... 145 8e-34 emb|Z46952|GMHSF21 G.max mRNA for heat shock transcription facto... 145 8e-34 emb|AW559623|AW559623 EST314671 DSIR Medicago truncatula cDNA cl... 144 2e-33 45 emb|AW222011|AW222011 EST298822 tomato fruit red ripe, TAMU Lyco... 144 2e-33 emb|AW930998|AW930998 EST356841 tomato fruit mature green, TAMU ... 143 4e-33 emb|AW906840|AW906840 EST342963 potato stolon, Cornell Universit... 140 2e-32 emb|AB014484|AB014484 Nicotiana tabacum NtHSF2 mRNA for heat sho... 140 3e-32 emb|AF208544|AF208544 Lycopersicon peruvianum heat stress transc... 139 4e-32 50 emb|AW738534|AW738534 EST339961 tomato flower buds, anthesis, Co... 139 5e-32 emb|AI725043|AI725043 942 PtIFG2 Pinus taeda cDNA clone 8824r, m... 139 5e-32 emb|AW874988|AW874988 00109 leafy spurge Lambda HybriZAP 2.1 two... 138 1e-31 emb|AW596493|AW596493 sj13a09.yl Gm-c1032 Glycine max cDNA clone... 138 1e-31 emb|AV415736|AV415736 AV415736 Lotus japonicus young plants (two... 138 1e-31 55 emb|AW979619|AW979619 EST341218 tomato root deficiency, Cornell ... 137 2e-31 emb|AW932142|AW932142 EST357985 tomato fruit mature green, TAMU ... 136 3e-31 emb|Z46954|GMHSF33 G.max mRNA for heat shock transcription facto... 135 9e-31 emb|AW569138|AW569138 si63g09.y1 Gm-r1030 Glycine max cDNA clone... 134 1e-30 emb|AW569256|AW569256 si64g09.yl Gm-r1030 Glycine max cDNA clone... 134 1e-30 60 emb|AW203851|AW203851 sf38h11.y1 Gm-c1028 Glycine max cDNA clone... 133 3e-30 emb|AW220758|AW220758 EST297227 tomato fruit mature green, TAMU ... 132 6e-30

,	emb AI728806 AI728806 BNLGHi11701 Six-day Cotton fiber Gossypium 108 2e-28 emb AW736596 AW736596 EST333088 KV3 Medicago truncatula cDNA clo 103 3e-28 emb AI895934 AI895934 EST265377 tomato callus, TAMU Lycopersicon 123 2e-27
5	emb Z46951 GMHSF29 G.max mRNA for heat shock transcription facto 120 2e-26 gb BE019974 BE019974 sm38b12.yl Gm-c1028 Glycine max cDNA clone 119 6e-26 emb Z46955 GMHSF31 G.max mRNA for heat shock transcription facto 115 8e-25 emb X67599 LEHSF8 L.esculentum Le-hsf8 gene for heat stress tran 114 2e-24
10	emb AQ579554 AQ579554 T135016b shotgun sub-library of BAC clone 113 4e-24 emb AW775388 AW775388 EST334453 DSIL Medicago truncatula cDNA cl 66 1e-23
10	emb AW931892 AW931892 EST357735 tomato fruit mature green, TAMU 104 2e-21 emb AQ579623 AQ579623 T135087b shotgun sub-library of BAC clone 103 4e-21 emb AW736595 AW736595 EST333087 KV3 Medicago truncatula cDNA clo 103 4e-21 emb AW697097 AW697097 NF112C08ST1F1065 Developing stem Medicago 103 4e-21
15	emb AV420766 AV420766 AV420766 Lotus japonicus young plants (two 102 8e-21 emb AV413314 AV413314 AV413314 Lotus japonicus young plants (two 102 8e-21 emb AW693546 AW693546 NF067D12ST1F1101 Developing stem Medicago 101 1e-20 emb AI895294 AI895294 EST264737 tomato callus, TAMU Lycopersicon 101 1e-20 emb AJ010644 PSA010643 Pisum sativum hsfA gene, exons 1 to 2, pa 99 7e-20
20	emb AW924303 AW924303 WS1_52_H11.b1_A002 Water-stressed 1 (WS1) 99 7e-20 emb AI895834 AI895834 EST265277 tomato callus, TAMU Lycopersicon 95 9e-19 emb AW756148 AW756148 s116e07.y1 Gm-c1036 Glycine max cDNA clone 93 4e-18 emb AW132703 AW132703 se09a08.y1 Gm-c1013 Glycine max cDNA clone 93 6e-18
25	gb M94683 YSPHSF Schizosaccharomyces pombe heat shock transcript 93 6e-18 emb X55149 KLHSFG K. lactis HSF gene for heat shock transcriptio 76 2e-17 emb AW933448 AW933448 EST359387 tomato fruit mature green, TAMU 89 8e-17 emb AI896906 AI896906 EST266349 tomato callus, TAMU Lycopersicon 89 1e-16 emb AZ045432 AZ045432 T234030b shotgun sub-library of BAC clone 84 2e-15
30	emb X83031 SCPOS9 S.cerevisiae POS9 gene. 83 5e-15 gb U00485 YSCSKN7 Saccharomyces cerevisiae putative transcriptio 83 5e-15 gb U00029 YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm 83 5e-15 emb Z69726 SPAC2E12 S.pombe chromosome I cosmid c2E12. 83 6e-15
35	gb M22040 YSCHSF1A S.cerevisiae heat shock transcription factor 81 2e-14 emb Z72596 SCYGL074C S.cerevisiae chromosome VII reading frame O 81 2e-14 gb J03139 YSCHSF S.cerevisiae heat shock factor gene (HSF), comp 81 2e-14 emb AI212342 AI212342 x3c12a1.rl Aspergillus nidulans 24hr asexu 73 8e-14 emb AW686674 AW686674 NF040F05NR1F1000 Nodulated root Medicago t 79 8e-14 emb AZ048458 AZ048458 PSB119 Barley PstI genomic clones Hordeum 78 2e-13
40	emb AW034135 AW034135 EST277706 tomato callus, TAMU Lycopersicon 57 9e-13 emb AW933529 AW933529 EST359288 tomato fruit mature green, TAMU 72 1e-11 emb AW307441 AW307441 sf57a06.yl Gm-c1009 Glycine max cDNA clone 70 5e-11 emb AW620962 AW620962 sj98b03.yl Gm-c1023 Glycine max cDNA clone 70 5e-11
45	Query= hsp176A_i_at 13277_i_at /id_source genbank /description emb caa74399.1 (y14070) heat shock protein 17.6a [arabidopsis thaliana] /blast_score 2.00e-75 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
50	post/entrez/query?db=n&form=6&dopt=g&uid=gb hsp176a /ncgi http://www.ncgr.org/cgi-bin/ff?hsp176a (613 letters)
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
55	Searchingdone
	Score E Sequences producing significant alignments: (bits) Value
60	gb M33901 PEAHSP177A Pisum sativum 17.7 kDa heat shock protein (126 3e-44 gb M99429 PHNSHSPA Ipomoea nil small heat shock protein, complet 171 4e-42

```
emb|X98617|MSSHP17KD M.sativa mRNA for 17kD heat shock protein.
       emb|AF159562|AF159562 Prunus dulcis cytosolic class II low molec... 105 7e-42
       gb|LA7740|PIAEMB29R Picea glauca class II cytoplasmic small mole... 169 2e-41
       emb|AW569703|AW569703 si79c12.yl Gm-c1031 Glycine max cDNA clone... 107 6e-41
  5
       emb[X99346]PASHSP P.abies mRNA for small heat shock protein.
       emb|AW667877|AW667877 GA_Ea0011C02 Gossypium arboreum 7-10 dpa ... 110 2e-40
       emb|AW725392|AW725392 GA_Ea0017J18 Gossypium arboreum 7-10 dpa ... 110 2e-40
       emb|AW569553|AW569553 si88e08.yl Gm-c1031 Glycine max cDNA clone... 107 1e-39
       emb|AW620261|AW620261 si93g10.yl Gm-c1031 Glycine max cDNA clone... 107 1e-39
 10
       gb|BE053976|BE053976 GA_Ea0002N06f Gossypium arboreum 7-10 dpa ... 110 3e-39
       emb|AW109163|AW109163 gate0002N06f Gossypium arboreum 7-10 dpa f... 110 3e-39
       emb|AW569987|AW569987 si85c01.yl Gm-c1031 Glycine max cDNA clone... 107 2e-38
       emb|X07159|GMHSP179 Soybean gene for heat shock protein Gmhsp17.... 103 2e-38
       emb|AW620254|AW620254 si93g03.yl Gm-c1031 Glycine max cDNA clone... 103 2e-38
15
       emb|AW569546|AW569546 si88e01.yl Gm-c1031 Glycine max cDNA clone... 103 2e-38
       emb|AW569992|AW569992 si85c07.yl Gm-c1031 Glycine max cDNA clone... 107 8e-38
       emb|AW570000|AW570000 si85d08.yl Gm-c1031 Glycine max cDNA clone... 104 1e-37
       emb|AW870031|AW870031 NXNV 123 C02 F Nsf Xylem Normal wood Verti... 153 1e-36
20
       emb|AI812703|AI812703 18B10 Pine Lambda Zap Xylem library Pinus ... 145 3e-34
       gb|U72396|LEU72396 Lycopersicon esculentum class II small heat s... 123 8e-31
       emb[X95716]PCSHSPGEN P.crispum mRNA for 17.9kDa heat shock prote... 105 3e-28
      emb|AI776971|AI776971 EST252063 tomato callus, TAMU Lycopersicon... 123 1e-27
      emb|AB027500|AB027500 Daucus carota Dchsp-1 mRNA, complete cds.
25
      emb|AJ225049|LPAJ5049 Lycopersicon peruvianum mRNA for Hsp20.2 p... 105 8e-26
      emb|AF090115|AF090115 Lycopersicon esculentum cytosolic class II... 106 3e-25
      emb|AI782242|AI782242 EST263121 tomato susceptible, Cornell Lyco... 106 4e-25
      emb|AF089846|AF089846 Funaria hygrometrica cytosolic II small he... 73 6e-25
      dbi|D21817|LILLIM11 Lily mRNA for small heat shock protein, part... 78 1e-24
30
      emb|AW569456|AW569456 si87d04.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW569687|AW569687 si79b06.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW568954|AW568954 si73e12.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW569158|AW569158 si75b01.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emblAW568867|AW568867 si73c04.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
35
      emb|AW569632|AW569632 si89d12.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW569640|AW569640 si89e09.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW568707|AW568707 si72b01.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW569586|AW569586 si88h09.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
      emb|AW620228|AW620228 si93d08.yl Gm-c1031 Glycine max cDNA clone... 111 7e-24
40
      gb|LA7717|PIAEMB27R Picea glauca heat shock protein 17.0 (EMB27)... 110 1e-23
      emb|AW570013|AW570013 si85f01.y1 Gm-c1031 Glycine max cDNA clone... 108 3e-23
      emb|AW185394|AW185394 se90h07.yl Gm-c1027 Glycine max cDNA clone... 108 3e-23
      emb|AW620212|AW620212 si93c03.yl Gm-c1031 Glycine max cDNA clone... 108 3e-23
      emb|AI900116|AI900116 sc01a11.yl Gm-c1012 Glycine max cDNA clone... 108 3e-23
45
      emb|AW569816|AW569816 si81h07.yl Gm-c1031 Glycine max cDNA clone... 108 3e-23
      emb|AW569179|AW569179 si75e02.yl Gm-c1031 Glycine max cDNA clone... 108 3e-23
      emb|AW289617|AW289617 NXNV003E01F Nsf Xylem Normal wood Vertical... 108 5e-23
      emb|Z29554|HA179HSP H.annuus (Sunweed) mRNA for 17.9 kDa heat-sh... 105 3e-22
      emb|X92983|PMLMWHSPA P.menziesii mRNA for low molecular weight h... 104 6e-22
50
      emb|AW569996|AW569996 si85c11.yl Gm-c1031 Glycine max cDNA clone... 104 6e-22
      emb|X92984|PMLMWHSPB P.menziesii mRNA for low molecular weight h... 104 6e-22
      dbi|D21816|LILLIM10 Lily mRNA for small heat shock protein, part... 68 1e-21
      emb|X58279|TAHSP173 T.aestivum mRNA for heat shock protein 17.3.
      gb|M99430|PHNSHSPB Ipomoea nil small heat shock protein, complet... 102 3e-21
55
      gb|M33899|PEAHSP181A Pisum sativum 18.1 kDa heat shock protein (... 65 5e-21
      emb|AF089843|AF089843 Funaria hygrometrica cytosolic I small hea... 64 9e-21
      gb|U63631|FXU63631 Fragaria x ananassa LMW heat shock protein mR... 63 2e-20
      gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 63 2e-20
      emb|X13431|TAHSPLW Wheat mRNA for putative low molecular weight ... 65 2e-20
60
      emb|AF123255|AF123255 Lycopersicon esculentum 17.7 kD class I sm... 61 3e-20
      emb|X58711|MSHSP182 M.sativa mRNA for heat shock protein (clone ... 61 3e-20
```

	emb AW929084 AW929084 EST337788 tomato flower buds 8 mm to pre-a 61 3e-20
	emb AW443699 AW443699 EST308629 tomato mixed elicitor, BTI Lycop 61 3e-20
	gb BE034047 BE034047 MG04B07 MG Mesembryanthemum crystallinum cD 61 4e-20
	gb U08601 PSU08601 Papaver somniferum low molecular weight heat 98 5e-20
5	emb AW289567 AW289567 NXNV002G05F Nsf Xylem Normal wood Vertical 98 5e-20
	emb X70688 NTHSP18P N.tabacum hsp18p mRNA for heat shock protein 61 8e-20
	emb AF022217 AF022217 Brassica rapa low molecular weight heat-sh 63 8e-20
	emb X07160 GMHSP185 Soybean gene for heat shock protein Gmhsp18 61 1e-19
	* 1 *
10	111111000000000000000000000000000000000
10	
	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1
	emb AW569326 AW569326 si76f03.yl Gm-c1031 Glycine max cDNA clone 61 1e-19
	emb X56138 LEHSPIR Lycopersicon esculentum mRNA for small heat-s 61 2e-19
1.5	emb A15448 A15448 tomato fruit ripening related gene pTOM66 Seq 61 2e-19
15	emb AF123256 AF123256 Lycopersicon esculentum 17.8 kD class I sm 61 2e-19
	emb AF087640 AF087640 Funaria hygrometrica cytosolic I small hea 66 3e-19
	emb AF123257 AF123257 Lycopersicon esculentum 17.6 kD class I sm 59 4e-19
	emb AJ225047 LPAJ5047 Lycopersicon peruvianum mRNA for Hsp19.9 p 59 4e-19
	emb AW029721 AW029721 EST272976 tomato callus, TAMU Lycopersicon 62 4e-19
20	emb AW221905 AW221905 EST298716 tomato fruit red ripe, TAMU Lyco 62 4e-19
	emb X58710 MSHSP181 M.sativa mRNA for heat shock protein (clone 58 4e-19
	emb AW980952 AW980952 EST392105 GVN Medicago truncatula cDNA clo 58 4e-19
	emb AW569926 AW569926 si83d04.yl Gm-c1031 Glycine max cDNA clone 63 4e-19
	emb AW569343 AW569343 si76g12.yl Gm-c1031 Glycine max cDNA clone 63 4e-19
25	emb AJ225046 LPAJ5046 Lycopersicon peruvianum mRNA for Hsp20.1 p 59 5e-19
	emb AW678863 AW678863 WS1 1 C05.g1 A002 Water-stressed 1 (WS1) S 95 6e-19
	emb AW678637 AW678637 WS1_1_C05.b1_A002 Water-stressed 1 (WS1) S 95 6e-19
	emb AW290614 AW290614 NXNV044B03F Nsf Xylem Normal wood Vertical 95 6e-19
	emb AW508849 AW508849 si41b03.y1 Gm-r1030 Glycine max cDNA clone 59 7e-19
30	emb AW569644 AW569644 si89f04.yl Gm-c1031 Glycine max cDNA clone 59 7e-19
	emb AW569636 AW569636 si89e04.y1 Gm-c1031 Glycine max cDNA clone 59 7e-19
	emb AW568435 AW568435 si70g06.yl Gm-c1031 Glycine max cDNA clone 59 1e-18
	emb AW567658 AW567658 si77b11.y1 Gm-c1031 Glycine max cDNA clone 63 1e-18
	emb AW569747 AW569747 si79h07.y1 Gm-c1031 Glycine max cDNA clone 59 1e-18
35	emb AF089845 AF089845 Funaria hygrometrica cytosolic II small he 94 1e-18
<i>.</i>	emb[X53852]DCHSP179 Carrot gene for a heat shock protein. 61 1e-18
	emb AW223810 AW223810 EST300621 tomato fruit red ripe, TAMU Lyco 57 1e-18
	omopi w 223010 pt w 223010 pt 1300021 tomato nun teu tipe, 17410 pt 1500 37 16-16
40	0 1 00 10000 111
40	Query=hsp83_s_at 13285_s_at /id_source genbank /description
	gb aaa32822.1 (m62984) heat shock protein 83 [arabidopsis thaliana]
	/blast_score 0
	(2411 letters)
45	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
50	Score E
50	Sequences producing significant alignments: (bits) Value
•	sequences producing significant anguments. (ons) value
	gb M99431 PHNHSP83A Pharbitis nil heat shock protein 83 (Hsp83) 597 0.0
	gb M96549 TOMHSC80P Tomato heat shock cognate protein 80 gene, 3 577 0.0
55	gb U55859 TAU55859 Triticum aestivum heat shock protein 80 mRNA, 575 0.0
-	emb X98582 TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0
•	emb[X63195]NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0
	· · · · · · · · · · · · · · · · · · ·
	emb AF123259 AF123259 Lycopersicon esculentum heat shock protein 483 0.0
60	emb AF165818 AF165818 Guillardia theta nucleomorph 5S ribosomal 505 0.0
v	emb AF042329 AF042329 Eimeria tenella heat shock protein 90 (hsp 514 0.0
	gb M57386 THEHSP90 T.parva heat shock protein 90 (hsp90) mRNA, c 500 0.0

emb|Z29667|PFHESHPR P.falciparum (7) mRNA for heat-shock protein. gb|U45449|EBU45449 Eimeria bovis heat shock protein 90 (hsp90) m... 495 0.0 emb|AF151114|AF151114 Tetrahymena thermophila strain B2086 hsp82... 486 0.0 emb|AF136649|AF136649 Babesia bovis heat shock protein 90 (HSP90... 487 0.0 gb]M15346|TRBHSC T.cruzi tandemly repeated gene encoding an 85 k... 457 0.0 5 emb[X14176]TBHSP83 Trypanosoma brucei HSP83 gene. gb|M73492|LEIHSP90 Leishmania donovani heat shock protein 90 mRN... 456 0.0 emb|X87770|LIHSP83GN L.infantum hsp83 gene. 454 0.0 gb|M92926|LEIHSP01 Leishmania amazonensis heat shock protein 83 ... 449 0.0 10 gb|U92465|AFU92465 Aspergillus fumigatus heat shock protein (Hsp... 458 e-165 emb|AF212996|AF212996 Neurospora crassa heat shock protein 80 ge... 473 e-165 emb|AL110469|SPAC926 S.pombe chromosome I cosmid c926. gb|L35550|YSPHSP90X Schizosaccharomyces pombe heat shock protein... 460 e-162 gb|U81165|PAU81165 Podospora anserina suppressor of vegetative i... 292 e-161 15 emb|Z67751|SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb). emb|Z73596|SCYPL240C S.cerevisiae chromosome XVI reading frame O... 448 e-159 gb[K01387|YSCHSP82A Yeast (S.cerevisiae) HSP82 (heat shock-induc... 448 e-159 emb|X81025|CAHSP90 C.albicans hsp90 gene. 451 e-159 emb|AF251005|AF251005 Candida tropicalis heat shock protein 90 g... 444 e-158 emb|Z49808|SC8010 S.cerevisiae chromosome XIII cosmid 8010. emb|AF221856|AF221856 Euphorbia esula heat-shock protein 80 mRNA... 292 e-158 gb[M26044]YSCHSC82 S. cerevisiae HSC82 gene encoding hsc82, the ... 447 e-157 25 emb|AI489832|AI489832 EST248171 tomato ovary, TAMU Lycopersicon ... 471 e-132 emb|AW982575|AW982575 HVSMEg0003K07f Hordeum vulgare pre-anthesi... 471 e-131 emb|AW774793|AW774793 EST333944 KV3 Medicago truncatula cDNA clo... 459 e-128 emb|AW221746|AW221746 EST298557 tomato fruit red ripe, TAMU Lyco... 350 e-128 emb|AW728021|AW728021 GA_Ea0029G22 Gossypium arboreum 7-10 dpa ... 315 e-127 30 gb|BE035845|BE035845 MO11A12 MO Mesembryanthemum crystallinum cD... 455 e-127 emb|AW650299|AW650299 EST328753 tomato germinating seedlings, TA... 455 e-127 emb|AW982497|AW982497 HVSMEg0003G20f Hordeum vulgare pre-anthesi... 439 e-126 emb|AF078070|AF078070 Griffithsia japonica heat-shock protein 90... 245 e-126 emb|AW218188|AW218188 EST303369 tomato radicle, 5 d post-imbibit... 452 e-126 35 emb|AW621485|AW621485 EST312283 tomato root during/after fruit s... 445 e-124 emb|AW905909|AW905909 EST342082 potato stolon, Cornell Universit... 331 e-124 emb|AW618647|AW618647 EST320633 L. pennellii trichome, Cornell U... 439 e-122 emb|AI730385|AI730385 BNLGHi6770 Six-day Cotton fiber Gossypium ... 439 e-122 40 emb|AW931002|AW931002 EST356845 tomato fruit mature green, TAMU ... 436 e-121 emb|AW186517|AW186517 se68g12.yl Gm-c1019 Glycine max cDNA clone... 432 e-120 gb|BE055051|BE055051 GA_Ea0031H10f Gossypium arboreum 7-10 dpa ... 381 e-118 emb|AW217359|AW217359 EST296010 tomato flower buds 0-3 mm, Corne... 427 e-118 emb[AW216642|AW216642 EST295356 tomato callus, TAMU Lycopersicon... 423 e-117 45 emb|AW217696|AW217696 EST296410 tomato flower buds 8 mm to pre-a... 422 e-117 emb|AW011081|AW011081 ST16E03 Pine TriplEx shoot tip library Pin... 421 e-116 emb|AI730419|AI730419 BNLGHi7100 Six-day Cotton fiber Gossypium ... 417 e-115 emb|AW907064|AW907064 EST343096 potato stolon, Cornell Universit... 413 e-114 emb|AW696590|AW696590 NF108G11ST1F1087 Developing stem Medicago ... 413 e-114 50 emb|AW738699|AW738699 EST340126 tomato flower buds, anthesis, Co... 412 e-114 emb|AI442468|AI442468 sa27d08.yl Gm-c1004 Glycine max cDNA clone... 412 e-114 emb|AW684853|AW684853 NF022C08NR1F1000 Nodulated root Medicago t... 403 e-114 emb|AW693965|AW693965 NF071A06ST1F1040 Developing stem Medicago ... 408 e-113 emb|AW690869|AW690869 NF036A07ST1F1000 Developing stem Medicago ... 390 e-113 emb|AW030608|AW030608 EST273863 tomato callus, TAMU Lycopersicon... 407 e-112 emb|AW983321|AW983321 HVSMEg0010D10f Hordeum vulgare pre-anthesi... 354 e-112 emb|AI726426|AI726426 BNLGHi5602 Six-day Cotton fiber Gossypium ... 407 e-112 emb|AW930252|AW930252 EST340709 tomato fruit mature green, TAMU ... 406 e-112 emb|AW979717|AW979717 EST341337 tomato root deficiency, Cornell ... 404 e-111 60 emb|AW695561|AW695561 NF096B09ST1F1076 Developing stem Medicago ... 404 e-111 emb|AW691505|AW691505 NF045G02ST1F1000 Developing stem Medicago ... 361 e-111

emb|AW735801|AW735801 EST336569 tomato flower buds 0-3 mm, Corne... 402 e-111 emb|AW737406|AW737406 EST338749 tomato flower buds, anthesis, Co... 402 e-111 emb|AL112936|CNS01AHC Botrytis cinerea strain T4 cDNA library un... 400 e-110 emb|AW217697|AW217697 EST296411 tomato flower buds 8 mm to pre-a... 400 e-110 5 emb|AW218948|AW218948 EST301430 tomato root during/after fruit s... 396 e-110 emb|AW220869|AW220869 EST297338 tomato fruit mature green, TAMU ... 398 e-109 emb|AW616417|AW616417 EST322828 L. hirsutum trichome, Cornell Un... 397 e-109 emb|AW688548|AW688548 NF008H04ST1F1000 Developing stem Medicago ... 396 e-109 emb|AW738535|AW738535 EST339962 tomato flower buds, anthesis, Co... 242 e-109 10 emb|AW649397|AW649397 EST327851 tomato germinating seedlings, TA... 394 e-108 emblAW693115|AW693115 NF060C10ST1F1081 Developing stem Medicago ... 226 e-107 emb|AI488065|AI488065 EST246387 tomato ovary, TAMU Lycopersicon ... 390 e-107 emb|AI726157|AI726157 BNLGHi5098 Six-day Cotton fiber Gossypium ... 226 e-107 gb|BE060856|BE060856 HVSMEg0013J20f Hordeum vulgare pre-anthesis... 388 e-107 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107 emb|AL111751|CNS019KF Botrytis cinerea strain T4 cDNA library un... 389 e-107 emb|AW092845|AW092845 EST286025 tomato mixed elicitor, BTI Lycop... 386 e-106 emb|AW983154|AW983154 HVSMEg0008G17f Hordeum vulgare pre-anthesi... 224 e-106 emb|AI780272|AI780272 EST261151 tomato susceptible, Cornell Lyco... 215 e-106 20 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106 emb|AW690804|AW690804 NF035B11ST1F1000 Developing stem Medicago ... 375 e-106 emb|AW154860|AW154860 EST290253 tomato root deficiency, Cornell ... 385 e-105 emb|AI780075|AI780075 EST260954 tomato susceptible, Cornell Lyco... 383 e-105 emb|AW928471|AW928471 EST337259 tomato flower buds 8 mm to pre-a... 382 e-105 25 gb|L34028|PFAHSP86B Plasmodium falciparum (clone HB3) heat shock... 382 e-105 emblAF030694|AF030694 Plasmodium falciparum strain Dd2 heat shoc... 382 e-105 gb|L34027|PFAHSP86A Plasmodium falciparum (clone Dd2) heat shock... 382 e-105 emb|AW737397|AW737397 EST338740 tomato flower buds, anthesis, Co... 381 e-104 emb|AW334905|AW334905 S40F8 AGS-1 Pneumocystis carinii f. sp. ca... 381 e-104 30 emb|AW035244|AW035244 EST280506 tomato callus, TAMU Lycopersicon... 380 e-104 Query= Mlolike2_s_at 13685_s_at /id source genbank /description gb|aad25552.1|ac005850_9 (ac005850) highly similar to mlo proteins 35 [arabidopsis thaliana] /blast_score 0 /ec number /family /chip nova /gb_link /ncgi (1752 letters) Database: plantfungal 40 661,018 sequences; 426,114,510 total letters Searching.....done Score 45 Sequences producing significant alignments: (bits) Value emb|A92838|A92838 Sequence 12 from Patent WO9804586. 258 e-123 emb|Z83834|HVMLO H.vulgare mRNA for Mlo protein. 261 e-116 emb|A92833|A92833 Sequence 7 from Patent WO9804586. 261 e-116 50 emb|A92828|A92828 Sequence 2 from Patent WO9804586. 261 e-116 emb|AW216578|AW216578 EST295292 tomato callus, TAMU Lycopersicon... 165 6e-78 emb|AJ005341|LUAJ5341 Linum usitatissimum mRNA for MLO-like prot... 287 2e-76 emblAW934153|AW934153 EST359996 tomato fruit mature green, TAMU ... 235 4e-74 emb|AW132264|AW132264 sd98f11.yl Gm-c1013 Glycine max cDNA clone... 128 2e-60 55 emb|AI779924|AI779924 EST260803 tomato susceptible, Cornell Lyco... 228 8e-59

gb|BE020055|BE020055 sm38e01.y1 Gm-c1028 Glycine max cDNA clone ... 199 2e-58 emb|AW132268|AW132268 sd98g11.y1 Gm-c1013 Glycine max cDNA clone... 124 5e-58 emb|AI729603|AI729603 BNLGHi13760 Six-day Cotton fiber Gossypium... 202 8e-51 emb|AI054629|AI054629 coau0001J02 Cotton Boll Abscission Zone cD... 133 2e-44

emb|AV426381|AV426381 AV426381 Lotus japonicus young plants (two... 145 3e-43 emb|AI729043|AI729043 BNLGHi12416 Six-day Cotton fiber Gossypium... 142 6e-42

60

	emb[Y14573]HVCH4H Hordeum vulgare DNA for chromosome 4H. 107 7e-41
	emb A92831 A92831 Sequence 5 from Patent WO9804586. 107 7e-41
	emb AI731933 AI731933 BNLGHi11440 Six-day Cotton fiber Gossypium 136 3e-40
	emb AI440563 AI440563 sa84c07.yl Gm-c1004 Glycine max cDNA clone 155 le-36
5	emb AI166945 AI166945 xylem.est.727 Poplar xylem Lambda ZAPII li 149 4e-35
Ĭ	emb A92829 A92829 Sequence 3 from Patent WO9804586. 107 4e-34
·	
	gb BE059771 BE059771 sn36h06.yl Gm-c1016 Glycine max cDNA clone 137 2e-31
	emb AB011444 AB011444 Triticum aestivum WESR3 mRNA, partial cds. 137 2e-31
10	emb AW350270 AW350270 GM210007B20B6R Gm-r1021 Glycine max cDNA 3 127 7e-3
10	emb A1778500 A1778500 EST259379 tomato susceptible, Cornell Lyco 76 3e-30
	emb AW299018 AW299018 EST305692 KV2 Medicago truncatula cDNA clo 125 1e-27
	emb AW442776 AW442776 EST307706 tomato mixed elicitor, BTI Lycop 117 2e-25
	emb AW719459 AW719459 LjNEST4h6r Lotus japonicus nodule library, 85 4e-25
	emb AW087034 AW087034 ga11d07.y1 Moss EST library CPU Ceratodon 83 5e-25
15	emb AW672144 AW672144 LG1_357_A11.b1_A002 Light Grown 1 (LG1) So 108 1e-22
-	emb AT000894 AT000894 AT000894 Brassica rapa guard cell Brassica 108 2e-22
	emb AW906979 AW906979 EST343206 potato stolon, Cornell Universit 98 2e-19
20	emb A92836 A92836 Sequence 10 from Patent WO9804586. 98 2e-19
20	emb A92832 A92832 Sequence 6 from Patent WO9804586. 98 2e-19
	emb AW570038 AW570038 si85h06.y1 Gm-c1031 Glycine max cDNA clone 96 6e-19
	emb AA660856 AA660856 00751 MtRHE Medicago truncatula cDNA 5', m 90 4e-17
	emb AT000630 AT000630 AT000630 Brassica rapa guard cell Brassica 87 5e-16
	gb BE022484 BE022484 sm74e08.yl Gm-c1015 Glycine max cDNA clone 84 3e-15
25	emb AW672173 AW672173 LG1_357 A11.g1 A002 Light Grown 1 (LG1) So 80 4e-14
	emb AI443125 AI443125 sa84f05.yl Gm-c1004 Glycine max cDNA clone 78 3e-13
	emb AW870276 AW870276 NXNV_128_G07_F Nsf Xylem Normal wood Verti 77 4e-13
	emb AW726816 AW726816 GA_ Ea0022N04 Gossypium arboreum 7-10 dpa 50 6e-13
	emb AI960937 AI960937 sc92h06.yl Gm-c1019 Glycine max cDNA clone 76 1e-12
30	emb AW569990 AW569990 si85c05.y1 Gm-c1031 Glycine max cDNA clone 75 1e-12
50	
	emb A 484886 A 484886 EST243149 tomato ovary, TAMU Lycopersicon 73 7e-12
	emb AW285009 AW285009 LG1_297_B09.g1_A002 Light Grown 1 (LG1) So 72 1e-11
	emb AW203816 AW203816 sf38e09.yl Gm-c1028 Glycine max cDNA clone 62 2e-08
35	emb AW719871 AW719871 LjNEST11d10r Lotus japonicus nodule librar 51 8e-08
22	emb AW757069 AW757069 sl02g02.y1 Gm-c1036 Glycine max cDNA clone 59 9e-08
	emb AW567653 AW567653 si77b05.yl Gm-c1031 Glycine max cDNA clone 55 2e-06
	emb AT000874 AT000874 AT000874 Brassica rapa guard cell Brassica 46 7e-04
	emb AI563090 AI563090 EST00214 watermelon lambda zap library Cit 37 0.010
	emb Z74921 BOK8A2 B.oleracea mRNA (unknown). 31 0.26
40	emb AZ221382 AZ221382 Gm_UMb001_002_A13R UMN Soybean BAC Library 33 0.65
	gb BE035329 BE035329 MM06C12 MM Mesembryanthemum crystallinum cD 36 0.71
	emb AW186503 AW186503 se68f07.y1 Gm-c1019 Glycine max cDNA clone 36 0.97
	emb AW218260 AW218260 EST303441 tomato radicle, 5 d post-imbibit 35 1.3
	emb AW693662 AW693662 NF067A11ST1F1084 Developing stem Medicago 35 1.3
45	emb AW688978 AW688978 NF014A05ST1F1000 Developing stem Medicago 35 1.3
	emb AI374173 AI374173 T6346 MVAT4 bloodstream form of serodeme W 35 1.3
	emb AW689953 AW689953 NF027B09ST1F1000 Developing stem Medicago 35 1.3
	emb AW218259 AW218259 EST303440 tomato radicle, 5 d post-imbibit 35 1.3
	emb X96770 SCLACHXVI S.cerevisiae chromosome XVI, left arm DNA. 35 1.8
50	4 1944 - 14 41 - 14 14 14 14 14 14 14 14 14 14 14 14 14
50	
	emb Z73500 SCYPL144W S.cerevisiae chromosome XVI reading frame O 35 1.8
	gb]U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi 35 1.8
	emb Z73499 SCYPL143W S.cerevisiae chromosome XVI reading frame O 35 1.8
	emb AJ242498 CCL242498 Candida cloacae mRNA for long chain fatty 35 1.8
55	emb AQ949106 AQ949106 Sheared DNA-49L9.TR Sheared DNA Trypanosom 35 2.5
	emb AQ650344 AQ650344 Sheared DNA-28J12.TF Sheared DNA Trypanoso 35 2.5
	emb AQ657515 AQ657515 Sheared DNA-3K7.TR Sheared DNA Trypanosoma 35 2.5
	emb Z74965 SCYOR057W S.cerevisiae chromosome XV reading frame OR 34 3.5
	emb AC007061 AC007061 Leishmania major chromosome 3 clone L1559 34 3.5
60	emb AQ642037 AQ642037 RPCI93-DpnII-29K3.TJ RPCI93-DpnII Trypanos 34 3.5
	embla 0445280 A 0445280 GSSTc01558 Transposoms crizi random genomi 34-3-5

5	emb AQ659145 AQ659145 Sheared DNA-16H2.TF Sheared DNA Trypanosom 34 3.5 gb U88830 SCU88830 Saccharomyces cerevisiae Sgt1p (SGT1) gene, c 34 3.5 emb AC005927 AC005927 Leishmania major chromosome 3 clone L3561 34 3.5 emb AQ637975 AQ637975 927P1-6A12.TV 927P1 Trypanosoma brucei gen 34 3.5 emb AL031744 PFMAL1P1 Plasmodium falciparum chromosome 1 strain 29 4.5
10	emb AF091345 AF091345 Schizosaccharomyces pombe N-terminal serin 34 4.7 emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC 34 4.7 emb AQ948416 AQ948416 Sheared DNA-38M22.TR Sheared DNA Trypanoso 34 4.7 emb AW257222 AW257222 EST305359 KV2 Medicago truncatula cDNA clo 34 4.7 emb Y13973 CACIP1 Candida sp. CIP1 gene. 34 4.7 emb AL031263 SPBC17F3 S.pombe chromosome II cosmid c17F3. 34 4.7
15	emb AF152552 AF152552 Sorghum bicolor chalcone synthase 5 (CHS5) 34 4.7 emb AQ655690 AQ655690 Sheared DNA-9G1.TR Sheared DNA Trypanosoma 34 4.7 emb AZ212373 AZ212373 Sheared DNA-101E1.TF Sheared DNA Trypanoso 34 4.7 emb AJ250726 TBR250726 Trypanosoma brucei HSP100 gene, GPI-PLC g 34 4.7 gb M17420 YSTHEP Saccharomyces cerevisiae heptapeptide repeat re 33 6.5
20	emb AI730517 AI730517 BNLGHi6942 Six-day Cotton fiber Gossypium 33 6.5 emb Z49511 SCYJR011C S.cerevisiae chromosome X reading frame ORF 33 6.5 gb U59312 HVU59312 Hordeum vulgare (1,4)-beta-xylan endohydrolas 33 6.5 emb Z74188 SCYDL140C S.cerevisiae chromosome IV reading frame OR 33 6.5 emb X87611 SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 33 6.5 emb AA003500 AA003500 T3189 MVAT4 bloodstream form of serodeme W 33 6.5
25	emb AQ951709 AQ951709 Sheared DNA-51E22.TF Sheared DNA Trypanoso 33 6.5
30	Query= NI115_at 13696_at /id_source genbank /description no hits found less than or equal to 1e-15. /blast_score /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ni115 /ncgi http://www.ncgr.org/cgi-bin/ff?ni115 (640 letters)
35	Database: plantfungal 661,018 sequences; 426,114,510 total letters
40	Searchingdone Score E
	Sequences producing significant alignments: (bits) Value
45	emb AI856734 AI856734 sb41e04.yl Gm-c1014 Glycine max cDNA clone 110 1e-23 gb C22284 C22284 C22284 Miyagawa-wase satsuma mandarin orange (M 103 1e-21 emb AW759850 AW759850 sl54h05.yl Gm-c1027 Glycine max cDNA clone 89 2e-17 emb AW565002 AW565002 LG1_313_B11.b1_A002 Light Grown 1 (LG1) So 89 2e-17 emb AW437881 AW437881 ST32702 Till Till Till Till Till Till Till Til
50	emb AW437881 AW437881 ST73F03 Pine TriplEx shoot tip library Pin 84 1e-15 emb AW760009 AW760009 sl56h04.yl Gm-c1027 Glycine max cDNA clone 83 3e-15 emb AW397963 AW397963 sg70e07.yl Gm-c1007 Glycine max cDNA clone 53 2e-06 emb AI440799 AI440799 sa48g03.yl Gm-c1004 Glycine max cDNA clone 47 1e-04 emb AI563168 AI563168 EST00292 watermelon lambda zap library Cit 47 1e-04
55	emb AI491014 AI491014 EST241723 tomato shoot, Cornell Lycopersic 44 0.001 emb AW034769 AW034769 EST278805 tomato callus, TAMU Lycopersicon 44 0.001 emb AI777269 AI777269 EST258234 tomato resistant, Cornell Lycope 44 0.001 emb AQ653339 AQ653339 Sheared DNA-6G13.TF Sheared DNA Trypanosom 34 1.5 dbj D50838 CREACTINA Chlamydomonas reinhardtii DNA for actin, co 33 2.0
60	emb AL109815 PFMAL13PA Plasmodium falciparum chromosome 13 strai 33 2.0 emb AW257048 AW257048 EST305185 KV2 Medicago truncatula cDNA clo 32 3.8 gb U52151 APU52151 Aspergillus parasiticus polyketide synthase P 32 3.8 emb AO644937 AO644937 RPC193-DnnH-27K24 TV RPC193-DnnH Trumpno 32 3.8

	emb AB009881 AB009881 Nicotiana tabacum mRNA for myo-inositol 1 32 3.8 emb AQ643140 AQ643140 RPCI93-EcoRI-6J20.TJ RPCI93-EcoRI Trypanos 32 3.8 emb X56441 GL35 G.lemaneiformis plasmid GL3.5 DNA starting at Ec 28 5.1
5	gb M60208 YSPHSP70 S.pombe mitochondrial heat shock protein (HSP 32 5.2
3	emb AF083468 AF083468 Emericella nidulans putative zinc finger p 32 5.2 emb AU011047 AU011047 AU011047 Schizosaccharomyces pombe late lo 32 5.2
	emb AL136235 SPAC664 S.pombe chromosome I cosmid c664. 32 5.2
	emb AL160493 LMFLCHR26 Leishmania major Friedlin assembled chrom 31 7.1 emb X70810 CLEGCGA Euglena gracilis chloroplast complete genome. 31 7.1
10	emb[X70810]CLEGCGA Euglena gracilis chloroplast complete genome. 31 7.1 emb[AW923451]AW923451 DG1_52_H09.b1_A002 Dark Grown 1 (DG1) Sorg 31 7.
	emb AQ845394 AQ845394 LMAJFV1 lm24h05.yl Leishmania major FV1 ra 31 7.1
	emb AQ908191 AQ908191 GSSTc08820 Trypanosome cruzi random genomi 31 7.1
	emb AV410934 AV410934 AV410934 Lotus japonicus young plants (two 31 7.1
15	emb Z11874 CHEGZ Euglena gracilis Z Chloroplast DNA. 31 7.1 emb AL049184 PFMAL13P3 Plasmodium falciparum chromosome 13 strai 31 9.8
Ļ	emb AL049184 PFMAL13P3 Plasmodium falciparum chromosome 13 strai 31 9.8 gb U33050 SCD8035 Saccharomyces cerevisiae chromosome IV cosmids 31 9.8
	emb AC007862 AC007862 Trypanosoma brucei chromosome II clone RPC 31 9.8
	emb X74406 HSPSEN102 Hemerocallis sp. mRNA for thiol-protease. 31 9.8
20	emb AF107822 AF107822 Hildenbrandia rubra country Mexico ribulos 31 9.8
20	emb AL031744 PFMAL1P1 Plasmodium falciparum chromosome 1 strain 31 9.8 emb AQ651798 AQ651798 Sheared DNA-20J13.TR Sheared DNA Trypanoso 31 9.8
	emb AQ875345 AQ875345 V123A8 mTn-3xHA/lacZ Insertion Library, st 31 9.8
	emb AF245210 AF245210 Thuja plicata clone Tp6 microsatellite seq 31 9.8
25	emb AC006281 AC006281 Plasmodium falciparum chromosome 12 clone 31 9.8
23	emb AI897641 AI897641 EST267084 tomato ovary, TAMU Lycopersicon 31 9.8 emb AF163675 AF163675 Sclerotium cepivorum strain SQ-48 anonymou 31 9.8
	emb AF163675 AF163675 Sclerotium cepivorum strain SQ-48 anonymou 31 9.8 emb AF163674 AF163674 Sclerotium cepivorum strain DE-1 anonymous 31 9.8
	•
30	Query= NI16_at 13697_at /id_source genbank /description no hits found.
	/blast_score /ec_number /family /chip nova/gb_link
	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ni16 /ncgi
	http://www.ncgr.org/cgi-bin/ff?ni16
35	(509 letters)
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
40	
•	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
45	emb AV397290 AV397290 AV397290 Chlamydomonas reinhardtii C9 Chla 36 0.20
	emb W35667 W35667 TgESTzy83e02.rl TgRH Tachyzoite cDNA Toxoplasm 28 0.49
	emb AL115822 CNS01CPI Botrytis cinerea strain T4 cDNA library un 33 1.5 emb AL031744 PFMAL1P1 Plasmodium falciparum chromosome 1 strain 33 2.0
	emb AW033792 AW033792 EST277363 tomato callus, TAMU Lycopersicon 33 2.5
50	emb Z49705 SC8520X S.cerevisiae chromosome XIII cosmid 8520. 32 3.8
	emb AB001684 AB001684 Chlorella vulgaris C-27 chloroplast DNA, c 32 3.8
	emb AL049185 PFMAL13P2 Plasmodium falciparum chromosome 13 strai 32 3.8
	emb AW101318 AW101318 sd77e03.yl Gm-c1009 Glycine max cDNA clone 32 3.8 emb AQ909718 AQ909718 GSSTc09185 Trypanosome cruzi random genomi 31 5.3
55	emb AW991095 AW991095 SsS0129 Suaeda salsa ZAP cDNA library Suae 28 5.9
	emb AJ273065 AJ273065 AJ273065 Metarhizium anisopliae ARSEF 2575 31 6.5
	emb AF057379 AF057379 Nicotiana tabacum clone G8-1 unknown mRNA. 31 6.5
	emb AB005455 AB005455 Antirrhinum majus DNA, genomic survey sequ 31 7.3 gb BE036743 BE036743 MP04G02 MP Mesembryanthemum crystallinum cD 31 7.3
50	gb BE036743 BE036743 MP04G02 MP Mesembryanthemum crystallinum cD 31 7.3 emb AI460510 AI460510 sa80h11.yl Gm-c1004 Glycine max cDNA clone 31 7.3
	embl A 10265001 A 1026500 TENI 10712 T. cruzi enimostigata no-selizad.

emb|AW651081|AW651081 EST329535 tomato germinating seedlings, TA... 30 10.0 emb|Z50113|SPAC31A2 S.pombe chromosome I cosmid c31A2. emb|AW728950|AW728950 GA_ Ea0018L17 Gossypium arboreum 7-10 dpa ... 30 10.0 gb|L38011|L38011 BNAF0228E Mustard flower buds Brassica rapa cDN... 30 10.0 Query= Novartis127_at 13751_at /id_source /description gb|aaf16751.1|ac010155 4 (ac010155) f3m18.8 [arabidopsis thaliana] /blast_score 2.00e-27 /ec_number /family /chip nova /gb link (341 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done Score Sequences producing significant alignments:

20

5

10

15

60

(bits) Value emb|AV428133|AV428133 AV428133 Lotus japonicus young plants (two... 53 9e-07 emb|AV412192|AV412192 AV412192 Lotus japonicus young plants (two... 53 9e-07 emb|AW350135|AW350135 GM210007B10E8R Gm-r1021 Glycine max cDNA 3... 51 2e-06 25 emb|AW349971|AW349971 GM210006B10B12R Gm-r1021 Glycine max cDNA ... 51 2e-06 emb|AW032575|AW032575 EST276134 tomato callus, TAMU Lycopersicon... 51 2e-06 emb|AW030108|AW030108 EST273363 tomato callus, TAMU Lycopersicon... 51 2e-06 emb|AI895822|AI895822 EST265265 tomato callus, TAMU Lycopersicon... 51 2e-06 emb|AI759855|AI759855 sb65c01.yl Gm-c1017 Glycine max cDNA clone... 51 2e-06 30 emb|AI777275|AI777275 EST258240 tomato resistant, Cornell Lycope... 51 2e-06 emb|AW625260|AW625260 EST319263 tomato radicle, 5 d post-imbibit... 51 2e-06 emb|AW441936|AW441936 EST311332 tomato fruit red ripe, TAMU Lyco... 51 2e-06 emb|AI441970|AI441970 sa82e02.yl Gm-c1004 Glycine max cDNA clone... 51 2e-06 emb|AW705827|AW705827 sk63d05.yl Gm-c1016 Glycine max cDNA clone... 51 3e-06 35 emb|AV428923|AV428923 AV428923 Lotus japonicus young plants (two... 51 3e-06 gb|BE124339|BE124339 EST393374 GVN Medicago truncatula cDNA clon... 48 2e-05 emb|AW442099|AW442099 EST311495 tomato fruit red ripe, TAMU Lyco... 48 3e-05 emb|AW625258|AW625258 EST319261 tomato radicle, 5 d post-imbibit... 47 4e-05 emb|AI779024|AI779024 EST259903 tomato susceptible, Cornell Lyco... 46 1e-04 40 emb|AW775746|AW775746 EST334811 DSIL Medicago truncatula cDNA cl... 46 1e-04 emb|AI960660|AI960660 sc87f03.yl Gm-c1018 Glycine max cDNA clone... 46 1e-04 emb|AW278224|AW278224 sf41c11.yl Gm-c1009 Glycine max cDNA clone... 45 3e-04 gb|BE059759|BE059759 sn36g02.yl Gm-c1016 Glycine max cDNA clone ... 45 3e-04 emb|AW348296|AW348296 GM210001B23C7R Gm-r1021 Glycine max cDNA 3... 44 4e-04 45 emb|AW685445|AW685445 NF029E11NR1F1000 Nodulated root Medicago t... 44 4e-04 emb|AI442537|AI442537 sa32g06.yl Gm-c1004 Glycine max cDNA clone... 41 0.004 emb|Z99164|SPAC29B12 S.pombe chromosome I cosmid c29B12. 41 0.005 emb|AW099733|AW099733 sd30f03.y2 Gm-c1012 Glycine max cDNA clone... 40 0.005 emb|AU011832|AU011832 AU011832 Schizosaccharomyces pombe late lo... 40 0.006 50 emb|AW622091|AW622091 EST312889 tomato root during/after fruit s... 39 0.017 emb|AW152886|AW152886 se32c07.yl Gm-c1015 Glycine max cDNA clone... 38 0.024 emb|AW661378|AW661378 833004H08.yl C. reinhardtii CC-125 -S, Lam... 38 0.033 emb|AW625785|AW625785 EST319692 tomato radicle, 5 d post-imbibit... 37 0.045 emb|AQ639212|AQ639212 927P1-10E7.TP 927P1 Trypanosoma brucei gen... 30 0.055 55 emb|X02873|DCEXTG Carrot gene for extensin. 37 0.062 emb|AW926428|AW926428 HVSMEg0007D04 Hordeum vulgare pre-anthesis... 35 0.063 emb|AI988320|AI988320 sc99b12.yl Gm-c1020 Glycine max cDNA clone... 36 0.086 emb|X55685|LEEXTEN5 Tomato extensin mRNA (clone uG-18). 36 0.12 emb|X55682|LEEXTEN2 Tomato extensin mRNA (clone wY). 35 0.16

gb|M34310|YSCTSDNAA S.cerevisiae telomeric sequence DNA, clone Y... 27 0.20

emb|X55681|LEEXTEN1 Tomato extensin mRNA (clone w17-1).

	emb AI780236 AI780236 EST261115 tomato susceptible, Cornell Lyco 35 0.22
	emb AW101170 AW101170 sd75a05.yl Gm-c1008 Glycine max cDNA clone 35 0.22
	emb AW775499 AW775499 EST334564 DSIL Medicago truncatula cDNA cl 35 0.22
	emb AI780235 AI780235 EST261114 tomato susceptible, Cornell Lyco 35 0.22
' 5	emb AI779223 AI779223 EST260102 tomato susceptible, Cornell Lyco 35 0.22
_	emb AW091576 AW091576 EST284852 tomato mixed elicitor, BTI Lycop 35 0.22
	1147000504147005554 44454 4 - 44454 4 - 4445
	emb A1900504 A1900504 sc11h04.yl Gm-c1012 Glycine max cDNA clone 35 0.22
	emb AF163959 AF163959 Saccharomyces cerevisiae isolate wt-20 tel 29 0.23
10	gb[M34311]YSCTSDNAB S.cerevisiae telomeric sequence DNA, clone Y 27 0.25
10	emb AF163953 AF163953 Saccharomyces cerevisiae isolate wt-2 telo 29 0.26
	emb X59720 SCCHRIII S.cerevisiae chromosome III complete DNA seq 28 0.30
	gb M15317 PFAHRPA P.lophurae histidine-rich protein mRNA, 3' end. 35 0.30
	emb AV408422 AV408422 AV408422 Lotus japonicus young plants (two 35 0.30
	emb AF163955 AF163955 Saccharomyces cerevisiae isolate wt-8 telo 33 0.34
15	emb AL116033 CNS01CVD Botrytis cinerea strain T4 cDNA library un 27 0.38
	gb BE034443 BE034443 MH05A01 MH Mesembryanthemum crystallinum cD 34 0.42
	gb M12922 YSCARSX Yeast (S.cerevisiae) chromosome III L terminal 28 0.44
	emb AF163958 AF163958 Saccharomyces cerevisiae isolate wt-13 tel 26 0.56
	emb[X91836]VUEXT26GN V.unguiculata Ext26G gene. 34 0.58
20	emb AI667994 AI667994 TENG0819 T. Cruzi epimastigote normalised 34 0.58
20	embly W029929 A W029929 ECT227616 to make flower but to 0
	emb AW928828 AW928828 EST337616 tomato flower buds 8 mm to pre-a 34 0.58
	emb X86030 VURNEXT26 V.unguiculata mRNA for extensine-like prote 34 0.58
	emb AF163960 AF163960 Saccharomyces cerevisiae isolate wt-21 tel 31 0.58
0.5	emb AF163947 AF163947 Saccharomyces cerevisiae strain yku70Delta 28 0.60
25	emb AF163957 AF163957 Saccharomyces cerevisiae isolate wt-11 tel 30 0.60
	emb AW722164 AW722164 a5d01nm.rl Neurospora crassa morning cDNA 34 0.72
	emb AI065410 AI065410 TENU2298 T. cruzi epimastigote normalized 33 0.79
	emb Y15372 MTY15372 Medicago truncatula mRNA for MtN4 gene, part 33 0.79
	emb AV393340 AV393340 AV393340 Chlamydomonas reinhardtii C9 Chla 33 0.79
30	emb AL117324 LMFL2719 Leishmania major Friedlin chromosome 23 co 33 0.79
	emb AW926294 AW926294 HVSMEg0006N09 Hordeum vulgare pre-anthesis 33 0.79
	emb AI895893 AI895893 EST265336 tomato callus, TAMU Lycopersicon 33 0.79
	emb AW926361 AW926361 HVSMEg0007A04 Hordeum vulgare pre-anthesis 33 0.79
	emb AW712341 AW712341 g1b02ne.f1 Neurospora crassa evening cDNA 33 0.79
35	emb AI066197 AI066197 TENU2588 T. cruzi epimastigote normalized 33 0.79
55	gb L16776 LEIGP63Z Leishmania guyanensis (clone Lg63c7) major su 29 1.0
	gb L07282 CREPETE Chlamydomonas reinhardtii plastocyanin (petE) 33 1.1
	emb AW471567 AW471567 si12b01.yl Gm-c1029 Glycine max cDNA clone 33 1.1
40	emb AI399511 AI399511 NCSP6D11T3 Subtracted Perithecial Neurospo 33 1.1
40	emb AW696703 AW696703 NF109H07ST1F1063 Developing stem Medicago 33 1.1
	emb AW164290 AW164290 se70e09.yl Gm-c1023 Glycine max cDNA clone 33 1.1
	emb AV410275 AV410275 AV410275 Lotus japonicus young plants (two 33 1.1
	emb AW507760 AW507760 si44g05.yl Gm-r1030 Glycine max cDNA clone 33 1.1
	emb X74106 NTGRPR N.tabacum gene for glycine-rich protein. 33 1.1
45	emb AW725658 AW725658 GA_Ea0019C15 Gossypium arboreum 7-10 dpa 27 1.5
	emb AA660327 AA660327 00198 MtRHE Medicago truncatula cDNA 5', m 32 1.5
	emb AW690202 AW690202 NF030A02ST1F1000 Developing stem Medicago 32 1.5
	gb BE123911 BE123911 EST394036 DSIL Medicago truncatula cDNA clo 32 1.5
	emb AI496548 AI496548 sb13b10.y1 Gm-c1004 Glycine max cDNA clone 32 1.5
50	emb AW686104 AW686104 NF034D07NR1F1000 Nodulated root Medicago t 32 1.5
-	gb M76670 TOMEXTENA L.esculentum extensin (class I) gene, comple 32 1.5
	chipenances in the complex of the co
	gb BE034655 BE034655 ML01E08 ML Mesembryanthemum crystallinum cD 32 1.5
	emb AL161025 L3320Y Leishmania major Friedlin cosmid L3320 t7 en 32 1.5
c	emb AW329194 AW329194 N200406e rootphos(-) Medicago truncatula c 32 1.5
55	emb AF163952 AF163952 Saccharomyces cerevisiae isolate wt-1 telo 27 1.5
	emb Z98532 SPAC1B1 S.pombe chromosome I cosmid c1B1. 28 1.6
	emb X01469 PLHRP1 Plasmodium gene fragment for histidine-rich pr 32 2.0
	gb U66179 SCU66179 Skeletonema costatum fucoxanthin-chlorophyll 32 2.0
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone 32 2.0
60	embla W277058 A

Query= Novartis22 at 13764 at /id source /description gb|aad39641.1|ac007591 6 (ac007591) f911.6 [arabidopsis thaliana] /blast score 2.00e-30 5 (973 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching......done Score E Sequences producing significant alignments: (bits) Value 15 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 260 e-123 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 260 e-121 emb|AI495914|AI495914 sb17g06.y1 Gm-c1004 Glycine max cDNA clone... 57 4e-10 emb|AW217278|AW217278 EST295992 tomato callus, TAMU Lycopersicon... 50 6e-10 emb|AF179222|AF179222 Brassica rapa subsp. pekinensis floral nec... 43 2e-08 20 emb|AW737522|AW737522 EST338949 tomato flower buds, anthesis, Co... 52 5e-06 emb|AW650581|AW650581 EST329035 tomato germinating seedlings, TA... 49-6e-06 emb|AW200887|AW200887 se94g08.yl Gm-c1027 Glycine max cDNA clone... 50 3e-05 emb|AW774361|AW774361 EST333512 KV3 Medicago truncatula cDNA clo... 48 1e-04 emb|AW033701|AW033701 EST277272 tomato callus, TAMU Lycopersicon... 47 2e-04 25 emb|AW738253|AW738253 EST339680 tomato flower buds, anthesis, Co... 46 5e-04 emb|AW285102|AW285102 LG1_300_F04.g1_A002 Light Grown 1 (LG1) So... 40 6e-04 emb|AI896626|AI896626 EST266069 tomato callus, TAMU Lycopersicon... 46 6e-04 emb|AW563740|AW563740 LG1_248_A08.g1_A002 Light Grown 1 (LG1) So... 43 0.004 emb|AW256640|AW256640 EST304777 KV2 Medicago truncatula cDNA clo... 42 0.006 30 emb|AF133053|AF133053 Clarkia breweri S-adenosyl-L-methionine:sa... 42 0.006 emb|AI773683|AI773683 EST254783 tomato resistant, Cornell Lycope... 41 0.011 emb|AW563321|AW563321 LG1_235_A01.b1_A002 Light Grown 1 (LG1) So... 40 0.021 emb|AJ234779|HVU234779 Hordeum vulgare genomic DNA fragment; clo... 37 0.26 emb|W66488|W66488 TgESTzy71b04.rl TgME49 Tachyzoite cDNA Toxopla... 36 0.50 35 emb|AW595921|AW595921 si95b09.y1 Gm-c1032 Glycine max cDNA clone... 35 0.94 emb|AW567624|AW567624 si65f05.yl Gm-r1030 Glycine max cDNA clone... 35 1.3 emb|AQ875548|AQ875548 V126F8 mTn-3xHA/lacZ Insertion Library, st... 35 1.3 emb|AI069155|AI069155 mgae0005dA02f Magnaporthe grisea Appressor... 34 1.8 emb|AW734368|AW734368 sk19c07.yl Gm-c1028 Glycine max cDNA clone... 34 1.8 40 gb[T02585]T02585 0228C3 cbsPfHB3.1, Debopam Chakrabarti Plasmodi... 34 2.4 emb|AC005507|AC005507 Plasmodium falciparum chromosome 12 clone ... 34 2.4 emb|AF134688|AF134688 Plasmodium falciparum strain MAI5 from Mal... 34 2.4 emb|AF134683|AF134683 Plasmodium falciparum strain UNK1 CG2 omeg... 34 2.4 emb|AB009111|AB009111 AB009111 Chlamydomonas W80 lambda ZAP II C... 34 2.4 45 emb|AL109814|PFMAL13PB Plasmodium falciparum chromosome 13 strai... 34 2.4 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. emb|AV397690|AV397690 AV397690 Chlamydomonas reinhardtii C9 Chla... 33 3.3 emb|AW695936|AW695936 NF100B08ST1F1064 Developing stem Medicago ... 33 3.3 emb|AV389414|AV389414 AV389414 Chlamydomonas reinhardtii C9 Chla... 33 3.3 50 emb|AF134698|AF134698 Plasmodium falciparum strain COM1 from Com... 33 3.3 gb|U60200|STU60200 Solanum tuberosum lipoxygenase (POTLX-1) mRNA... 33 4.6 emb|AF039651|AF039651 Solanum tuberosum 5-lipoxygenase mRNA, com... 33 4.6 emb|AQ447600|AQ447600 mgxb0008I05f CUGI Rice Blast BAC Library P... 33 4.6 emb|Z15131|ASBGLUCAN A.sativa mRNA for beta glucanase. 55 gb|BE126052|BE126052 DG1_65_G12.b1_A002 Dark Grown 1 (DG1) Sorgh... 33 4.6 emb[Y18548|STU18548 Solanum tuberosum mRNA for lipoxygenase. emb|AF019614|AF019614 Solanum tuberosum lipoxygenase (plox2) mRN... 33 4.6 emb|X79107|STLOX1 S.tuberosum (Desiree) mRNA for lipoxygenase. emb|AQ400078|AQ400078 mgxb0017C10f CUGI Rice Blast BAC Library P... 33 4.6

emb|X95516|STLIPOT13 S.tuberosum mRNA for lipoxygenase (clone T13). 33 4.6 dbj|D85900|ASNPDIA Aspergillus oryzae DNA for protein disulfide ... 33 4.6

60

	emb AQ396525 AQ396525 mgxb0011J08f CUGI Rice Blast BAC Library P 33 4.6 gb U60201 STU60201 Solanum tuberosum lipoxygenase (POTLX-2) mRNA 33 4.6 cmb AW750228 AW7750228 AW750228 W75028 A
	emb AW759238 AW759238 sl38f10.yl Gm-c1027 Glycine max cDNA clone 33 4.6 emb AQ399938 AQ399938 mgxb0012O04f CUGI Rice Blast BAC Library P 33 4.6
5	emb AF019613 AF019613 Solanum tuberosum lipoxygenase (plox1) mRN 33 4.6
	emb X95512 STLIPOXT6 S.tuberosum mRNA for lipoxygenase (clone T6). 33 4.6
	emb AW278834 AW278834 sf99c02.yl Gm-c1019 Glycine max cDNA clone 32 6.3
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom 32 6.3
10	emb AB005555 AB005555 Triticum aestivum mRNA for wga20, complete 32 6.3
10	emb AA786508 AA786508 m3a04a1.rl Aspergillus nidulans 24hr asexu 32 6.3
	emb AJ274333 AJ274333 AJ274333 Metarhizium anisopliae ARSEF 2575 32 6.3
	emb Y14007 TAY14007 Triticum aestivum mRNA for gibberellin 20-ox 32 6.3 emb AW234216 AW234216 sf22f02.yl Gm-c1028 Glycine max cDNA clone 27 6.8
	emb AW234216 AW234216 sf22f02.yl Gm-c1028 Glycine max cDNA clone 27 6.8 emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S 32 8.6
15	emb AA273033 AA273033 T4296 MVAT4 bloodstream form of serodeme W 32 8.6
	emb AZ215931 AZ215931 Sheared DNA-116D3.TR Sheared DNA Trypanoso 32 8.6
	emb AA495648 AA495648 c078 Zhou and Ragan 1993 Gracilaria gracil 32 8.6
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai 32 8.6
•	emb X56775 HVGLB1 H.vulgare Glb 1 gene for 1-3,1-4-beta-D-glucan 32 8.6
20	emb Z72916 SCYGR131W S.cerevisiae chromosome VII reading frame O 32 8.6
	emb Z72915 SCYGR130C S.cerevisiae chromosome VII reading frame O 32 8.6
	gb U10083 TGU10083 Toxoplasma gondii RH hypoxanthine-guanine pho 32 8.6
	emb AB026835 AB026835 Toxoplasma gondii mRNA for hypoxanthine-gu 32 8.6
25	gb U09219 TGU09219 Toxoplasma gondii RH hypoxanthine-guanine pho 32 8.6
25	gb U10247 TGU10247 Toxoplasma gondii RH hypoxanthine-xanthine-gu 32 8.6
	emb AB012774 AB012774 AB012774 Toxoplasma gondii mRNA (T.Koyama) 32 8.6
	gb S73865 S73865 linoleate:oxygen oxidoreductase [Solanum tubero 32 8.6 emb AW761275 AW761275 sl65d12.yl Gm-c1027 Glycine max cDNA clone 32 8.6
	emb AL112245 CNS019Y5 Botrytis cinerea strain T4 cDNA library un 32 8.6
30	emb X56260 HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC 32 8.6
	emb AI162017 AI162017 A011P07U Hybrid aspen plasmid library Popu 30 9.4
35	Query= Novartis31_at 14141_at /id_source /description no hits found less than or equal to 1e-15. /blast score
	/ec_number /family /chip nova /gb_link /ncgi (309 letters)
	Database: plantfungal
40	661,018 sequences; 426,114,510 total letters
	001,010 soquences, 420,114,510 total fettels
	Searchingdone
	Score E
45	Sequences producing significant alignments: (bits) Value
	LIVOGI AQIYA CIVID CINAYA
	emb X87143 HACYTB5RN H.annuus mRNA for extraplastidial fusion pr 34 0.49
	emb X74782 BNSACPD1 B.napus gene for stearoyl-acyl carrier prote 32 1.3 emb AW560462 AW560462 EST315510 DSIR Medicago truncatula cDNA cl 32 1.3
50	emb AW560462 AW560462 EST315510 DSIR Medicago truncatula cDNA cl 32 1.3 emb AW687516 AW687516 NF010D12RT1F1101 Developing root Medicago 32 1.3
	emb AW256825 AW256825 EST304962 KV2 Medicago truncatula cDNA clo 32 1.3
	emb X07644 NTALSURA Tobacco acetolactate synthase gene, ALS SuRA 32 1.7
	emb AA451568 AA451568 AOB213F Onion seedling leaf cDNA library A 31 2.4
	emb AW067623 AW067623 SBcD89 Sugar beet leaf cDNA library Beta v 31 3.3
55	emb AF030694 AF030694 Plasmodium falciparum strain Dd2 heat shoc 31 3.3
	emb X12493 SCADR6 Yeast ADR6 gene for transcription factor. 30 4.5
	gb U14726 SCU14726 Saccharomyces cerevisiae Syg1p (SYG1) gene, c 30 4.5
	emb Z46861 SC9905 S.cerevisiae chromosome IX cosmid 9905 and lam 30 4.5
40	gb L29456 TOBHIC12X Nicotiana tabacum histone H1 (H1C12) mRNA, c 30 4.5
60	gb[U33335[U33335 Saccharomyces cerevisiae chromosome XVI, left a 30 4.5 emblAJ290663[PAB290663 Picea abjes copia like retroelement parti 30 6.2
	VIDURALA ZUUUDIE MADA ZUUUD EILEM MDIES CODIN IIKE TEITOEIEMENT NATU 40 K 7

```
emb|ALI 15708|CNS01CMC Botrytis cinerea strain T4 cDNA library un... 30 6.2
       emb|Z71630|SCYNR015W S.cerevisiae chromosome XIV reading frame O... 29 8.5
       emb|Z71629|SCYNR014W S.cerevisiae chromosome XIV reading frame O... 29 8.5
       emb|AQ875584|AQ875584 V127B11 mTn-3xHA/lacZ Insertion Library, s... 29 8.5
  5
       gb|L16451|YSAAPRP Candida albicans acid proteinase-related prote... 29 8.5
       emb|AW981797|AW981797 PC18H02 Pine TriplEx pollen cone library P... 29 8.5
       emb|AQ644958|AQ644958 RPCI93-DpnII-30N9.TJ RPCI93-DpnII Trypanos... 29 8.5
       emb|AW672524|AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So... 29 8.5
       emb[AW564851]AW564851 LG1_310_D10.b1_A002 Light Grown 1 (LG1) So... 29 8.5
10
       emb|AI895394|AI895394 EST264837 tomato callus, TAMU Lycopersicon... 27 9.6
       Query= Novartis35_at 14145_at /id_source
      /description "dbj|baa22813.1| (d26015) cnd41, chloroplast nucleoid dna
      binding protein [nicotiana tabacum]" /blast_score 8.00e-58 /ec_number
15
      /family /chip nova /gb link /ncgi
           (783 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
20
                                         Score E
      Sequences producing significant alignments:
                                                        (bits) Value
25
      gb|BE053273|BE053273 GA_Ea0035A10f Gossypium arboreum 7-10 dpa ... 149 4e-61
      dbj|D26015|D26015 Nicotiana tabacum mRNA for CND41, chloroplast ... 148 9e-56
      emb|AI487587|AI487587 EST245909 tomato ovary, TAMU Lycopersicon ... 152 4e-54
      emb|AI489151|AI489151 EST247490 tomato ovary, TAMU Lycopersicon ... 152 4e-54
30
      emb|AI483907|AI483907 EST249778 tomato ovary, TAMU Lycopersicon ... 152 1e-52
      emb|AW931514|AW931514 EST357357 tomato fruit mature green, TAMU ... 145 4e-52
      emb|AI771546|AI771546 EST252646 tomato ovary, TAMU Lycopersicon ... 144 2e-49
      emb|AW736637|AW736637 EST333129 KV3 Medicago truncatula cDNA clo... 142 6e-48
      emb|AI166286|AI166286 xylem.est.133 Poplar xylem Lambda ZAPII li... 151 6e-40
35
      emb|AW693272|AW693272 NF064A05ST1F1000 Developing stem Medicago ... 143 3e-39
      emb|AW736636|AW736636 EST333128 KV3 Medicago truncatula cDNA clo... 145 5e-39
      emb|AW559446|AW559446 EST314494 DSIR Medicago truncatula cDNA cl... 143 1e-38
      emb|AW730900|AW730900 GA_Ea0029G11 Gossypium arboreum 7-10 dpa ... 146 2e-37
      emb|AW692307|AW692307 NF049H04ST1F1043 Developing stem Medicago ... 143 1e-36
40
      emb|AW737187|AW737187 EST338614 tomato flower buds, anthesis, Co... 149 3e-36
      emb|AW688595|AW688595 NF009D06ST1F1000 Developing stem Medicago ... 137 8e-35
      emb|AI974844|AI974844 T113327e KV2 Medicago truncatula cDNA clon... 143 3e-33
      emb|AW773698|AW773698 EST332684 KV3 Medicago truncatula cDNA clo... 129 1e-32
      emb|AV408654|AV408654 AV408654 Lotus japonicus young plants (two... 135 6e-32
45
      emb|AW688941|AW688941 NF013E03ST1F1000 Developing stem Medicago ... 121 4e-30
      emb|AI725786|AI725786 BNLGHi12992 Six-day Cotton fiber Gossypium... 66 7e-29
      emb|AW677148|AW677148 DG1_5_C02.b1_A002 Dark Grown 1 (DG1) Sorgh... 92 4e-27
      emb|AW932074|AW932074 EST357917 tomato fruit mature green, TAMU ... 116 3e-26
      emb|AI731300|AI731300 BNLGHi9147 Six-day Cotton fiber Gossypium ... 50 9e-25
50
      emb|AW933383|AW933383 EST359322 tomato fruit mature green, TAMU ... 57 5e-23
      emb|AW034232|AW034232 EST277803 tomato callus, TAMU Lycopersicon... 63 4e-22
      emb|AW221352|AW221352 EST297821 tomato fruit mature green, TAMU ... 63 2e-21
      emblAW307535|AW307535 sf58b08.yl Gm-c1009 Glycine max cDNA clone... 63 2e-21
      emb|AI974298|AI974298 T110300e KV0 Medicago truncatula cDNA clon... 90 5e-21
55
      emb|AI772366|AI772366 EST253466 tomato resistant, Cornell Lycope... 63 7e-21
      emb|AV423168|AV423168 AV423168 Lotus japonicus young plants (two... 63 2e-20
      emb|AW928704|AW928704 EST337492 tomato flower buds 8 mm to pre-a... 67 8e-20
      emb|AW219354|AW219354 EST301836 tomato root during/after fruit s... 64 le-19
60
      emb|AW695746|AW695746 NF098B04ST1F1032 Developing stem Medicago ... 60 4e-19
      emb|AW729560|AW729560 GA_Ea0025G03 Gossypium arboreum 7-10 dpa ... 64 5e-19
```

```
emb|AW774011|AW774011 EST332997 KV3 Medicago truncatula cDNA clo... 63 1e-18
      emb|AW691624|AW691624 NF047B12ST1F1000 Developing stem Medicago ... 60 1e-18
      emb|AW690628|AW690628 NF036F05ST1F1000 Developing stem Medicago ... 60 1e-18
      emb|AW398635|AW398635 EST309135 L. pennellii trichome, Cornell U... 48 1e-18
 5
      gb|BE033948|BE033948 MG02E01 MG Mesembryanthemum crystallinum cD... 68 2e-18
      emb|AW980831|AW980831 EST391984 GVN Medicago truncatula cDNA clo... 48 2e-17
      emb|AW266728|AW266728 L48-63T3 Ice plant Lambda Uni-Zap XR expre... 89 4e-17
      emb|AI726953|AI726953 BNLGHi6948 Six-day Cotton fiber Gossypium ... 66 5e-17
10
      emb|AW666733|AW666733 GA_Ea0005N06 Gossypium arboreum 7-10 dpa ... 64 7e-17
      emb|AW693054|AW693054 NF059C10ST1F1081 Developing stem Medicago ... 63 1e-16
      emb|AW692433|AW692433 NF055F02ST1F1000 Developing stem Medicago ... 60 2e-16
      emb|AW560983|AW560983 EST316031 DSIR Medicago truncatula cDNA cl... 61 3e-16
      emb|AW686542|AW686542 NF039C04NR1F1000 Nodulated root Medicago t... 60 4e-16
15
      emb|AW726749|AW726749 GA_Ea0022J22 Gossypium arboreum 7-10 dpa ... 64 6e-16
      emb|AW689509|AW689509 NF021E09ST1F1000 Developing stem Medicago ... 63 6e-16
      emblAV411180|AV411180 AV411180 Lotus japonicus young plants (two... 75 9e-16
      emb|AW697936|AW697936 NXNV 072 C04 F Nsf Xylem Normal wood Verti... 42 1e-15
      emb|AW692507|AW692507 NF052C09ST1F1000 Developing stem Medicago ... 60 2e-15
20
      emb|AW685394|AW685394 NF028G11NR1F1000 Nodulated root Medicago t... 60 2e-15
      emb|AI725103|AI725103 1002 PtIFG2 Pinus taeda cDNA clone 8942r, ... 54 3e-15
      emb|AW133056|AW133056 se13g09.y1 Gm-c1013 Glycine max cDNA clone... 69 4e-15
      emb|AW695422|AW695422 NF094F05ST1F1046 Developing stem Medicago ... 52 5e-15
      emb|AW693273|AW693273 NF064A06ST1F1000 Developing stem Medicago ... 60 7e-15
25
      emb|AI727564|AI727564 BNLGHi8414 Six-day Cotton fiber Gossypium ... 66 le-14
      emb|AW254916|AW254916 ML134 peppermint glandular trichome Mentha... 67 3e-14
      emb|AI166906|AI166906 xylem.est.692 Poplar xylem Lambda ZAPII li... 59 5e-14
      emb|AW648535|AW648535 EST326989 tomato germinating seedlings, TA... 64 7e-14
      emb|AW691201|AW691201 NF038H04ST1F1000 Developing stem Medicago ... 45 2e-13
30
      emb|AW691254|AW691254 NF042G01ST1F1000 Developing stem Medicago ... 71 6e-13
      emb|AI771903|AI771903 EST253003 tomato ovary, TAMU Lycopersicon ... 58 2e-12
      emb|AW755537|AW755537 sl05b09.yl Gm-c1036 Glycine max cDNA clone... 43 2e-12
      emb|AW690391|AW690391 NF030B07ST1F1000 Developing stem Medicago ... 49 3e-12
      gbBE125956BE125956 DG1_60_B12.b1_A002 Dark Grown 1 (DG1) Sorgh... 56 2e-11
35
      emb|AW933549|AW933549 EST359308 tomato fruit mature green, TAMU ... 46 3e-11
      emb|AW573921|AW573921 EST316512 GVN Medicago truncatula cDNA clo... 59 6e-11
      emb|AV425214|AV425214 AV425214 Lotus japonicus young plants (two... 54 6e-11
      emb|AW621185|AW621185 EST311983 tomato root during/after fruit s.... 62 1e-10
      emb|AW720132|AW720132 LjNEST14h12r Lotus japonicus nodule librar... 57 1e-10
40
      emb|AW697024|AW697024 NF111E05ST1F1038 Developing stem Medicago ... 43 1e-10
      emb|AI727398|AI727398 BNLGHi7916 Six-day Cotton fiber Gossypium ... 66 2e-10
      emb|AW317889|AW317889 sg58e01.yl Gm-c1007 Glycine max cDNA clone... 64 2e-10
      emb|AI773497|AI773497 EST254597 tomato resistant, Cornell Lycope... 66 6e-10
      emb|AI779047|AI779047 EST259926 tomato susceptible, Cornell Lyco... 66 6e-10
45
      emb|AW160290|AW160290 EST290148 L. pennellii trichome, Cornell U... 66 6e-10
      emb|AW690159|AW690159 NF028E04ST1F1000 Developing stem Medicago ... 40 9e-10
      emb|AW697130|AW697130 NF112E12ST1F1098 Developing stem Medicago ... 40 9e-10
      emb|AA739537|AA739537 302 PtIFG2 Pinus taeda cDNA clone 8497M 3'... 57 9e-10
      emb|AW934683|AW934683 EST353575 tomato flower buds 0-3 mm, Corne... 44 1e-09
50
      emblAW217676|AW217676 EST296390 tomato flower buds 8 mm to pre-a... 44 1e-09
      gb|L47871|L47871 BNAF1521 Mustard flower buds Brassica rapa cDNA... 47 1e-09
      emb|AI163871|AI163871 A050p31u Hybrid aspen plasmid library Popu... 59 1e-09
      emb|AW728602|AW728602 GA_Ea0017E06 Gossypium arboreum 7-10 dpa ... 64 1e-09
      emb|AW617945|AW617945 EST314019 L. pennellii trichome, Cornell U... 46 2e-09
55
     emb|AW647996|AW647996 EST326450 tomato germinating seedlings, TA... 64 2e-09
      emb|AW218271|AW218271 EST303452 tomato radicle, 5 d post-imbibit... 64 2e-09
     emb|AI776062|AI776062 EST257162 tomato resistant, Cornell Lycope... 64 2e-09
     emb|AW036254|AW036254 EST278333 tomato seed, TAMU Lycopersicon e... 64 2e-09
     emb|AW650814|AW650814 EST329268 tomato germinating seedlings, TA... 64 2e-09
60
     emb|AI443133|AI443133 sa84g05.yl Gm-c1004 Glycine max cDNA clone... 63 3e-09
     emb|AW906997|AW906997 EST343224 potato stolon, Cornell Universit... 63 3e-09
```

	gb BE053949 BE053949 GA_Ea0031D21f Gossypium arboreum 7-10 dpa 48 4e-09 emb AW730655 AW730655 GA_Ea0018A01 Gossypium arboreum 7-10 dpa 48 4e-09
5	
	Query= Novartis36_at 14146_at /id_source /description gb aad25550.1 ac005850_7 (ac005850) hypothetical protein [arabidopsis thaliana] /blast_score 7.00e-26 /ec_number /family /chip nova /gb link
10	(507 letters)
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
15	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
20	emb AV427887 AV427887 AV427887 Lotus japonicus young plants (two 61 6e-17
	emb AV419761 AV419761 AV419761 Lotus japonicus young plants (two 56 le-15
	emb AI967590 AI967590 Ljirnpest06-480-c9 Ljirnp Lambda HybriZap 68 2e-14
	emb AW684644 AW684644 NF019C10NR1F1000 Nodulated root Medicago t 62 9e-12 gb BE036389 BE036389 MO24B03 MO Mesembryanthemum crystallinum cD 44 2e-06
25	gb BE034652 BE034652 ML01E04 ML Mesembryanthemum crystallinum cD 44 2e-06
	emb AC005308 AC005308 Plasmodium falciparum chromosome 12 clone 35 0.57
	gb[N60116]N60116 TgESTzy01b10.r1 TgRH Tachyzoite cDNA Toxoplasma 34 0.78
	emb AF161334 AF161334 Raphanus raphanistrum subsp. raphanistrum 33 1.5
20	gb L37356 PUMPAL3A Petroselinum crispum phenylalanine ammonia-ly 33 2.0
30	emb AI974840 AI974840 T113322e KV2 Medicago truncatula cDNA clon 32 2.8
	gb U36470 NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu 32 2.8 emb AI938788 AI938788 sc60a05.y1 Gm-c1016 Glycine max cDNA clone 32 2.8
	emb AI938788 AI938788 sc60a05.y1 Gm-c1016 Glycine max cDNA clone 32 2.8 emb AF114794 AF114794 Porphyra purpurea mitochondrion, complete 32 3.8
	emb AI374339 AI374339 T6652 MVAT4 bloodstream form of serodeme W 32 3.8
35	emb AI374387 AI374387 T6725 MVAT4 bloodstream form of serodeme W 32 3.8
	emb AI374381 AI374381 T6716 MVAT4 bloodstream form of serodeme W 32 3.8
	emb AI894927 AI894927 EST264370 tomato callus, TAMU Lycopersicon 31 5.2
	emb AA550548 AA550548 1711m3 gmbPfHB3.1, G. Roman Reddy Plasmodi 31 5.2 emb AJ223459 ANAJ3459 Aspergillus nidulans prnA gene. 31 5.2
40	emb AJ223459 ANAJ3459 Aspergillus nidulans prnA gene. 31 5.2 emb AJ390536 CAL390536 Candida albicans DNA, clone 222g9. 31 5.2
,,,	emb AW119888 AW119888 sd54b09.y1 Gm-c1016 Glycine max cDNA clone 31 5.2
	emb AI431203 AI431203 sa22f12.y2 Gm-c1006 Glycine max cDNA clone 31 5.2
	emb AF161331 AF161331 Sinapis arvensis S-locus related 1 (SLR1) 31 7.2
15	emb AF137311 AF137311 Miscanthus sinensis phytochrome B (PHYB) g 31 7.2
45	gb[T36711[T36711 EST101701 S. cerevisiae strain X2180-1A Sacchar 31 7.2
	emb AW781868 AW781868 sl97g02.yl Gm-c1027 Glycine max cDNA clone 31 7.2 emb AW755482 AW755482 sl04e07.yl Gm-c1036 Glycine max cDNA clone 30 9.9
	emb AW694935 AW694935 NF081F05ST1F1046 Developing stem Medicago 30 9.9
	emb AZ215370 AZ215370 Sheared DNA-56C1.TF Sheared DNA Trypanosom 30 9.9
50	emb AQ945786 AQ945786 Sheared DNA-30C5.TR Sheared DNA Trypanosom 30 9.9
	emb AA739646 AA739646 411 PtIFG2 Pinus taeda cDNA clone 8694M 3' 30 9.9
	emb AL034353 SPBC1271 S.pombe chromosome II cosmid c1271. 30 9.9
	gb N69599 N69599 TgESTzy41b11.r1 TgRH Tachyzoite cDNA Toxoplasma 30 9.9
55	
	Query= Novartis38_at 14148_at /id_source
	/description gb/aaf34713.1/af224762_1 (af224762) siga binding protein
	[arabidopsis thaliana] /blast_score 4.00e-53 /ec_number /family
60	/chip nova /gb_link
60	(770 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters 5 Score Sequences producing significant alignments: (bits) Value emb|AW266797|AW266797 L48-136T3 Ice plant Lambda Uni-Zap XR expr... 59 5e-08 emb|AI776331|AI776331 EST257431 tomato resistant, Cornell Lycope... 51 8e-06 10 emb|AI938454|AI938454 sc45e10.yl Gm-c1015 Glycine max cDNA clone... 44 0.001 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 36 0.38 emb|AV406828|AV406828 AV406828 Lotus japonicus young plants (two... 31 0.49 emb|AI731942|AI731942 BNLGHi11450 Six-day Cotton fiber Gossypium... 35 0.71 15 emb|AQ255443|AQ255443 mgxb0014I21r CUGI Rice Blast BAC Library P... 35 0.71 emb|AQ940346|AQ940346 Sheared DNA-33M2.TF Sheared DNA Trypanosom... 34 1.3 emb|AI210373|AI210373 i0e05a1.rl Aspergillus nidulans 24hr asexu... 34 1.8 emb|AQ935542|AQ935542 CpG2525A CpIOWAgDNA1 Cryptosporidium parvu... 33 2.5 gb|T18147|T18147 0722c3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 33 2.5 20 emb|AW651276|AW651276 EST329730 tomato germinating seedlings, TA... 33 3.5 emb|AI392128|AI392128 NCSM1B1T7 Subtracted Mycelial Neurospora c... 32 4.8 emb|AW330094|AW330094 TENU4840 T.cruzi epimastigote normalized c... 32 4.8 emb|AF055296|AF055296 Zantedeschia aethiopica geranylgeranyl red... 32 4.8 emb|AI725804|AI725804 BNLGHi13200 Six-day Cotton fiber Gossypium... 32 4.8 25 emb|AW686984|AW686984 NF004F11RT1F1094 Developing root Medicago ... 32 6.6 emb|AJ273808|AJ273808 AJ273808 Metarhizium anisopliae ARSEF 2575... 32 6.6 emb|AQ943530|AQ943530 Sheared DNA-42D24.TR Sheared DNA Trypanoso... 31 9.0 emb|AQ941987|AQ941987 Sheared DNA-42F7.TR Sheared DNA Trypanosom... 31 9.0 emb|AW620371|AW620371 sj04d01.yl Gm-c1032 Glycine max cDNA clone... 31 9.0 30 emb|AI973930|AI973930 sd13g08.y1 Gm-c1020 Glycine max cDNA clone... 31 9.0 emb|AF069470|AF069470 Phleum pratense group V allergen Phl p 5.0... 31 9.0 emb|AL160716|P406R Leishmania major Friedlin PAC P406 right end-... 31 9.0 emb|AQ851400|AQ851400 LMAJFV1 lm40b04.yl Leishmania major FV1 ra... 31 9.0 emb|AF061068|AF061068 Phleum pratense clone 10029 major allergen... 31 9.0 35 emb|AQ953188|AQ953188 Sheared DNA-50B12.TF Sheared DNA Trypanoso... 31 9.0 emb|AW719942|AW719942 LjNEST12c6r Lotus japonicus nodule library... 31 9.0 emb[X74735]PPHLP5 P. pratense mRNA for PhlpV. emb|AW396374|AW396374 sh27d05.yl Gm-c1016 Glycine max cDNA clone... 31 9.0 gb[N60997]N60997 TgESTzy23f10.r1 TgRH Tachyzoite cDNA Toxoplasma... 31 9.0 40 emb|AI164737|AI164737 A068P10U Hybrid aspen plasmid library Popu... 31 9.0 emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 26 9.5 emb|AW309665|AW309665 sf22g06.x1 Gm-c1028 Glycine max cDNA clone... 26 9.5 emb|AW310247|AW310247 sf33d01.x1 Gm-c1028 Glycine max cDNA clone... 26 9.5 emb|AW508196|AW508196 si50d10.yl Gm-r1030 Glycine max cDNA clone... 27 9.6 45 emb|AW102012|AW102012 sd81h10.yl Gm-c1009 Glycine max cDNA clone... 26 9.8 emb|AW309166|AW309166 sg05b01.yl Gm-c1019 Glycine max cDNA clone... 26 9.8 emb|AW598779|AW598779 sj46h06.yl Gm-c1033 Glycine max cDNA clone... 26 9.8 emb|AW311252|AW311252 sg34d09.yl Gm-c1025 Glycine max cDNA clone... 26 9.8 50 Query= Novartis73_at 14201_at /id_source /description no hits found less than or equal to 1e-15. /blast score /ec_number /family /chip nova /gb link (430 letters) 55 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 60

Score E

Sequences producing significant alignments: (bits) Value emb|AQ952678|AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso... 35 0.32 emb|AW698685|AW698685 R125 non-glandular-haired subtracted cDNA ... 32 1.4 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. emb|AL031854|SPBC337 S.pombe chromosome II cosmid c337. emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 31 5.6 emb|AC006280|AC006280 Plasmodium falciparum chromosome 12 clone ... 31 5.6 gb|M74062|YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl... 31 5.6 emb|AQ947500|AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso... 31 5.6 10 gb|M83307|YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl... 31 5.6 emb|AL031856|SPBC1734 S.pombe chromosome II cosmid c1734. emb|AC073246|AC073246 Trypanosoma brucei chromosome II clone RPC... 30 7.7 emb|AL031535|SPCC16C4 S.pombe chromosome III cosmid c16C4. 15 emb|AC012647|AC012647 Trypanosoma brucei chromosome II clone RPC... 30 7.7 gb|L28038|TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc... 30 7.7 emb|AB004322|AB004322 Nicotiana sylvestris NsPMT1 gene for putre... 30 7.7 emb|AQ941496|AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso... 30 7.7 emb|AQ946940|AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom... 30 7.7 20 emb|AQ942433|AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom... 30 7.7 emb|AF133529|AF133529 Candida albicans mRNA cap methyltransferas... 30 7.7 Query= Novartis73 RC at 14202 at /id source 25 /description no hits found less than or equal to 1e-15. /blast_score /ec_number /family /chip nova /gb_link (430 letters) Database: plantfungal 30 661,018 sequences; 426,114,510 total letters Searching......done Score E 35 Sequences producing significant alignments: (bits) Value emb|AQ952678|AQ952678 Sheared DNA-48H20.TF Sheared DNA Trypanoso... 35 0.32 emb|AW698685|AW698685 R125 non-glandular-haired subtracted cDNA ... 32 1.4 emb|AF061282|AF061282 Sorghum bicolor 22 kDa kafirin cluster. 40 emb|AL031854|SPBC337 S.pombe chromosome II cosmid c337. emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 31 5.6 emb|AC006280|AC006280 Plasmodium falciparum chromosome 12 clone ... 31 5.6 gb[M74062|YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl... 31 5.6 emb|AQ947500|AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso... 31 5.6 45 gb]M83307|YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl... 31 5.6 emb[AL031856]SPBC1734 S.pombe chromosome II cosmid c1734. emb|AC073246|AC073246 Trypanosoma brucei chromosome II clone RPC... 30 7.7 emb|AL031535|SPCC16C4 S.pombe chromosome III cosmid c16C4. emb|AC012647|AC012647 Trypanosoma brucei chromosome II clone RPC... 30 7.7 50 gb|L28038|TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc... 30 7.7 emb|AB004322|AB004322 Nicotiana sylvestris NsPMT1 gene for putre... 30 7.7 emb|AQ941496|AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso... 30 7.7 emb|AQ946940|AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom... 30 7.7 emb|AQ942433|AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom... 30 7.7 55 ... emb|AF133529|AF133529 Candida albicans mRNA cap methyltransferas... 30 7.7 Query= Novartis9 at 14223 at /id source /description emb|caa19683.1| (al024486) putative protein [arabidopsis 60 thaliana] /blast_score 0 /ec number /family /chip nova /gb_link (1761 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters 5 Searching......done Score E Sequences producing significant alignments: (bits) Value 10 emb|AW745943|AW745943 WS1_38 H06.b1_A002 Water-stressed I (WS1) ... 240 3e-62 gb|BE023215|BE023215 sm70a04.yl Gm-c1028 Glycine max cDNA clone ... 236 5e-61 emb|AW399343|AW399343 EST309843 L. pennellii trichome, Cornell U... 234 2e-60 emb|AW618318|AW618318 EST320304 L. pennellii trichome, Cornell U... 177 1e-53 emb|AW310982|AW310982 sg31b02.x1 Gm-c1024 Glycine max cDNA clone... 97 1e-51 15 emb|AI442277|AI442277 sa66a04.yl Gm-c1004 Glycine max cDNA clone... 200 2e-50 emb|AW687759|AW687759 NF013B05RT1F1044 Developing root Medicago ... 160 1e-46 emb|AW684122|AW684122 NF012F06NR1F1000 Nodulated root Medicago t... 83 2e-44 emb|AW309867|AW309867 sf25g10.x1 Gm-c1028 Glycine max cDNA clone... 89 5e-43 gb|BE020423|BE020423 sm40e08.yl Gm-c1028 Glycine max cDNA clone ... 88 2e-39 20 emb|AW691118|AW691118 NF041D08ST1F1000 Developing stem Medicago ... 78 2e-35 emb|AW160235|AW160235 EST290093 L. pennellii trichome, Cornell U... 120 6e-32 emb|AI960862|AI960862 sc91f07.y1 Gm-c1019 Glycine max cDNA clone... 74 5e-30 emb|AW349633|AW349633 GM210006A11B3R Gm-r1021 Glycine max cDNA 3... 89 8e-29 emb|AW775076|AW775076 EST334227 KV3 Medicago truncatula cDNA clo... 81 6e-26 25 gb|BE020331|BE020331 sm40d08.yl Gm-c1028 Glycine max cDNA clone ... 69 4e-23 emb|AW746031|AW746031 WS1_39 A03.b1_A002 Water-stressed I (WS1) ... 74 8e-23 emb|AW621546|AW621546 EST312344 tomato root during/after fruit s... 64 le-13 emb|AW622846|AW622846 EST306916 tomato flower buds 3-8 mm, Corne... 54 2e-12 gb|L43984|BLYBD Hordeum vulgare (clone ABG377) chromosome 3H STS... 69 8e-11 30 emb|AW774216|AW774216 EST333367 KV3 Medicago truncatula cDNA clo... 69 1e-10 emb|AW774324|AW774324 EST333475 KV3 Medicago truncatula cDNA clo... 69 1e-10 emb|AW686169|AW686169 NF038H07NR1F1000 Nodulated root Medicago t... 68 2e-10 emb|AW160234|AW160234 EST290092 L. pennellii trichome, Cornell U... 46 2e-08 emb|AW685496|AW685496 NF030G02NR1F1000 Nodulated root Medicago t... 45 2e-07 35 emb|AW684082|AW684082 NF011H08NR1F1000 Nodulated root Medicago t... 55 2e-06 emb|AW693839|AW693839 NF069F08ST1F1074 Developing stem Medicago ... 53 6e-06 emb|AI163659|AI163659 A046p04u Hybrid aspen plasmid library Popu... 53 6e-06 emb|AW033404|AW033404 EST276975 tomato callus, TAMU Lycopersicon... 49 le-04 emb|AI054662|AI054662 coau0001K11 Cotton Boll Abscission Zone cD... 37 2e-04 40 emb|AW758414|AW758414 874008A01.y1 C. reinhardtii CC-1690, Lambd... 41 0.022 emb|AW746188|AW746188 WS1_39_A03.g1_A002 Water-stressed 1 (WS1) ... 41 0.022 emb|Z99126|SPAC26H5 S.pombe chromosome I cosmid c26H5. emb|AJ225805|EDKCHALPH Egeria densa mRNA for inward potassium ch... 39 0.14 emb|AI488725|AI488725 EST247064 tomato ovary, TAMU Lycopersicon ... 38 0.20 45 emb|Z69731|SPAC6C3 S.pombe chromosome I cosmid c6C3. 36 0.71 emb|Z38061|SC9168 S.cerevisiae chromosome IX cosmid 9168. emb|AW925349|AW925349 HVSMEg0001B12 Hordeum vulgare pre-anthesis... 36 0.71 emb|AW671585|AW671585 LG1_348_H11.b1_A002 Light Grown 1 (LG1) So... 36 0.97 gb|BE024935|BE024935 894007A03.x1 C. reinhardtii CC-1690, normal... 36 0.97 50 emb|AW216501|AW216501 EST295215 tomato callus, TAMU Lycopersicon... 36 0.97 emb|AW680841|AW680841 WS1_7_E11.g1_A002 Water-stressed 1 (WS1) S... 35 1.3 emb|AQ911629|AQ911629 LMAJFV1_lm96c04.yl Leishmania major FV1 ra... 35 1.3 emb|AW100578|AW100578 sd57b08.y1 Gm-c1008 Glycine max cDNA clone... 35 1.3 emb|AW010724|AW010724 ST11E02 Pine TriplEx shoot tip library Pin... 35 1.8 emb|AL138854|SPAC23G3 S.pombe chromosome I cosmid c23G3. emb|AW934681|AW934681 EST353573 tomato flower buds 0-3 mm, Corne... 34 3.5 emb|Z98975|SPAC19E9 S.pombe chromosome I cosmid c19E9. emb|AW690479|AW690479 NF035A03ST1F1000 Developing stem Medicago ... 34 3.5 emb|Z50142|SPAC2F7 S.pombe chromosome I cosmid c2F7. 60

emb|AA728334|AA728334 LmLv39p7/70M Leishmania major promastigote... 34 4.8 emb|AI779448|AI779448 EST260327 tomato susceptible, Cornell Lyco... 34 4.8

	·
	emb AQ639314 AQ639314 927P1-2A10.TV 927P1 Trypanosoma brucei gen 34 4.8
	emb AW725460 AW725460 GA_Ea0018B02 Gossypium arboreum 7-10 dpa 34 4.8
	emb AW256577 AW256577 EST304714 KV2 Medicago truncatula cDNA clo 34 4.8
	emb AW234006 AW234006 st33a07.yl Gm-c1028 Glycine max cDNA clone 34 4.8
5	emb AW727061 AW727061 GA_Ea0011B08 Gossypium arboreum 7-10 dpa 34 4.8
•	114 700404714 7004047 01 4 7044 4 704 704 704 704 704
	1147701000147701000 7077040100
	emb A/81303 A1/81303 ES1262182 tomato susceptible, Cornell Lyco 34 4.8
	emb AA898817 AA898817 NCP3G4T7 Perithecial Neurospora crassa cDN 34 4.8
10	emb AI329539 AI329539 b6b04ne.f1 Neurospora crassa evening cDNA 33 6.6
10	emb AW754602 AW754602 PC04B10 Pine TriplEx pollen cone library P 33 6.6
	emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai 33 6.6
	emb AW756307 AW756307 s119a02.y1 Gm-c1036 Glycine max cDNA clone 33 6.6
	emb AC004145 AC004145 Leishmania major chromosome 3 clone L5801 33 6.6
	emb AI778201 AI778201 EST259080 tomato susceptible, Cornell Lyco 33 9.0
15	emb AZ215585 AZ215585 Sheared DNA-74E7.TR Sheared DNA Trypanosom 33 9.0
	emb AF216960 AF216960 Pichia pastoris strain GS115 Sec12 (SEC12) 33 9.0
	1 A TOO C A O O A TOO C A O O TOO C C C C C C C C C C C C C C C C
	emb AV6700101AV6700101 G1 266 B11 b1 A002 I into Green A G C C C C C C C C C C C C C C C C C C
	emb AW670919 AW670919 LG1_266_B11.b1_A002 Light Grown 1 (LG1) So 33 9.0.
20	emb AQ842680 AQ842680 CpG1185B CpIOWAgDNA1 Cryptosporidium parvu 33 9.0
20	emb AW982007 AW982007 PC23H10 Pine TriplEx pollen cone library P 33 9.0
	gb U51030 YSCD9954 Saccharomyces cerevisiae chromosome IV cosmid 33 9.0
	emb AQ988815 AQ988815 11E1D03NE.R1 C. parvum Lambda Zap Express 33 9.0
	emb AV419655 AV419655 AV419655 Lotus japonicus young plants (two 33 9.0
	emb AQ023613 AQ023613 CpGR0073A Cryptosporidium parvum genomic r 33 9.0
25	gb BE024936 BE024936 894007A03.yl C. reinhardtii CC-1690, normal 33 9.0
	gb L31407 YSCAKR Saccharomyces cerevisiae ankyrin repeat-contain 33 9.0
	emb AQ648055 AQ648055 RPCI93-DpnII-30G1.TJ RPCI93-DpnII Trypanos 33 9.0
	emb AQ641411 AQ641411 RPCI93-DpnII-28C15.TJ RPCI93-DpnII Trypano 33 9.0
	1.14.701.600014.701.6000.01 1.7574.0000.000 or
30	
20	emb AW282605 AW282605 LG1_310_E08.g1_A002 Light Grown 1 (LG1) So 29 9.8
	Query= Novartis95_at 14232_at /id_source
25	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155 9 (ac010155) f3m18.20 [arabidopsis
35	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova
35	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
35	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova
35	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters)
35	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
35 40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters)
	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searchingdone Score E Sequences producing significant alignments: (bits) Value emb AV417327 AV417327 AV417327 Lotus japonicus young plants (two 28 0.003 emb AV411846 AV411846 AV411846 Lotus japonicus young plants (two 28 0.005 emb AV423458 AV423458 AV423458 Lotus japonicus young plants (two 28 0.005 emb AV422547 AV422547 AV422547 Lotus japonicus young plants (two 28 0.006 emb AV406554 AW706554 sj58h12.y1 Gm-c1033 Glycine max cDNA clone 28 0.010
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40	Query= Novartis95_ at 14232_ at /id_ source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	Query= Novartis95_ at 14232_ at /id_ source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searchingdone Score E Sequences producing significant alignments: (bits) Value 28 0.003 emb AV417327 AV417327 AV417327 Lotus japonicus young plants (two 28 0.005 28 0.005 emb AV41846 AV411846 AV411846 Lotus japonicus young plants (two 28 0.005 28 0.005 emb AV4223458 AV423458 AV423458 Lotus japonicus young plants (two 28 0.005 28 0.005 emb AV422547 AV422547 AV422547 Lotus japonicus young plants (two 28 0.006 28 0.006 emb AV906554 AW706554 sj58h12.y1 Gm-c1033 Glycine max cDNA clone 28 0.016 28 0.010 emb AW308852 AW508852 si41b07.y1 Gm-r1030 Glycine max cDNA clone 28 0.015 28 0.015 emb AW32586 AW432586 sh76d11.y1 Gm-c1015 Glycine max cDNA clone 28 0.021 28 0.021 emb AI965714 AI965714 sc77f01.y1 Gm-c1018 Glycine max cDNA clone 28 0.031 28 0.031 emb AW100187 AW100187 sd26g01.y1 Gm-c1015 Glycine max cDNA clone 28 0.031 28 0.031 emb AW153030 AW153030 se34a10.y1 Gm-c1015 Glycine max cDNA clone 30 0.13 30 0.19 gb BE055645 BE055645 GA_Ea0021E15f Goss
40 45 50	Query= Novartis95_ at 14232_ at /id_ source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_ score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Score E Searching
40 45 50	Query= Novartis95_at 14232_at /id_source /description gb aaf16756.1 ac010155_9 (ac010155) f3m18.20 [arabidopsis thaliana] /blast_score 7.00e-32 /ec_number /family /chip nova /gb_link /ncgi (447 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searchingdone Score E Sequences producing significant alignments: (bits) Value 28 0.003 emb AV417327 AV417327 AV417327 Lotus japonicus young plants (two 28 0.005 28 0.005 emb AV41846 AV411846 AV411846 Lotus japonicus young plants (two 28 0.005 28 0.005 emb AV4223458 AV423458 AV423458 Lotus japonicus young plants (two 28 0.005 28 0.005 emb AV422547 AV422547 AV422547 Lotus japonicus young plants (two 28 0.006 28 0.006 emb AV906554 AW706554 sj58h12.y1 Gm-c1033 Glycine max cDNA clone 28 0.016 28 0.010 emb AW308852 AW508852 si41b07.y1 Gm-r1030 Glycine max cDNA clone 28 0.015 28 0.015 emb AW32586 AW432586 sh76d11.y1 Gm-c1015 Glycine max cDNA clone 28 0.021 28 0.021 emb AI965714 AI965714 sc77f01.y1 Gm-c1018 Glycine max cDNA clone 28 0.031 28 0.031 emb AW100187 AW100187 sd26g01.y1 Gm-c1015 Glycine max cDNA clone 28 0.031 28 0.031 emb AW153030 AW153030 se34a10.y1 Gm-c1015 Glycine max cDNA clone 30 0.13 30 0.19 gb BE055645 BE055645 GA_Ea0021E15f Goss

	gb M11221 DAREXTA Carrot (D.carota) extensin mRNA, partial cds. 35 0.47
	emb AW306694 AW306694 sf47b08.yl Gm-c1009 Glycine max cDNA clone 27 0.5
	emb AW035648 AW035648 EST281480 tomato callus, TAMU Lycopersicon 28 0.5
	emb AW559374 AW559374 EST314422 DSIR Medicago truncatula cDNA cl 27 0.5
5	emb AV411578 AV411578 AV411578 Lotus japonicus young plants (two 26 0.68
	emb AW618112 AW618112 EST314162 L. pennellii trichome, Cornell U 28 0.72
1	emb AW164515 AW164515 se74g06.yl Gm-c1023 Glycine max cDNA clone 27 0.7
	emb AI900852 AI900852 sb95c05.yl Gm-c1012 Glycine max cDNA clone 27 0.75
	emb AW328989 AW328989 N200181e rootphos(-) Medicago truncatula c 27 0.81
10	114774070041477407004477407004
	emb A V 4 2 5 8 0 4 A V 4 2 5 8 0 4 A V 4 2 5 8 0 4 Lotus japonicus young plants (two 34 0.89 emb A V 4 2 7 2 3 2 A V 4 2 7 2 3 2 Lotus japonicus young plants (two 34 0.89
	emb AI775562 AI775562 EST256662 tomato resistant, Cornell Lycope 28 1.2
	1117404800117404800
15	emb A1486798 A1486798 EST245120 tomato ovary, TAMU Lycopersicon 28 1.3
13	emb AW568194 AW568194 si57g03.y1 Gm-r1030 Glycine max cDNA clone 29 1.3
	emb AW031184 AW031184 EST274722 tomato callus, TAMU Lycopersicon 28 1.3
	emb AW622531 AW622531 EST313331 tomato root during/after fruit s 28 1.3
	dbj D38124 TOBBY4B Tobacco mRNA for EREBP-3, complete cds. 28 1.4
20	emb AW695699 AW695699 NF097F03ST1F1029 Developing stem Medicago 31 1.4
20	emb AW186005 AW186005 se62d09.yl Gm-c1019 Glycine max cDNA clone 29 1.5
	emb AW306715 AW306715 sf47d10.yl Gm-c1009 Glycine max cDNA clone 28 1.6
	dbj D86853 D86853 Catharanthus roseus cycl5 mRNA for extensin, c 33 1.7
	emb AW650803 AW650803 EST329257 tomato germinating seedlings, TA 33 1.7
~-	emb X63339 SRENOD2 S.rostrata Enod2 gene for nodulin. 32 2.3
25	gb C95684 C95684 C95684 Marchantia polymorpha immature sex organ 32 2.3
	gb[M12865]YSCRSCATC Yeast (S.cerevisiae) CAT repetitive element, 27 2.7
	emb AW040234 AW040234 EST282740 tomato mixed elicitor, BTI Lycop 28 3.0
	emb AW720424 AW720424 LjNEST22g2r Lotus japonicus nodule library 32 3.2
	emb AW686730 AW686730 NF041H01NR1F1000 Nodulated root Medicago t 32 3.2
30	emb AV412432 AV412432 AV412432 Lotus japonicus young plants (two 26 3.2
	emb AV407890 AV407890 AV407890 Lotus japonicus young plants (two 26 3.4
	gb[U91982 SHU91982 Stylosanthes hamata EREBP-3 homolog mRNA, com 28 3.5
	emb AV413265 AV413265 AV413265 Lotus japonicus young plants (two 26 3.6
	gb[U10398]YSCH9315 Saccharomyces cerevisiae chromosome VIII cosm 27 3.6
35	emb AV412856 AV412856 AV412856 Lotus japonicus young plants (two 26 3.7
	emb AV420682 AV420682 AV420682 Lotus japonicus young plants (two 26 3.9
	emb AW099863 AW099863 sd17e06.y2 Gm-c1012 Glycine max cDNA clone 27 3.9
	emb[AV419065]AV419065 AV419065 Lotus japonicus young plants (two 26 4.0
	emb AV413080 AV413080 AV413080 Lotus japonicus young plants (two 26 4.0
40	emb AV425734 AV425734 AV425734 Lotus japonicus young plants (two 26 4.3
	emb AV413154 AV413154 AV413154 Lotus japonicus young plants (two 28 4.3
•	emb AQ944381 AQ944381 Sheared DNA-53H12.TF Sheared DNA Trypanoso 31 4.3
	emb AI166472 AI166472 xylem.est.300 Poplar xylem Lambda ZAPII li 31 4.3
	emb AI495395 AI495395 sa97d11.y1 Gm-c1004 Glycine max cDNA clone 25 4.9
45	emb AW278410 AW278410 sf43g05.y1 Gm-c1009 Glycine max cDNA clone 25 5.0
	emb AV425829 AV425829 AV425829 Lotus japonicus young plants (two 28 5.2
	emb AV414990 AV414990 AV414990 Lotus japonicus young plants (two 28 5.2
	emb AV426605 AV426605 AV426605 Lotus japonicus young plants (two 28 5.9
	emb AW722435 AW722435 b3b06nm.rl Neurospora crassa morning cDNA 31 6.0
50	emb AW724180 AW724180 f4c08nm.rl Neurospora crassa morning cDNA 31 6.0
-	114 7700 400 - 14 - 100 400 - 1 - 1 - 1 - 1 - 1 - 1 - 1
	111 1 ///000011 1 ///0000 000 145 / 5
	emb AV395215 AV395215 AV395215 Chlamydomonas reinhardtii C9 Chla 31 6.0
55	emb AW720526 AW720526 LjNEST18f4r Lotus japonicus nodule library 31 6.0
))	emb AW717057 AW717057 h6e06nm.rl Neurospora crassa morning cDNA 31 6.0
	emb AW038232 AW038232 EST279889 tomato mixed elicitor, BTI Lycop 31 6.0
	emb AW234792 AW234792 sf19c08.y1 Gm-c1028 Glycine max cDNA clone 31 6.0
	emb AV406499 AV406499 AV406499 Lotus japonicus young plants (two 31 6.0
60	emb AI900301 AI900301 sc03g01.yl Gm-c1012 Glycine max cDNA clone 31 6.0
60	emb AI487770 AI487770 EST246092 tomato ovary, TAMU Lycopersicon 28 6.6
	emblAA840807lAA840807 CFB53 Floral bud cDNA library of Hot penne 23 68

emb|AF056182|AF056182 Emericella nidulans G-protein beta subunit... 30 8.2 emb|AC007862|AC007862 Trypanosoma brucei chromosome II clone RPC... 30 8.2 emb|AC010851|AC010851 Leishmania major chromosome 22 clone L4134... 30 8.2 emb|AW707173|AW707173 sk10f12.yl Gm-c1023 Glycine max cDNA clone... 30 8.2 5 emb|AW686992|AW686992 NF004G07RT1F1055 Developing root Medicago ... 30 8.2 emb|AW618891|AW618891 EST320877 L. pennellii trichome, Cornell U... 30 8.2 emb|AW507786|AW507786 si45a10.yl Gm-r1030 Glycine max cDNA clone... 30 8.2 emb|AQ910557|AQ910557 GSSTc05793 Trypanosome cruzi random genomi... 28 8.5 emb|AW032140|AW032140 EST275594 tomato callus, TAMU Lycopersicon... 26 8.7 10 emb|AW932239|AW932239 EST358082 tomato fruit mature green, TAMU ... 26 8.7 emb|AW933044|AW933044 EST358887 tomato fruit mature green, TAMU ... 26 8.7 emb|AW030545|AW030545 EST273800 tomato callus, TAMU Lycopersicon... 26 8.8 emb|AW932961|AW932961 EST358804 tomato fruit mature green, TAMU ... 26 8.8 15. Query= PAD3 at 14248 at /id source genbank /description "gb|aad31062.1|ac007357 11 (ac007357) strong similarity to gb|x97864 cytochrome p450 from arabidopsis thaliana and is a member of the pf|00067 cytochrome p450 family. ests gb|n65665, gb|t14112, 20 gb|t76255, gb|t20906 and gb|ai100027 come from this gene." /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|pad3| /ncgi http://www.ncgr.org/cgi-bin/ff?pad3 25 (1635 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 30 Searching......done Score Sequences producing significant alignments: (bits) Value 35 emblAF029858|AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... 220 e-104 gb[M32885]AVOCYP Avocado cytochrome P-450LXXIA1 (cyp7JA1) mRNA.... 173 3e-89 gb|BE054146|BE054146 GA_Ea0034H12f Gossypium arboreum 7-10 dpa ... 167 7e-50 gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 144 2e-48 emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. 40 dbj|D14588|PETHF1 Petunia hybrida Hf1 mRNA for flavonoid-3',5'-h... 77 9e-47 emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 71 2e-44 dbi|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 85 8e-44 emb|AW234222|AW234222 sf22f08.yl Gm-c1028 Glycine max cDNA clone... 147 5e-43 emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 126 8e-40 45 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 127 2e-39 gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 136 3e-39 emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 135 3e-39 emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 134 4e-39 emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 130 9e-39 gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 124 2e-38 50 emb|AW255799|AW255799 ML868 peppermint glandular trichome Mentha... 116 2e-38 emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 123 1e-37 emb|AF022460|AF022460 Glycine max cytochrome P450 monooxygenase ... 116 3e-37 emb|AW349428|AW349428 GM210007A20E11R Gm-r1021 Glycine max cDNA ... emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. emb|AW830233|AW830233 sm24f03.y1 Gm-c1028 Glycine max cDNA clone... 110 2e-36 emb|AW668053|AW668053 GA_ Ea0012G23 Gossypium arboreum 7-10 dpa ... 129 3e-36 emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 126 3e-36 emb|AW690420|AW690420 NF033B04ST1F1000 Developing stem Medicago ... 79 5e-36 60 emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 140 2e-35 emb|AW774664|AW774664 EST333815 KV3 Medicago truncatula cDNA clo... 144 6e-35

emb|AF191772|AF191772 Papaver somniferum (S)-N-methylcoclaurine ... 138 8e-35 emb|AW832405|AW832405 sm09e01.yl Gm-c1027 Glycine max cDNA clone... 147 2e-34 emb|AW432372|AW432372 sh73b04.yl Gm-c1015 Glycine max cDNA clone... 147 3e-34 emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 122 4e-34 5 emb|X70981|SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 119 7e-34 emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 145 1e-33 emb|AW156616|AW156616 se27f06.yl Gm-c1015 Glycine max cDNA clone... 90 1e-33 emb|AF107765|AF107765 Prunus dulcis cytochrome P450 (P450) gene,... 144 1e-33 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 117 2e-33 10 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 117 2e-33 emb|X71130|PHPET1 P.hybrida mRNA for P450 hydroxylase. emb|AF166332|AF166332 Nicotiana tabacum cytochrome P450 gene, co... 127 2e-33 emb|Y09424|NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... 117 2e-33 emb|AI895521|AI895521 EST264964 tomato callus, TAMU Lycopersicon... 142 7e-33 15 emb|AQ917284|AQ917284 T233265b Medicago truncatula BAC library M... 142 9e-33 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 115 2e-32 emb|AF029857|AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C... 78 2e-32 emb|X71654|SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. 115 3e-32 dbj|D14990|POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... 115 3e-32 20 emb|AW310655|AW310655 sg22h01.x1 Gm-c1024 Glycine max cDNA clone... 140 3e-32 emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 139 4e-32 emb|AB028151|AB028151 Antirrhinum majus AFNS2 mRNA for cytochrom... 66 7e-32 emb|AF150881|AF150881 Lycopersicon esculentum x Lycopersicon per... 78 3e-31 emb|Y10493|GMC450CP7 G.max mRNA for putative cytochrome P450, cl... 137 3e-31 emb|AW569661|AW569661 si89h01.y1 Gm-c1031 Glycine max cDNA clone... 137 3e-31 25 emb|AW569417|AW569417 si86h05.yl Gm-c1031 Glycine max cDNA clone... 137 3e-31 emb|AW676782|AW676782 DG1_14_D06.g1_A002 Dark Grown 1 (DG1) Sorg... 135 4e-31 emb|AW677294|AW677294 DG1_5_H08.g1_A002 Dark Grown 1 (DG1) Sorgh... 136 4e-31 emb|AW623139|AW623139 EST321084 tomato flower buds 3-8 mm, Corne... 117 5e-31 30 emb|AW256491|AW256491 EST304628 KV2 Medicago truncatula cDNA clo... 136 6e-31 dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 66 6e-31 emb|AW922446|AW922446 DG1_19_F10.g1_A002 Dark Grown 1 (DG1) Sorg... 135 1e-30 gb|U09610|U09610 Berberis stolonifera cytochrome P-450 CYP80 mRN... 125 2e-30 emb|AW031613|AW031613 EST275067 tomato callus, TAMU Lycopersicon... 73 2e-30 35 emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 133 3e-30 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 63 3e-30 emb|AW218579|AW218579 EST303762 tomato radicle, 5 d post-imbibit... 133 4e-30 emb|AB028152|AB028152 Torenia hybrida TFNS5 mRNA for cytochrome ... 64 4e-30 emb|AI489371|AI489371 EST247722 tomato ovary, TAMU Lycopersicon ... 111 6e-30 40 emb|AF000403|AF000403 Lotus japonicus putative cytochorome P450 ... 131 2e-29 emb|AW394303|AW394303 sh31c01.yl Gm-c1017 Glycine max cDNA clone... 130 3e-29 emb|AW560246|AW560246 EST315294 DSIR Medicago truncatula cDNA cl... 130 3e-29 emb|AW458764|AW458764 sh82d02.yl Gm-c1016 Glycine max cDNA clone... 130 3e-29 emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 73 4e-29 45 emb|AF014800|AF014800 Eschscholzia californica (S)-N-methylcocla... 105 5e-29 emb|AW923050|AW923050 DG1 48 G09.g1 A002 Dark Grown 1 (DG1) Sorg... 129 7e-29 emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 115 8e-29 emb|AI938505|AI938505 sb46e03.yl Gm-c1015 Glycine max cDNA clone... 128 9e-29 emb|AW728587|AW728587 GA__Ea0017C12 Gossypium arboreum 7-10 dpa ... 101 le-28 50 emb|AW922486|AW922486 DG1_19_B12.g1_A002 Dark Grown 1 (DG1) Sorg... 128 1e-28 emb|AW759717|AW759717 sl47a12.yl Gm-c1027 Glycine max cDNA clone... 127 2e-28 emb|AF014801|AF014801 Eschscholzia californica (S)-N-methylcocla... 104 3e-28 emb|AW278861|AW278861 sf99f08.yl Gm-c1019 Glycine max cDNA clone... 126 4e-28 emb|AF014802|AF014802 Eschscholzia californica (S)-N-methylcocla... 72 4e-28 55 emb|AI776223|AI776223 EST257323 tomato resistant, Cornell Lycope... 126 6e-28 emb|AW255421|AW255421 ML442 peppermint glandular trichome Mentha... 125 8e-28 emb|AW256010|AW256010 MW364 peppermint glandular trichome Mentha... 125 8e-28 emb|AW156752|AW156752 se30c09.yl Gm-c1015 Glycine max cDNA clone... 125 8e-28 emb|X70824|SMPEG1 S.melongena pEG1 mRNA for hydroxylase P450. 60 dbj|E05111|E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... emb|AB006790|AB006790 Petunia x hybrida IMT-2 mRNA for cytochrom... 75 1e-27

emb|AW255848|AW255848 ML931 peppermint glandular trichome Mentha... 124 2e-27 emblAW255619lAW255619 ML666 peppermint glandular trichome Mentha... 124 2e-27 emb|AW255274|AW255274 ML276 peppermint glandular trichome Mentha... 124 2e-27 emb|AF124817|AF124817 Mentha x piperita cytochrome p450 isoform ... 124 2e-27 5 emb|AW032343|AW032343 EST275797 tomato callus, TAMU Lycopersicon... 123 2e-27 emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 105 2e-27 emb|AW255953|AW255953 MW299 peppermint glandular trichome Mentha... 123 3e-27 emb|AI988440|AI988440 sd02b09.yl Gm-c1020 Glycine max cDNA clone... 123 3e-27 emb|AW038144|AW038144 EST279801 tomato mixed elicitor, BTI Lycop... 123 3e-27 emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 123 3e-27 10 emb|AW255346|AW255346 ML357 peppermint glandular trichome Mentha... 123 4e-27 emb|AF139532|AF139532 Liquidambar styraciflua aldehyde 5-hydroxy... 78 5e-27 15 Query= PAD4_i_at 14249_i_at /id_source genbank /description emb|cab43438.1| (al050300) putative protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|pad4| /ncgi 20 http://www.ncgr.org/cgi-bin/ff?pad4 (1732 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 25 Searching.....done Score Sequences producing significant alignments: (bits) Value 30 emb|AW981483|AW981483 EST392636 DSIL Medicago truncatula cDNA cl... 126 8e-59 emb|AW684289|AW684289 NF015A11NR1F1000 Nodulated root Medicago t... 124 5e-37 emb|AW032082|AW032082 EST275536 tomato callus, TAMU Lycopersicon... 112 2e-29 emb|AI781175|AI781175 EST262054 tomato susceptible, Cornell Lyco... 62 4e-24 35 emb|AW011208|AW011208 ST18A05 Pine TriplEx shoot tip library Pin... 107 2e-23 emb|AW225676|AW225676 ST70B12 Pine TriplEx shoot tip library Pin... 95 2e-20 emb|AV423915|AV423915 AV423915 Lotus japonicus young plants (two... 98 6e-20 emb|AI778594|AI778594 EST259473 tomato susceptible, Cornell Lyco... 95 2e-19 emb|AW032676|AW032676 EST276235 tomato callus, TAMU Lycopersicon... 95 2e-19 40 emb|AW559251|AW559251 EST306087 DSIR Medicago truncatula cDNA cl... 97 4e-19 emb|AW774727|AW774727 EST333878 KV3 Medicago truncatula cDNA clo... 97 4e-19 emb|AW707128|AW707128 sk10a03.yl Gm-c1023 Glycine max cDNA clone... 58 4e-17 emb|AW560897|AW560897 EST315945 DSIR Medicago truncatula cDNA cl... 73 1e-16 emb|AW257406|AW257406 EST305543 KV2 Medicago truncatula cDNA clo... 73 le-16 45 emb|AW685948|AW685948 NF036G07NR1F1000 Nodulated root Medicago t... 73 1e-16 emb|AW698315|AW698315 NXNV_071 G01_F Nsf Xylem Normal wood Verti... 75 3e-16 emb|AZ051219|AZ051219 Gm_UMb001_062_F16R UMN Soybean BAC Library... 55 2e-15 emb|AW587665|AW587665 ST63B10 Pine TriplEx shoot tip library Pin... 78 2e-15 emb|AW217058|AW217058 EST295772 tomato callus, TAMU Lycopersicon... 71 2e-15 50 emb|AW888098|AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti... 72 1e-14 emb|AW560122|AW560122 EST315170 DSIR Medicago truncatula cDNA cl... 51 4e-14 emb|AW980840|AW980840 EST391993 GVN Medicago truncatula cDNA clo... 51 4e-14 emb|AW560121|AW560121 EST315169 DSIR Medicago truncatula cDNA cl... 51 7e-14 emb|AI920196|AI920196 1726 Pine Lambda Zap Xylem library Pinus t... 59 1e-13 55 emb|AW559836|AW559836 EST314884 DSIR Medicago truncatula cDNA cl... 78 2e-13 emb|AW290408|AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical... 73 3e-13 gb|BE049795|BE049795 NXNV_144_C08_F Nsf Xylem Normal wood Vertic... 52 7e-13 emb|AW687647|AW687647 NF011F10RT1F1090 Developing root Medicago ... 51 9e-13 emb|AW687408|AW687408 NF009C08RT1F1065 Developing root Medicago ... 49 2e-10 60 emb|AW870069|AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti... 58 2e-10 emb|AI855891|AI855891 sc30h08.yl Gm-c1014 Glycine max cDNA clone... 58 1e-09

```
emb|AW349142|AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3... 57 3e-09
      emb|AW065112|AW065112 ST39G09 Pine TriplEx shoot tip library Pin... 62 1e-08
      emb|AW736866|AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti... 52_2e-08
      emb[AW685287]AW685287 NF027B11NR1F1000 Nodulated root Medicago t... 46 4e-08
 5
      emb|AW031593|AW031593 EST275047 tomato callus, TAMU Lycopersicon... 35 2e-07
      emblAW560074|AW560074 EST315122 DSIR Medicago truncatula cDNA cl... 48 5e-07
      emblAW773999lAW773999 EST332985 KV3 Medicago truncatula cDNA clo... 51 5e-07
      emb|AW704685|AW704685 sk39c02.yl Gm-c1028 Glycine max cDNA clone... 39 5e-07
      gb|BE123705|BE123705 NXNV 151 H02 F Nsf Xylem Normal wood Vertic... 53 1e-06
10
      emb|AW349364|AW349364 GM210004B12G1R Gm-r1021 Glycine max cDNA 3...
      emb|AW560073|AW560073 EST315121 DSIR Medicago truncatula cDNA cl... 46 1e-06
      emb|AW432244|AW432244 sh71a11.yl Gm-c1015 Glycine max cDNA clone... 52 2e-06
      emblAW773847|AW773847 EST332833 KV3 Medicago truncatula cDNA clo... 39 4e-06
      emblAW694970|AW694970 NF082B02ST1F1015 Developing stem Medicago ... 37 8e-06
15
      emb|AW687653|AW687653 NF011G04RT1F1035 Developing root Medicago ... 49 1e-04
      emb|AI416889|AI416889 sa19d09.x1 Gm-c1005 Glycine max cDNA clone... 49 1e-04
      emb|AW438038|AW438038 ST83G07 Pine TriplEx shoot tip library Pin... 49 1e-04
      emb|AI780239|AI780239 EST261118 tomato susceptible, Cornell Lyco... 34 4e-04
      emb|AW985058|AW985058 NXNV 130 D03 F Nsf Xylem Normal wood Verti... 31 7e-04
20
      emb|AZ214023|AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso... 46 9e-04
      emblAZ214029|AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso... 46 0.001
      emb|AW933515|AW933515 EST359274 tomato fruit mature green, TAMU ... 32 0.003
      emb|AZ213147|AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso... 36 0.003
      emb|AW616497|AW616497 EST322908 L. hirsutum trichome, Cornell Un... 35 0.004
25
      emb|AW870252|AW870252 NXNV 128 C06 F Nsf Xylem Normal wood Verti... 44 0.004
      emb|AW687535|AW687535 NF010F08RT1F1074 Developing root Medicago ... 43 0.006
      gb|BE123796|BE123796 NXNV 156 E06 F Nsf Xylem Normal wood Vertic... 31 0.006
      emb|AW618666|AW618666 EST320652 L. pennellii trichome, Cornell U... 33 0.009
      emb|AW317531|AW317531 sg51e11.yl Gm-c1025 Glycine max cDNA clone... 41 0.013
30
      emb|AW686129|AW686129 NF033H12NR1F1000 Nodulated root Medicago t... 32 0.023
      emb|AV417662|AV417662 AV417662 Lotus japonicus young plants (two... 30 0.025
      emb|AW010126|AW010126 ST02C06 Pine TriplEx shoot tip library Pin... 41 0.029
      emb|AW686977|AW686977 NF004F04RT1F1042 Developing root Medicago ... 33 0.031
      emb|AW329638|AW329638 N200899e rootphos(-) Medicago truncatula c... 40 0.075
35
      emb|AW687805|AW687805 NF013F08RT1F1074 Developing root Medicago ... 32 0.14
      emb|AW775153|AW775153 EST334304 KV3 Medicago truncatula cDNA clo... 29 0.14
      emb|AI812757|AI812757 18G10 Pine Lambda Zap Xylem library Pinus ... 39 0.14
      emb|AW774485|AW774485 EST333636 KV3 Medicago truncatula cDNA clo... 39 0.14
      emb|AW693919|AW693919 NF070E05ST1F1038 Developing stem Medicago ... 39 0.14
      emb|AW685575|AW685575 NF029B05NR1F1000 Nodulated root Medicago t... 39 0.14
40
      emb|AW705444|AW705444 sk49b08.yl Gm-c1019 Glycine max cDNA clone... 39 0.14
      emb|AW695353|AW695353 NF094C07ST1F1053 Developing stem Medicago ... 39 0.14
      emb|AW257266|AW257266 EST305403 KV2 Medicago truncatula cDNA clo... 39 0.14
      emb|AW934555|AW934555 EST353447 tomato flower buds 0-3 mm, Corne... 38 0.27
45
      emb|AW307176|AW307176 sf53g04.y1 Gm-c1009 Glycine max cDNA clone... 31 0.36
      emb|AL031525|SPCC1682 S.pombe chromosome III cosmid c1682.
      emb|AW698283|AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti... 28 0.66
      emb|AW698011|AW698011 NXNV_079_E11_F Nsf Xylem Normal wood Verti... 29 0.88
      emb|AW693913|AW693913 NF070E02ST1F1017 Developing stem Medicago ... 36 0.96
50
      emb|AW686305|AW686305 NF036D07NR1F1000 Nodulated root Medicago t... 36 0.96
      emb|AW685079|AW685079 NF024H05NR1F1000 Nodulated root Medicago t... 36 0.96
      emb|AW043221|AW043221 ST30G04 Pine TriplEx shoot tip library Pin... 36 0.96
      emb|AF127256|AF127256 Laureliopsis philippiana rpl16 gene, chlor... 35 1.8
      emb|AF127255|AF127255 Laurelia sempervirens rpl16 gene, chloropl... 35 1.8
      emb|AF127257|AF127257 Nemuaron vieillardii rpl16 gene, chloropla... 35 1.8
55
      emblAW508953|AW508953 si38d01.yl Gm-r1030 Glycine max cDNA clone... 28 2.1
      emblAW719424|AW719424 LjNEST4d11r Lotus japonicus nodule library... 28 2.1
      emb|AW032864|AW032864 EST276423 tomato callus, TAMU Lycopersicon... 29 2.1
      emb|AW306559|AW306559 se52d10.yl Gm-c1017 Glycine max cDNA clone... 35 2.5
60
      emb|AI399344|AI399344 NCW01D11T7 Westergaards Neurospora crassa ... 35 2.5
      emb|AI485040|AI485040 EST243320 tomato ovary, TAMU Lycopersicon ... 34 3.4
```

	emb Z49212 SC9952X S.cerevisiae chromosome XIII cosmid 9952. 34 3.4 emb AA741585 AA741585 LmLv39p3/132B Leishmania major promastigot 34 3.4 emb X81715 SCMDYGENE S.cerevisiae partial MDY gene. 34 3.4 emb X73956 TBMAP292 T.brucei Tb-292 mRNA for membrane associated 34 3.4
5	emb AZ212769 AZ212769 Sheared DNA-66C3.TR Sheared DNA Trypanosom 34 3.4 emb X82612 SCATM1 S.cerevisiae ATM1 gene. 34 3.4 emb AC005139 AC005139 Plasmodium falciparum chromosome 12, *** S 34 4.7 emb AA649446 AA649446 T4369 MVAT4 bloodstream form of serodeme W 34 4.7
10	Query= PAD4_r_at 14250_r_at /id_source genbank /description
	emb cab43438.1 (al050300) putative protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
15	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb pad4 /ncgi
	http://www.ncgr.org/cgi-bin/ff?pad4 (1732 letters)
20	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
	Score E
25 -	Sequences producing significant alignments: (bits) Value
30	emb AW981483 AW981483 EST392636 DSIL Medicago truncatula cDNA cl 126 8e-59 emb AW684289 AW684289 NF015A11NR1F1000 Nodulated root Medicago t 124 5e-37 emb AW032082 AW032082 EST275536 tomato callus, TAMU Lycopersicon 112 2e-29
30	emb AI781175 AI781175 EST262054 tomato susceptible, Cornell Lyco 62 4e-24 emb AW011208 AW011208 ST18A05 Pine TriplEx shoot tip library Pin 107 2e-23 emb AW225676 AW225676 ST70B12 Pine TriplEx shoot tip library Pin 95 2e-20 emb AV423915 AV423915 AV423915 Lotus japonicus young plants (two 98 6e-20 emb AI778594 AI778594 EST259473 tomato susceptible, Cornell Lyco 95 2e-19
35	emb AI778594 AI778594 EST259473 tomato susceptible, Cornell Lyco 95 2e-19 emb AW032676 AW032676 EST276235 tomato callus, TAMU Lycopersicon 95 2e-19 emb AW559251 AW559251 EST306087 DSIR Medicago truncatula cDNA cl 97 4e-19 emb AW774727 AW774727 EST333878 KV3 Medicago truncatula cDNA clo 97 4e-19 emb AW707128 AW707128 sk10a03.y1 Gm-c1023 Glycine max cDNA clone 58 4e-17 emb AW560897 AW560897 EST315945 DSIR Medicago truncatula cDNA cl 73 1e-16
40 45	emb AW257406 AW257406 EST305543 KV2 Medicago truncatula cDNA clo 73 1e-16 emb AW685948 AW685948 NF036G07NR1F1000 Nodulated root Medicago t 73 1e-16 emb AW698315 AW698315 NXNV_071_G01_F Nsf Xylem Normal wood Verti 75 3e-16 emb AZ051219 AZ051219 Gm_UMb001_062_F16R UMN Soybean BAC Library 55 2e-15 emb AW587665 AW587665 ST63B10 Pine TriplEx shoot tip library Pin 78 2e-15
50	emb AW217058 AW217058 EST295772 tomato callus, TAMU Lycopersicon 71 2e-15 emb AW888098 AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti 72 1e-14 emb AW560122 AW560122 EST315170 DSIR Medicago truncatula cDNA cl 51 4e-14 emb AW980840 AW980840 EST391993 GVN Medicago truncatula cDNA cl 51 4e-14 emb AW560121 AW560121 EST315169 DSIR Medicago truncatula cDNA cl 51 7e-14 emb AI920196 AI920196 1726 Pine Lambda Zap Xylem library Pinus t 59 1e-13
	emb AW559836 AW559836 EST314884 DSIR Medicago truncatula cDNA cl 78 2e-13 emb AW290408 AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical 73 3e-13 gb BE049795 BE049795 NXNV_144_C08_F Nsf Xylem Normal wood Vertic 52 7e-13 emb AW687647 AW687647 NF011F10RT1F1090 Developing root Medicago 51 9e-13
55	emb AW687408 AW687408 NF009C08RT1F1065 Developing root Medicago 49 2e-10 emb AW870069 AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti 58 2e-10 emb AI855891 AI855891 sc30h08.y1 Gm-c1014 Glycine max cDNA clone 58 1e-09 emb AW349142 AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3 57 3e-09 emb AW065112 AW065112 ST39G09 Pine TriplEx shoot tip library Pin 62 1e-08
60	emb AW065112 AW065112 S139G09 Pine TriplEx shoot tip library Pin 62 1e-08 emb AW736866 AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti 52 2e-08 emb AW685287 AW685287 NF027B11NR1F1000 Nodulated root Medicago t 46 4e-08

```
emb|AW031593|AW031593 EST275047 tomato callus, TAMU Lycopersicon... 35 2e-07
      emb|AW560074|AW560074 EST315122 DSIR Medicago truncatula cDNA cl... 48 5e-07
      emb|AW773999|AW773999 EST332985 KV3 Medicago truncatula cDNA clo... 51 5e-07
      emb|AW704685|AW704685 sk39c02.yl Gm-c1028 Glycine max cDNA clone... 39 5e-07
 5
      gb|BE123705|BE123705 NXNV 151 H02 F Nsf Xylem Normal wood Vertic... 53 1e-06
      emb|AW349364|AW349364 GM210004B12G1R Gm-r1021 Glycine max cDNA 3... 56 1e-06
      emb|AW560073|AW560073 EST315121 DSIR Medicago truncatula cDNA cl... 46 1e-06
      emb|AW432244|AW432244 sh71a11.yl Gm-c1015 Glycine max cDNA clone... 52 2e-06
      emb|AW773847|AW773847 EST332833 KV3 Medicago truncatula cDNA clo... 39 4e-06
10
      emb|AW694970|AW694970 NF082B02ST1F1015 Developing stem Medicago ... 37 8e-06
      emb|AW687653|AW687653 NF011G04RT1F1035 Developing root Medicago ... 49 1e-04
      emb|AI416889|AI416889 sa19d09.x1 Gm-c1005 Glycine max cDNA clone... 49 1e-04
      emb|AW438038|AW438038 ST83G07 Pine TriplEx shoot tip library Pin... 49 1e-04
      emb|AI780239|AI780239 EST261118 tomato susceptible, Cornell Lyco... 34 4e-04
      emb|AW985058|AW985058 NXNV_130_D03_F Nsf Xylem Normal wood Verti... 31 7e-04
15
      emblAZ214023|AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso... 46 9e-04
      emb|AZ214029|AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso... 46 0.001
      emb|AW933515|AW933515 EST359274 tomato fruit mature green, TAMU ... 32 0.003
      emblAZ213147\AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso... 36 0.003
      emb|AW616497|AW616497 EST322908 L. hirsutum trichome, Cornell Un... 35 0.004
20
      emb|AW870252|AW870252 NXNV 128 C06 F Nsf Xylem Normal wood Verti... 44 0.004
      emb|AW687535|AW687535 NF010F08RT1F1074 Developing root Medicago ... 43 0.006
      gb|BE123796|BE123796 NXNV 156 E06 F Nsf Xylem Normal wood Vertic... 31 0.006
      emb|AW618666|AW618666 EST320652 L. pennellii trichome, Cornell U... 33 0.009
25
      emb|AW317531|AW317531 sg51e11.yl Gm-c1025 Glycine max cDNA clone... 41 0.013
      emb|AW686129|AW686129 NF033H12NR1F1000 Nodulated root Medicago t... 32 0.023
      emb|AV417662|AV417662 AV417662 Lotus japonicus young plants (two... 30 0.025
      emb|AW010126|AW010126 ST02C06 Pine TriplEx shoot tip library Pin... 41 0.029
      emb|AW686977|AW686977 NF004F04RT1F1042 Developing root Medicago ... 33 0.031
30
      emb|AW329638|AW329638 N200899e rootphos(-) Medicago truncatula c... 40 0.075
      emb|AW687805|AW687805 NF013F08RT1F1074 Developing root Medicago ... 32 0.14
      emb|AW775153|AW775153 EST334304 KV3 Medicago truncatula cDNA clo... 29 0.14
      emb|AI812757|AI812757 18G10 Pine Lambda Zap Xylem library Pinus ... 39 0.14
      emb|AW774485|AW774485 EST333636 KV3 Medicago truncatula cDNA clo... 39 0.14
35
      emb|AW693919|AW693919 NF070E05ST1F1038 Developing stem Medicago ... 39 0.14
      emb|AW685575|AW685575 NF029B05NR1F1000 Nodulated root Medicago t... 39 0.14
      emb|AW705444|AW705444 sk49b08.yl Gm-c1019 Glycine max cDNA clone... 39 0.14
      emb|AW695353|AW695353 NF094C07ST1F1053 Developing stem Medicago ... 39 0.14
      emb|AW257266|AW257266 EST305403 KV2 Medicago truncatula cDNA clo... 39 0.14
40
      emb|AW934555|AW934555 EST353447 tomato flower buds 0-3 mm, Corne... 38 0.27
      emb|AW307176|AW307176 sf53g04.y1 Gm-c1009 Glycine max cDNA clone... 31 0.36
      emb|AL031525|SPCC1682 S.pombe chromosome III cosmid c1682.
      emb|AW698283|AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti... 28 0.66
      emb|AW698011|AW698011 NXNV_079_E11_F Nsf Xylem Normal wood Verti... 29 0.88
45
      emb|AW693913|AW693913 NF070E02ST1F1017 Developing stem Medicago ... 36 0.96
      emb|AW686305|AW686305 NF036D07NR1F1000 Nodulated root Medicago t... 36 0.96
      emb|AW685079|AW685079 NF024H05NR1F1000 Nodulated root Medicago t... 36 0.96
      emb|AW043221|AW043221 ST30G04 Pine TriplEx shoot tip library Pin... 36 0.96
      emb|AF127256|AF127256 Laureliopsis philippiana rpl16 gene, chlor... 35 1.8
50
      emb|AF127255|AF127255 Laurelia sempervirens rpl16 gene, chloropl... 35 1.8
      emb|AF127257|AF127257 Nemuaron vieillardii rpl16 gene, chloropla... 35 1.8
      emblAW508953|AW508953 si38d01.yl Gm-r1030 Glycine max cDNA clone... 28 2.1
      emb|AW719424|AW719424 LjNEST4d11r Lotus japonicus nodule library... 28 2.1
      emblAW032864|AW032864 EST276423 tomato callus, TAMU Lycopersicon... 29 2.1
55
      emb|AW306559|AW306559 se52d10.yl Gm-c1017 Glycine max cDNA clone... 35 2.5
      emb|AI399344|AI399344 NCW01D11T7 Westergaards Neurospora crassa ... 35 2.5
      emb|AI485040|AI485040 EST243320 tomato ovary, TAMU Lycopersicon ... 34 3.4
      emb|Z49212|SC9952X S.cerevisiae chromosome XIII cosmid 9952.
                                                                     34 3.4
      emb|AA741585|AA741585 LmLv39p3/132B Leishmania major promastigot... 34 3.4
60
      emb|X81715|SCMDYGENE S.cerevisiae partial MDY gene.
                                                                    34 3.4
      emb|X73956|TBMAP292 T.brucei Tb-292 mRNA for membrane associated... 34 3.4
```

emblAZ212769lAZ212769 Sheared DNA-66C3.TR Sheared DNA Trypanosom... 34 3.4 emb|X82612|SCATM1 S.cerevisiae ATM1 gene. 34 3.4 emb|AC005139|AC005139 Plasmodium falciparum chromosome 12. *** S... 34 4.7 emb|AA649446|AA649446 T4369 MVAT4 bloodstream form of serodeme W... 34 4.7 5 Query= PAL1-mRNA s at 14254 s at /id source genbank /description gb|aad18156.2| (ac006260) phenylalanine ammonia lyase (pal1) [arabidopsis /blast_score 1.00e-134 /ec number /family /chip nova 10 /gb link /ncgi (848 letters) Database: plantfungal 661,018 sequences: 426,114,510 total letters 15 Searching......done E Score Sequences producing significant alignments: (bits) Value 20 emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 419 e-115 emblAJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 412 e-113 dbijD83076jD83076 Lithospermum erythrorhizon mRNA for phenylalan... 411 e-113 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 408 e-112 25 emb[Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 331 e-112 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 407 e-112 gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 407 e-112 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 328 e-111 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 403 e-111 30 dbj D26596 CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 403 e-111 emb|X58180|MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 398 e-109 gb|L11747|POPPALGA Populus tricocarpa X Populus deltoides (hybri... 318 e-109 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 396 e-109 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 395 e-108 35 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 319 e-108 emb[X78269[NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 312 e-106 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 312 e-105 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 373 e-102 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 174 e-102 40 emb|X81158|PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 173 e-101 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 214 2e-95 emb|AW667320|AW667320 GA_Ea0008P06 Gossypium arboreum 7-10 dpa ... 349 8e-95 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 347 3e-94 dbi|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 347 3e-94 45 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 291 3e-94 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 314 3e-91 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 326 6e-88 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 319 1e-85 50 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 220 2e-85 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 154 5e-85 gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 296 9e-81 emb|AW774460|AW774460 EST333611 KV3 Medicago truncatula cDNA clo... 302 1e-80 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 196 6e-79 55 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 292 8e-78 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 292 1e-77 emb|AI899906|AI899906 sb96a02.yl Gm-c1012 Glycine max cDNA clone... 287 3e-76 emb|AW691458|AW691458 NF045B11ST1F1000 Developing stem Medicago ... 286 6e-76 emb|AW696215|AW696215 NF103G12ST1F1099 Developing stem Medicago ... 283 7e-76 60 emb|AW688208|AW688208 NF004F12ST1F1000 Developing stem Medicago ... 278 1e-73

emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 275 9e-73

emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 275 2e-72 emblAW560722|AW560722 EST315770 DSIR Medicago truncatula cDNA cl... 269 7e-71 emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 262 1e-68 emb|AV407891|AV407891 AV407891 Lotus japonicus young plants (two... 260 3e-68 5 emb|AI729040|AI729040 BNLGHi12413 Six-day Cotton fiber Gossypium... 258 1e-67 emb|AI780119|AI780119 EST260998 tomato susceptible, Cornell Lyco... 237 3e-66 emb[X99705]TAPALGEN1 T.aestivum PAL gene. emb|AW694081|AW694081 NF072E06ST1F1050 Developing stem Medicago ... 225 8e-65 emb|AW688761|AW688761 NF011C12ST1F1000 Developing stem Medicago ... 246 7e-64 emblAW684895|AW684895 NF022G07NR1F1000 Nodulated root Medicago t... 237 3e-63 10 emb|AW267882|AW267882 EST306160 DSIR Medicago truncatula cDNA cl... 240 4e-62 emb|AW685144|AW685144 NF025D11NR1F1000 Nodulated root Medicago t... 232 5e-61 emb|AW686498|AW686498 NF042A10NR1F1000 Nodulated root Medicago t... 168 2e-60 gb|U39792|PTU39792 Pinus taeda phenylalanine ammonia-lyase (lpPA... 129 5e-60 15 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas... 231 2e-59 emb|AW720528|AW720528 LjNEST18f8r Lotus japonicus nodule library... 146 7e-58 emb|AI563248|AI563248 EST00372 watermelon lambda zap library Cit... 222 7e-57 emb|AJ289609|BPE289609 Betula pendula partial pal gene for pheny... 133 3e-56 emb|AW685192|AW685192 NF027D11NR1F1000 Nodulated root Medicago t... 219 6e-56 20 emb|AJ278116|BPE278116 Betula pendula partial pal1 gene for phen... 131 9e-56 emb|AW033848|AW033848 EST277419 tomato callus, TAMU Lycopersicon... 218 1e-55 emb|AW039368|AW039368 EST281625 tomato mixed elicitor, BTI Lycop... 218 1e-55 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 215 8e-55 emb|AW031670|AW031670 EST275124 tomato callus, TAMU Lycopersicon... 215 8e-55 25 emb|AW650661|AW650661 EST329115 tomato germinating seedlings, TA... 213 4e-54 emb|AB015870|AB015870 Vitis vinifera gene for phenylalanine ammo... 213 4e-54 emb[X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 213 5e-54 emb|AW219754|AW219754 EST302236 tomato root during/after fruit s... 211 2e-53 emb|AW690758|AW690758 NF033B06ST1F1000 Developing stem Medicago ... 210 3e-53 30 dbi|D30656|POPPALA Populus kitakamiensis gene for phenylalanine ... 208 1e-52 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalani... 208 2e-52 emb|AW689402|AW689402 NF018G12ST1F1000 Developing stem Medicago ... 207 2e-52 gb|M91192|TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 197 3e-52 emblAW034358|AW034358 EST277929 tomato callus, TAMU Lycopersicon... 190 1e-51 35 emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 204 2e-51 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonialyase (tpa1) gen... 204 2e-51 gbM90692[TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 203 5e-51 emb[Y07654]PCPAL1 P.crispum pal1 gene. dbi|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 201 2e-50 40 emb|AI495627|AI495627 sb11c09.yl Gm-c1004 Glycine max cDNA clone... 140 4e-50 gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 199 7e-50 dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 198 1e-49 emb|AW034782|AW034782 EST278818 tomato callus, TAMU Lycopersicon... 141 1e-49 emb|AW689099|AW689099 NF015D05ST1F1000 Developing stem Medicago ... 197 3e-49 45 emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 195 6e-49 emb|X15473|PCPAL1GN P.crispum PAL-1 gene for phenylalanine ammon... 120 6e-49 emb[X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 193 5e-48 emblAI974372|AI974372 T110225e KV0 Medicago truncatula cDNA clon... 191 2e-47 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 185 9e-46 50 emb|AF019965|AF019965 Pinus monticola phenylalanine ammonia lyas... 130 4e-45 emb|AI778115|AI778115 EST258994 tomato susceptible, Cornell Lyco... 166 le-44 emblAW031859|AW031859 EST275313 tomato callus, TAMU Lycopersicon... 165 4e-44 emb[X16772]PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 173 1e-42 emb|AW757191|AW757191 sl30c12.yl Gm-c1027 Glycine max cDNA clone... 174 2e-42 55 emb|AI484637|AI484637 EST242898 tomato ovary, TAMU Lycopersicon ... 174 2e-42 emb|AW683457|AW683457 NF012E02LF1F1017 Developing leaf Medicago ... 173 3e-42 emb|AI495119|AI495119 sb03f10.yl Gm-c1004 Glycine max cDNA clone... 169 7e-41 emb|AW922611|AW922611 DG1_46 C11.b1_A002 Dark Grown 1 (DG1) Sorg... 102 1e-40 emb|AV409143|AV409143 AV409143 Lotus japonicus young plants (two... 166 3e-40

60

Query= pall-intron_f_at 14256_f_at /id_source genbank /description gb[aad18156.2] (ac006260) phenylalanine ammonia lyase (pal1) [arabidopsis thaliana] /blast score 7.00e-77 /ec number /family /chip nova /gb link /ncgi (3115 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

10 Searching......done

5

Score Sequences producing significant alignments: (bits) Value 15 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 232 9e-60 dbj|D10001|PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 232 9e-60 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas... 231 2e-59 emb|AW774460|AW774460 EST333611 KV3 Medicago truncatula cDNA clo... 228 2e-58 emb|AW688761|AW688761 NF011C12ST1F1000 Developing stem Medicago ... 226 5e-58 20 emb|AW694081|AW694081 NF072E06ST1F1050 Developing stem Medicago ... 225 1e-57 emblAW684895|AW684895 NF022G07NR1F1000 Nodulated root Medicago t... 222 9e-57 emb|AI899906|AI899906 sb96a02.yl Gm-c1012 Glycine max cDNA clone... 220 5e-56 emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 220 6e-56 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 220 6e-56 25 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 219 9e-56 emb|X58180|MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 219 9e-56 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 215 1e-54 dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 215 2e-54 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 214 4e-54 30 emblAW667320|AW667320 GA_Ea0008P06 Gossypium arboreum 7-10 dpa ... 214 4e-54 emb|AB015870|AB015870 Vitis vinifera gene for phenylalanine ammo... 213 5e-54 emb|AW725857|AW725857 GA_Ea0019O22 Gossypium arboreum 7-10 dpa ... 212 1e-53 emb|AW696215|AW696215 NF103G12ST1F1099 Developing stem Medicago ... 211 2e-53 emb|AW691458|AW691458 NF045B11ST1F1000 Developing stem Medicago ... 211 2e-53 35 dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 211 2e-53 gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 211 3e-53 emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 210 5e-53 emb[Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 205 7e-53 emb|AW267882|AW267882 EST306160 DSIR Medicago truncatula cDNA cl... 209 9e-53 40 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 209 9e-53 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 209 1e-52 emb|AW685192|AW685192 NF027D11NR1F1000 Nodulated root Medicago t... 209 1e-52 emb|AW690758|AW690758 NF033B06ST1F1000 Developing stem Medicago ... 209 1e-52 emb|AW688208|AW688208 NF004F12ST1F1000 Developing stem Medicago ... 209 1e-52 45 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 208 2e-52 emb|AW689402|AW689402 NF018G12ST1F1000 Developing stem Medicago ... 207 3e-52 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalani... 207 3e-52 gblM91192|TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 197 3e-52 dbj|D30656|POPPALA Populus kitakamiensis gene for phenylalanine ... 207 5e-52 50 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 207 5e-52 gb|M90692|TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 207 5e-52 emb|AI729040|AI729040 BNLGHi12413 Six-day Cotton fiber Gossypium... 206 6e-52 emb|AW686498|AW686498 NF042A10NR1F1000 Nodulated root Medicago t... 153 9e-52 gb|L11747|POPPALGA Populus tricocarpa X Populus deltoides (hybri... 205 2e-51 55 emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 204 2e-51 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonialyase (tpa1) gen... 204 2e-51 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 204 3e-51 emb|AW033848|AW033848 EST277419 tomato callus, TAMU Lycopersicon... 203 8e-51 emb|AW650661|AW650661 EST329115 tomato germinating seedlings, TA... 203 8e-51 60 emb|AW219754|AW219754 EST302236 tomato root during/after fruit s... 203 8e-51 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 203 8e-51

	emb AW039368 AW039368 EST281625 tomato mixed elicitor, BTI Lycop 203 8e-51
	dbj D78640 IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni 202 1e-50
	emb AI563248 AI563248 EST00372 watermelon lambda zap library Cit 202 2e-50
	emb AW031670 AW031670 EST275124 tomato callus, TAMU Lycopersicon 202 2e-50
5	emb Y07654 PCPAL1 P.crispum pal1 gene. 173 2e-50
_	dbj D43803 POPPALG4B Populus kitakamiensis gene for phenylalanin 201 3e-50
	embly \$1.150 in CDA 1.2 Designation and National Section in Principles and the Control of the Co
	emb X81159 PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 174 4e-50
	emb X17462 PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia 199 4e-50
10	emb X81158 PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 173 7e-50
10	emb AJ238754 CCL238754 Citrus clementina X Citrus reticulata mRN 199 7e-50
	emb X78269 NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine 195 1e-49
	gb M83314 TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon 199 1e-49
	emb AJ238753 CCL238753 Citrus clementina X Citrus reticulata mRN 199 1e-49
	dbj D85850 D85850 Daucus carota gDcPAL1 gene for phenylalanine a 198 2e-49
15	dbj D17467 TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase, 195 3e-49
	emb AW685111 AW685111 NF026A05NR1F1000 Nodulated root Medicago t 197 4e-49
	emb AW720528 AW720528 LjNEST18f8r Lotus japonicus nodule library 116 5e-49
	emb AW689099 AW689099 NF015D05ST1F1000 Developing stem Medicago 197 5e-49
	emb X63103 STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon 197 5e-49
20	emb AF218453 AF218453 Coffea arabica clone 369.1.6r phenylalanin 196 7e-49
	emb AB008199 AB008199 Nicotiana tabacum palA gene for phenylalan 195 9e-49
	emb X15473 PCPAL1GN P.crispum PAL-1 gene for phenylalanine ammon 120 9e-49
	emb AF218454 AF218454 Coffea arabica clone 430.4 phenylalanine a 195 2e-48
	emb X99997 BFPAL B.finlaysoniana mRNA for phenylalanine ammonia 194 2e-48
25	emb AF165998 AF165998 Vigna unguiculata phenylalanine ammonia-ly 194 2e-48
	emb AW560722 AW560722 EST315770 DSIR Medicago truncatula cDNA cl 194 2e-48
	emb AV407891 AV407891 AV407891 Lotus japonicus young plants (two 193 9e-48
	emb X63104 STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon 193 9e-48
	emb AJ250836 CAR250836 Cicer arietinum mRNA for phenylalanine am 191 3e-47
30	dbj D30657 POPPALB Populus kitakamiensis gene for phenylalanine 185 1e-45
•	emb AI974372 AI974372 T110225e KV0 Medicago truncatula cDNA clon 185 2e-45
	emb AW034782 AW034782 EST278818 tomato callus, TAMU Lycopersicon 141 3e-45
	emb AW685144 AW685144 NF025D11NR1F1000 Nodulated root Medicago t 179 5e-45
	gb U16130 PAU16130 Persea americana phenylalanine ammonia lyase 183 7e-45
35	
33	emb X76130 CMPAL C.melo (cantaloupe) pal mRNA. 181 3e-44 emb X16772 PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo 173 2e-42
	emb AI484637 AI484637 EST242898 tomato ovary, TAMU Lycopersicon 174 3e-42
	emb AW683457 AW683457 NF012E02LF1F1017 Developing leaf Medicago 173 5e-42
	emb Z49147 HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine 154 1e-40
40	emb AI495119 AI495119 sb03f10.yl Gm-c1004 Glycine max cDNA clone 169 1e-40
10	embla W7571011A W757101 120012 v1 Cm 01027 Charing way a DNA 11 v1 100 0 100
	emb AW757191 AW757191 sl30c12.yl Gm-c1027 Glycine max cDNA clone 168 2e-40
	emb AW929506 AW929506 EST338294 tomato flower buds 8 mm to pre-a 96 4e-40
	emb AV409143 AV409143 AV409143 Lotus japonicus young plants (two 166 6e-40
45	emb AW694394 AW694394 NF075F09ST1F1078 Developing stem Medicago 114 3e-38
+3	emb AI495627 AI495627 sb11c09.yl Gm-c1004 Glycine max cDNA clone 100 3e-38
	emb AW979905 AW979905 EST341554 tomato root deficiency, Cornell 157 4e-37
	emb X99705 TAPALGEN1 T.aestivum PAL gene. 156 4e-37
	emb AW694606 AW694606 NF078C03ST1F1020 Developing stem Medicago 151 6e-36
-	emb AW922611 AW922611 DG1_46_C11.b1_A002 Dark Grown 1 (DG1) Sorg 87 9e-36
50	emb AI780119 AI780119 EST260998 tomato susceptible, Cornell Lyco 130 1e-35
	emb AI778115 AI778115 EST258994 tomato susceptible, Cornell Lyco 130 1e-35
•	emb AI773582 AI773582 EST254682 tomato resistant, Cornell Lycope 130 1e-35
	emb AW034358 AW034358 EST277929 tomato callus, TAMU Lycopersicon 130 4e-35
55	Onom - DATI 14600 4/11
	Query= PAT1_s_at 14620_s_at /id_source genbank /description
	gb aaa32835.1 (m96073) phosphoribosylanthranilate transferase
	[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
50	/gb_link /ncgi
w	(1602 letters)

Database: plantfungal

```
661,018 sequences; 426,114,510 total letters
      Searching.....done
 5
                                         Score
                                                E
      Sequences producing significant alignments:
                                                        (bits) Value
      emb|AW687938|AW687938 NF001B11ST1F1000 Developing stem Medicago ... 393 e-108
10
      emb|AW039382|AW039382 EST281639 tomato mixed elicitor, BTI Lycop... 369 e-101
      emb|AW096850|AW096850 EST46F4 potato shoot cDNA library Solanum ... 263 2e-69
      emb|AW688778|AW688778 NF011E05ST1F1000 Developing stem Medicago ... 244 1e-65
      emb|AW906002|AW906002 EST342043 potato stolon, Cornell Universit... 234 6e-63
      emb|AI855689|AI855689 sc23a07.yl Gm-c1013 Glycine max cDNA clone... 191 le-47
15
      emb|AW622744|AW622744 EST306881 tomato flower buds 3-8 mm, Corne... 171 2e-41
      emb|AW041025|AW041025 EST283889 tomato mixed elicitor, BTI Lycop... 171 2e-41
      emb|AL023554|SPBC16G5 S.pombe chromosome II cosmid c16G5.
      gb|BE053060|BE053060 GA Ea0020N16f Gossypium arboreum 7-10 dpa ... 132 7e+30
      gb|BE035432|BE035432 MO05D07 MO Mesembryanthemum crystallinum cD... 111 1e-23
20
      emb|AJ273068|AJ273068 AJ273068 Metarhizium anisopliae ARSEF 2575... 54 2e-16
      emb|AV412566|AV412566 AV412566 Lotus japonicus young plants (two... 78 2e-16
      emb|AV421776|AV421776 AV421776 Lotus japonicus young plants (two... 72 4e-13
      gb[U28372|YSCD9476 Saccharomyces cerevisiae chromosome IV cosmid... 49 &e-09
      emb|X04273|SCTRP4 Yeast TRP4 gene for anthranilate phosphoribosy... 49 9e-09
25
      emb|AQ874893|AQ874893 V118C3 mTn-3xHA/lacZ Insertion Library, st... 49 1e-07
      emb|AJ228925|AJ228925 AJ228925 Barley leaf, 8 day old seedling H... 57 4e-07
      emb|AW220409|AW220409 EST302892 tomato root during/after fruit s... 53 5e-06
      emb|AW737074|AW737074 CAF50 Peronospora parasitica cDNA-AFLP fra... 46 8e-04
      emb[X73297|SCSETRP4 S.cerevisiae spacer element.
                                                               29 0.002
30
      gb[U10274|SCU10274 Saccharomyces cerevisiae thioredoxin reductas... 44 0.004
      emb|AW933535|AW933535 EST359294 tomato fruit mature green, TAMU ... 38 0.016
      emb|AW922212|AW922212 DG1_17_B11.b1_A002 Dark Grown 1 (DG1) Sorg... 41 0.027
      gb|BE125449|BE125449 DG1 25 B11.b1 A002 Dark Grown 1 (DG1) Sorgh... 41 0.027
      emb|AV407038|AV407038 AV407038 Lotus japonicus young plants (two... 40 0.037
35
      emb|AI730383|AI730383 BNLGHi6768 Six-day Cotton fiber Gossypium ... 40 0.037
      emb|AW201070|AW201070 se97e05.y1 Gm-c1027 Glycine max cDNA clone... 40 0.050
      dbj E08275 E08275 cDNA encoding cystathionine gamma-lyase.
                                                                   37 0.46
      dbj|E08276|E08276 gDNA encoding cystathionine gamma-lyase.
      emb|AL113519|CNS01AXJ Botrytis cinerea strain T4 cDNA library un... 36 0.88
40
      emb Z31724 PCREPELEM P.chrysosporium DNA for repetitive element.
      emb|AW695815|AW695815 NF099E03ST1F1021 Developing stem Medicago ... 34 1.4
      emb|A46806|A46806 Sequence 3 from Patent EP0684312.
                                                                  35 1.7
      emb|Z37978|NTCYCMRN Nicotiana tabacum mRNA for cyclin B1 (cycB1 ... 35 1.7
      45
      emb|A46810|A46810 Sequence 7 from Patent EP0684312.
      emb|AL354572|LMFL5808 Leishmania major Friedlin chromosome 19 co... 35 2.3
      gb|BE052827|BE052827 GA_Ea0033G24f Gossypium arboreum 7-10 dpa ... 29 2.5
      emb|AW661030|AW661030 832009F12.x1 C. reinhardtii CC-125 nutrien... 34 3.1
      emb|AQ447557|AQ447557 mgxb0008C17f CUGI Rice Blast BAC Library P... 34 3.1
50
      emb|AW257438|AW257438 EST305575 KV2 Medicago truncatula cDNA clo... 34 3.1
      emb|AW563834|AW563834 LG1_272 A11.b1 A002 Light Grown 1 (LG1) So... 34 3.1
      emb|AQ654417|AQ654417 Sheared DNA-20C20.TF Sheared DNA Trypanoso... 34 4.3
      emb|AW756224|AW756224 s117f04.y1 Gm-c1036 Glycine max cDNA clone... 34 4.3
      emb|X89715|SCAOGENES S.cerevisiae AOB567, AOF1001, AOE110, AOE26... 34 4.3
55
      emb|AF134853|AF134853 Cuphea hookeriana acyl-ACP carrier protein... 34 4.3
      emb|Z74896|SCYOL154W S.cerevisiae chromosome XV reading frame OR... 34 4.3
      gb|U15935|CWKAS3A Cuphea wrightii beta-ketoacyl-ACP synthase III... 34 4.3
      gb|BE033595|BE033595 MF04D10 MF Mesembryanthemum crystallinum cD... 34 4.3
      emb|AQ952764|AQ952764 Sheared DNA-43G7.TR Sheared DNA Trypanosom... 33 5.9
60
      emb|X61281|PBPOLII9 P.berghei RNA polymerase largest subunit.
      emb|Z36097|SCYBR228W S.cerevisiae chromosome II reading frame OR... 33 5.9
```

5	emb AL113095 CNS01ALR Botrytis cinerea strain T4 cDNA library un 33 5.9 gb U36470 NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu 33 5.9 emb Z78011 ANAXHA A.niger CBS 120.49 axhA gene. 33 5.9 gb BE023153 BE023153 sm79a01.y1 Gm-c1015 Glycine max cDNA clone 33 5.9 emb X71807 ANUAPA A.nidulans uapA gene for uric acid-xanthine pe 33 5.9 emb AI213031 AI213031 y6f05a1.r1 Aspergillus nidulans 24hr asexu 33 5.9 emb AQ874871 AQ874871 V117H8 mTn-3xHA/lacZ Insertion Library, st 26 6.5 gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids 33 8.1 emb AF006304 AF006304 Saccharomyces cerevisiae protein tyrosine 33 8.1
10	gb U18814 SCE3612 Saccharomyces cerevisiae chromosome V lambda c 33 8.1 emb AW719293 AW719293 LjNEST_C6r Lotus japonicus nodule library, 33 8.1 emb AI441951 AI441951 sa83b07.yl Gm-c1004 Glycine max cDNA clone 33 8.1 emb AI443684 AI443684 sa50b09.yl Gm-c1004 Glycine max cDNA clone 33 8.1 emb AW932067 AW932067 EST357910 tomato fruit mature green, TAMU 33 8.1
15	emb AW720549 AW720549 LjNEST10b1rc Lotus japonicus nodule librar 33 8.1 emb AW706285 AW706285 sj54d11.y1 Gm-c1033 Glycine max cDNA clone 33 8.1 emb Z69368 SPAC27F1 S.pombe chromosome I cosmid c27F1. 33 8.1 emb X55664 SVPEPCA Sorghum vulgare mRNA for phosphoenolpyruvate 33 8.1 emb AW299016 AW299016 EST305690 KV2 Medicago truncatula cDNA clo 33 8.1
20	emb AW171746 AW171746 N100640e rootphos(-) Medicago truncatula c 33 8.1 emb AI960269 AI960269 sc81b07.yl Gm-c1018 Glycine max cDNA clone 27 9.1
25	Query=PDF1.2_at 14621_at /id_source genbank /description gb aac31244.1 (ac004747) putative antifungal protein [arabidopsis thaliana] /blast_score 1.00e-31 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb pdf1 /ncgi
30	http://www.ncgr.org/cgi-bin/ff?pdfl (400 letters)
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
35	Searchingdone
	Score E Sequences producing significant alignments: (bits) Value
40	emb A26875 A26875 R.sativus AFP1 gene. 160 5e-39 gb U18557 RSU18557 Raphanus sativus antifungal protein 1 preprot 159 1e-38 gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl 127 6e-37 gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot 138 1e-35 emb X97318 RSAFP4 R.sativus mRNA for antifungal protein 4. 145 3e-34
45	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3. emb A26963 A26963 D.merkii AMP1 sequence. emb X53375 HASF18 Sunflower anther-specific mRNA SF18. emb A27062 A27062 C.benedictus AMP2 sequence. emb A26906 A26906 C.benedictus AMP1 sequence. emb A26906 A26906 C.benedictus AMP1 sequence. emb A26906 A26906 C.benedictus AMP1 sequence. emb A26906 A26906 C.benedictus AMP1 sequence.
50	gb L47901 L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA 65 2e-10 emb AT001728 AT001728 AT001728 Flower bud cDNA Brassica rapa sub 65 3e-10 emb A27064 A27064 C.ternatea AMP1 sequence. 58 7e-09 emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub 52 2e-06 emb AW870017 AW870017 NXNV_122_A10_F Nsf Xylem Normal wood Verti 35 7e-06
55	emb AW064751 AW064751 ST35D04 Pine TriplEx shoot tip library Pin 36 7e-06 emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put 40 1e-05 emb AW621708 AW621708 EST312506 tomato root during/after fruit s 43 9e-05 emb AW220215 AW220215 EST302698 tomato root during/after fruit s 43 1e-04
60	emb AW220231 AW220231 EST302714 tomato root during/after fruit s 43 1e-04 emb AW219164 AW219164 EST301646 tomato root during/after fruit s 43 1e-04 emb AW219793 AW219793 EST302275 tomato root during/after fruit s 43 1e-04

```
emb|AW621529|AW621529 EST312327 tomato root during/after fruit s...
      emb|AW622375|AW622375 EST313174 tomato root during/after fruit s...
      emb|AW622390|AW622390 EST313189 tomato root during/after fruit s...
      emb|AW621171|AW621171 EST311969 tomato root during/after fruit s...
 5
      dbj|D29679|TOBPIT1A Tobacco pit1 mRNA (which expression is induc... 44 7e-04
      emb|AW622051|AW622051 EST312849 tomato root during/after fruit s...
      emb|AW622079|AW622079 EST312877 tomato root during/after fruit s...
                                                                       40 9e-04
      emb|AW621330|AW621330 EST312128 tomato root during/after fruit s...
                                                                       40 9e-04
      emb|AW219347|AW219347 EST301829 tomato root during/after fruit s...
10
      emb|AW220086|AW220086 EST302569 tomato root during/after fruit s...
      emb|AW621962|AW621962 EST312760 tomato root during/after fruit s... 40 0.001
      emb|AW621634|AW621634 EST312432 tomato root during/after fruit s... 37 0.005
      emb|AW623112|AW623112 EST321057 tomato flower buds 3-8 mm, Corne...
                                                                           40 0.006
      emb|AW683448|AW683448 NF012D04LF1F1041 Developing leaf Medicago ... 40 0.006
15
      emb|AI487824|AI487824 EST246146 tomato ovary, TAMU Lycopersicon ... 40 0.006
      emb|AI483999|AI483999 EST249870 tomato ovary, TAMU Lycopersicon ...
      gb|U20591|SLU20591 Solanum lycopersicum flower-specific gamma-th... 40 0.007
      emb|AW622923|AW622923 EST306993 tomato flower buds 3-8 mm, Corne... 40 0.007
      emb|AW929929|AW929929 EST354199 tomato flower buds 8 mm to pre-a... 40 0.007
20
      emb|AW929939|AW929939 EST354209 tomato flower buds 8 mm to pre-a... 40 0.007
      emb|AI897392|AI897392 EST266835 tomato ovary, TAMU Lycopersicon ...
                                                                          40 0.008
      emb|AI490243|AI490243 EST248569 tomato ovary, TAMU Lycopersicon ...
                                                                          40 0.008
      emb|AI487859|AI487859 EST246181 tomato ovary, TAMU Lycopersicon ...
      emb|AW217552|AW217552 EST296266 tomato flower buds 3-8 mm, Corne... 40 0.009
25
      emb|AI489818|AI489818 EST248157 tomato ovary, TAMU Lycopersicon ... 40 0.009
      emb|AI487398|AI487398 EST245720 tomato ovary, TAMU Lycopersicon ... 40 0.009
      emb|AW217379|AW217379 EST296063 tomato flower buds 0-3 mm, Corne... 40 0.010
      emb|AI898009|AI898009 EST267452 tomato ovary, TAMU Lycopersicon ... 40 0.010
      emb|AI897456|AI897456 EST266899 tomato ovary, TAMU Lycopersicon ... 40 0.010
30
      emb|AI483612|AI483612 EST249462 tomato ovary, TAMU Lycopersicon ...
                                                                          40 0.010
      emb|AI485550|AI485550 EST243871 tomato ovary, TAMU Lycopersicon ...
                                                                          40 0.010
      emb|AI484887|AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...
      emb|AI484497|AI484497 EST242507 tomato ovary, TAMU Lycopersicon ...
      emb|AI490062|AI490062 EST248401 tomato ovary, TAMU Lycopersicon ...
35
      emb|AW775186|AW775186 EST331908 GVN Medicago truncatula cDNA clo... 39 0.016
      emb|AI486656|AI486656 EST244977 tomato ovary, TAMU Lycopersicon ... 38 0.024
      emb|AI485044|AI485044 EST243324 tomato ovary, TAMU Lycopersicon ... 37 0.041
      emb|AW399651|AW399651 EST310151 L. pennellii trichome, Cornell U... 38 0.042
      emb|A26964|A26964 D.merkii AMP2 sequence.
                                                               37 0.080
40
      emb|X77993|HASF18A H.annuus SF18 gene.
                                                               31 0.14
      emb|A27063|A27063 L.cicera AFP sequence.
                                                             34 0.74
      emb|AI757757|AI757757 EtESTea34d02.yl Eimeria S5-2 Sporozoite st... 34 0.74
      emb|AW217119|AW217119 EST295833 tomato callus, TAMU Lycopersicon... 27 0.90
      emb|X95363|CAGT C.annuum gamma thionin gene.
                                                                 33 1.0
45
      emb|X95730|CAGTHIOGN Capsicum annuum defensin gene.
                                                                      33 1.0
      emb|AL035477|PFMAL4P4 Plasmodium falciparum chromosome 4 strain ... 33 1.0
      emb|AL117384|LMFL5883 Leishmania major Friedlin chromosome 23 co... 29 1.3
      emb|Z74387|SCYDR262W S.cerevisiae chromosome IV reading frame OR... 33 1.4
      emb|Z68329|SC9320A S.cerevisiae chromosome IV cosmid 9320A.
50
      emb|Z70202|SC9320X S.cerevisiae chromosome IV cosmid 9320X.
      emb|AQ846121|AQ846121 LMAJFV1 lm14f01.yl Leishmania major FV1 ra... 29 1.7
      emb|AV387503|AV387503 AV387503 Chlamydomonas reinhardtii C9 Chla... 32 2.6
      emb|AQ947439|AQ947439 Sheared DNA-50L12.TF Sheared DNA Trypanoso... 31 3.6
      emb|AA836739|AA836739 L30-187T3 Ice plant Lambda Uni-Zap XR expr... 31 3.6
      gb|M65164|PAR51C P.tetraurelia 51C surface protein gene, complet... 31 3.6
      emb|X16877|VUSTORED Vigna unguiculata cDNA for stored cotyledon ... 31 3.6
      emb|AW736134|AW736134 EST332130 KV3 Medicago truncatula cDNA clo...
      emb|AL034381|SPCC61 S.pombe chromosome III cosmid c61.
60
      emb|AQ642382|AQ642382 RPCI93-DpnII-29C10.TV RPCI93-DpnII Trypano...
      gb|L01579|PEADRR230B Pea (pi39) disease resistance response prot... 31 5.0
```

5	emb AW186932 AW186932 BNLGHi7476 Six-day Cotton fiber Gossypium 31 5.0 emb AI727997 AI727997 BNLGHi9540 Six-day Cotton fiber Gossypium 31 5.0 emb AI728914 AI728914 BNLGHi12020 Six-day Cotton fiber Gossypium 31 5.0 gb B07260 B07260 G236T7 MVAT4 sheared genomic library Trypanosom 31 5.0 emb AI728815 AI728815 BNLGHi11757 Six-day Cotton fiber Gossypium 31 5.0 emb AI726605 AI726605 BNLGHi6250 Six-day Cotton fiber Gossypium 31 5.0 gb BE033595 BE033595 MF04D10 MF Mesembryanthemum crystallinum cD 30 6.8 emb AW508408 AW508408 si40e08.y1 Gm-r1030 Glycine max cDNA clone 30 6.8
10	emb AW830659 AW830659 sm05b06.y1 Gm-c1027 Glycine max cDNA clone 30 6.8 emb AW266371 AW266371 L30-3125T3 Ice plant Lambda Uni-Zap XR exp 30 6.8 emb AW266222 AW266222 L30-2930T3 Ice plant Lambda Uni-Zap XR exp 30 6.8 emb AW093819 AW093819 EST286999 tomato mixed elicitor, BTI Lycop 30 6.8 emb AI774224 AI774224 EST255419 tomato resistant, Cornell Lycope 30 6.8 emb AA962873 AA962873 L30-403T3 Ice plant Lambda Uni-Zap XR expr 30 6.8
15	emb AA962873 AA962873 L30-403T3 Ice plant Lambda Uni-Zap XR expr 30 6.8 emb AL034557 PFMALAP1 Plasmodium falciparum chromosome 4 strain 30 6.8 emb AQ905826 AQ905826 GSSTc010408 Trypanosome cruzi random genom 30 6.8 emb AW053406 AW053406 L30-1317T3 Ice plant Lambda Uni-Zap XR exp 30 6.8
20	Query= PR.1_s_at 14635_s_at /id_source genbank /description gb aac69381.1 (ac005398) pathogenesis-related pr-1-like protein [arabidopsis thaliana] /blast_score 1.00e-94 /ec_number /family /chip nova /gb_link /ncgi (738 letters)
25	Database: plantfungal 661,018 sequences; 426,114,510 total letters
30	Searchingdone
	Score E Sequences producing significant alignments: (bits) Value
35	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P 323 3e-88 gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds. 323 3e-88 gb U64806 BNU64806 Brassica napus pathogenesis-related protein P 209 4e-85 emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl 311 4e-84 emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl 165 3e-62
40	emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon 152 4e-60 emb AW219671 AW219671 EST302153 tomato root during/after fruit s 151 1e-59 emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop 151 1e-59 emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit 151 1e-59
45	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW040983 AW040983 EST283847 tomato mixed elicitor, BTI Lycop 151 1e-59 emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW219480 AW219480 EST301878 tomato root during/after fruit s 151 1e-59 emb AW219480 AW219480 EST301878 tomato root during/after fruit s 151 1e-59
50	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop 151 1e-59 emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop 151 1e-59 emb AW034454 AW034454 EST278025 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW032723 AW032723 EST276282 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW033873 AW033873 EST277444 tomato callus, TAMU Lycopersicon 151 1e-59
55	emb AI894650 AI894650 EST264093 tomato callus, TAMU Lycopersicon 151 1e-59 emb AW033593 AW033593 EST277164 tomato callus, TAMU Lycopersicon 151 3e-59 emb AW034724 AW034724 EST278526 tomato callus, TAMU Lycopersicon 148 7e-59 emb AW041033 AW041033 EST283897 tomato mixed elicitor, BTI Lycop 148 7e-59 emb X66942 NTPRB1B N.tabacum prb-1b gene. 146 9e-59
60	emb AW559895 AW559895 EST314943 DSIR Medicago truncatula cDNA cl 160 1e-58 emb AW329241 AW329241 N200453e rootphos(-) Medicago truncatula c 160 1e-58 emb AW559894 AW559894 EST314942 DSIR Medicago truncatula cDNA cl 159 5e-58

```
emb|AW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 145 6e-58
       emb|AW032139|AW032139 EST275593 tomato callus, TAMU Lycopersicon... 145 6e-58
       emb|AW034330|AW034330 EST277901 tomato callus, TAMU Lycopersicon... 144 2e-57
       emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57
  5
       emb|AI352771|AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl... 220 2e-57
       emblAW032749|AW032749 EST276308 tomato callus, TAMU Lycopersicon... 149 3e-57
       emb|AI894391|AI894391 EST263846 tomato callus, TAMU Lycopersicon... 142 4e-57
       emb|AI896249|AI896249 EST265692 tomato callus, TAMU Lycopersicon... 142 5e-57
       emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 7e-57
 10
       emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56
       emb|AW981257|AW981257 EST392410 DSIL Medicago truncatula cDNA cl... 128 9e-56
       emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 149 2e-55
       emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55
       emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 4e-55
 15
       emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55
       emblAW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53
       emb[X52555]NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 116 1e-52
       gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 112 4e-52
       emb|AW053720|AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-52
20
       emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52
       emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51
       emb[X17681]NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51
       emb[X05454]NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.
                                                                         111 2e-51
       emb[X12487]NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51
25
       emb|AJ011520|LES011520 Lycopersicon esculentum prla (P4) gene.
                                                                        98 1e-50
       gb[M69247]TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
       emb|A22634|LEPI4GENE L.esculentum P14 gene.
                                                                  98 le-50
       emblAJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50
       emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50
30
       emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
       emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50
       emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50
       dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50
      emb[X05959]NTPR1AG Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
.35
       emb[X12737[NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
       emb[X06361]NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
       emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
       emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 116 5e-50
       emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
40
       emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50
       emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 95 7e-50
      emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
      emb[AW031086]AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
      emb[X74939]HVPR1AR H.vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
45
       emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
       emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49
       emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 3e-49
       emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 3e-49
      dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein.
                                                                         103 3e-49
50
      emb[Y08804|LEPR1B1 L.esculentum mRNA for PR protein.
                                                                      92 6e-49
      gb]M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 6e-49
      emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(p1... 92 6e-49
      emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 6e-49
      emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 6e-49
55
      emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 6e-49
      emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 6e-49
      emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco...
      emb|AI782822|AI782822 EST263701 tomato susceptible, Cornell Lyco...
      emb|AI778686|AI778686 EST259565 tomato susceptible, Cornell Lyco... 92 6e-49
60
      emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 6e-49
      emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 92 6e-49
```

5	emb AI779287 AI779287 EST260166 tomato susceptible, Cornell Lyco 92 6e-49 emb AI773130 AI773130 EST254230 tomato resistant, Cornell Lycope 92 6e-49 emb AI778790 AI778790 EST259669 tomato susceptible, Cornell Lyco 92 6e-49 emb AI778791 AI778791 EST259670 tomato susceptible, Cornell Lyco 92 6e-49 emb AI778985 AI778985 EST259864 tomato susceptible, Cornell Lyco 92 6e-49 emb AW032026 AW032026 EST275480 tomato callus, TAMU Lycopersicon 92 6e-49 emb AI782288 AI782288 EST263167 tomato susceptible, Cornell Lyco 92 6e-49 emb AI779013 AI779013 EST259892 tomato susceptible, Cornell Lyco 92 6e-49
10	emb AI781431 AI781431 EST262298 tomato susceptible, Cornell Lyco 92 6e-49 emb AI780973 AI780973 EST261852 tomato susceptible, Cornell Lyco 92 6e-49 emb AI895236 AI895236 EST264679 tomato callus, TAMU Lycopersicon 92 6e-49
15	Query= PRXcb_s_at 14638_s_at /id_source genbank /description emb caa50677.1 (x71794) peroxidase [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1236 letters)
20	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
25	Score E Sequences producing significant alignments: (bits) Value
30	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge 744 0.0 emb A00741 A00741 A.rusticana synthetic gene (reverse complement 692 0.0 emb A00740 A00740 A.rusticana synthetic gene for peroxidase. 692 0.0 dbj E01651 E01651 cDNA encoding horseradish peroxidase. 692 0.0 gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge 371 e-133 emb X97349 PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P 473 e-132
35	emb X97350 PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P 469 e-131 dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds. 468 e-131 gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge 363 e-130 emb X97348 PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P 463 e-129 dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part 441 e-123 emb X97361 PTPXPAPER P. trichocarpa mRNA for peroxidase, part 441 e-123
40	emb[X97351]PTPXP4PER P. trichocarpa mRNA for anionic peroxidase P 383 e-120 dbj[D30653]POPPB Populus kitakamiensis mRNA for peroxidase, part 356 e-112 emb[AF149277]AF149277 Phaseolus vulgaris peroxidase 1 precursor 227 e-107 gb[L36157]ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple 229 e-107 emb[AF007211]AF007211 Glycine max peroxidase precursor (GMIPER1) 229 e-106 gb]L07554]LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA 381 e-105
45	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A. 211 e-105 dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i 296 e-103 emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod 138 2e-97 emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor 142 4e-97 emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B. 231 1e-95
50	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C. 226 7e-94 gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 210 2e-89 emb AI959837 AI959837 sc94h07.yl Gm-c1019 Glycine max cDNA clone 228 6e-89 emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs 208 9e-88 emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl 236 1e-87 emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo 236 7e-8
55	emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox 215 2e-86 emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl 236 2e-85 emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per 209 2e-85 emb AF244923 AF244923 Spinacia oleracea peroxidase prx14 precurs 205 9e-85
60	emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g 253 1e-83 emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl 236 6e-83 emb Y10466 SOPRXR5 S.oleracea mRNA for peroxidase, clone PC18. 218 3e-82

emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81 emb]AW685437|AW685437 NF029D09NR1F1000 Nodulated root Medicago t... 230 9e-80 emb|AB024439|AB024439 Scutellaria baicalensis mRNA for peroxidas... 209 2e-79 emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79 emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. emb|AW776273|AW776273 EST335338 DSIL Medicago truncatula cDNA cl... 222 le-77 emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76 emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76 emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 207 7e-76 10 emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76 emb|AW775890|AW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 3e-74 emb|AW257195|AW257195 EST305332 KV2 Medicago truncatula cDNA clo... 214 Se-74 gb[M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73 gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73 15 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73 gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73 gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73 emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 '9e-73 emb|AW278775|AW278775 sf97d02.y1 Gm-c1019 Glycine max cDNA clone... 155 1e-72 20. emb|X71593|LECEVI1A L.esculentum CEVI-1 mRNA. 99 2e-72 gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72 emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72 emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70 emb|Y10467|SOPRXR6 S.oleracea mRNA for peroxidase, clone PC23. 105 le-69 25 dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 196 2e-69 gb|M74103|TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69 emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68 gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68 emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67 30 emb[Y10465]SOPRXR4 S.oleracea mRNA for peroxidase, clone PC44. emblAW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67 emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67 emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66 emb|AW185769|AW185769 se59d08.y1 Gm-c1019 Glycine max cDNA clone... 219 4e-65 35 emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64 gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidas... 205 7e-64 gblM91374|CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63 gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63 40 gblM91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63 emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63 emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63 emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62 gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62 45 emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61 emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 163 3e-61 emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). emb|AI496388|AI496388 sb04a11.yl Gm-c1004 Glycine max cDNA clone... 224 6e-61 50 emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61 dbj|D38050|POPP1 Aspen prxA3a gene for peroxidase, complete cds. 121 9e-61 emb|AW704659|AW704659 sk54h10.y1 Gm-c1019 Glycine max cDNA clone... 149 9e-61 emb|Y10464|SOPRXR3 S.oleracea mRNA for peroxidase, clone PC42. 80 3e-60 emb|AW705730|AW705730 sk51b02.yl Gm-c1019 Glycine max cDNA clone... 149 8e-60 55 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60 gb|U12314|CCU12314 Cenchrus ciliaris clone PX7 peroxidase mRNA, ... 105 9e-60 emb|AI938533|AI938533 sb46h09.y1 Gm-c1015 Glycine max cDNA clone... 145 1e-59 emb|AW705617|AW705617 sk50d03.y1 Gm-c1019 Glycine max cDNA clone... 149 2e-59 emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59 60 emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 90 3e-59 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59

emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59 emblAF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58 emblAW705946|AW705946 sk52h07.yl Gm-c1019 Glycine max cDNA clone... 224 6e-58 5. Query= TSA1_s_at 14672_s_at /id_source genbank /description gb|aac49117.1| (u18993) tryptophan synthase alpha chain [arabidopsis thaliana] /blast score 1.00e-158 /ec number /family /chip nova 10 /gb link /ncgi (939 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 15 Searching......done Score E Sequences producing significant alignments: (bits) Value 20 emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75 25 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70 emb|Z21642|CHASTRNAA Antithamnion sp. Chloroplast trnK,trnE,trpA... 255 4e-67 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59 gb|BE121873|BE121873 894015F07.yl C. reinhardtii CC-1690, normal... 227 1e-58 30 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56 emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49 35 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46 dbi|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43 40 emb[V01342]SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32 45 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycope... 138 5e-32 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 le-21 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19 50 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10 emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptopha... 64 1e-09 55 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 le-09 emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09 emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09 emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09 emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09 60 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08 emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06

	emb AW693052 AW693052 NF059C08ST1F1065 Developing stem Medicago 51 1e-05
	emb AV390244 AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla 49 4e-05
	emb AW616467 AW616467 EST322878 L. hirsutum trichome, Cornell Un 48 7e-05
	emb AL354022 P761R Leishmania major Friedlin PAC P761 right end 44 0.002
5	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1 43 0.005
	emb AQ903789 AQ903789 GSSTc04230 Trypanosome cruzi random genomi 35 0.24
•	emb AW727215 AW727215 GA_ Ea0023N23 Gossypium arboreum 7-10 dpa 36 0.52
	gb M91654 CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1 36 0.52
	emb AW728975 AW728975 GA_Ea0018P19 Gossypium arboreum 7-10 dpa 35 0.64
10	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC 35 0.87
	emb AW926438 AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis 34 1.2
•	emb AA965348 AA965348 e9d04a1.rl Aspergillus nidulans 24hr asexu 34 1.3
	gb U12630 ENU12630 Emericella nidulans R153 core histone H3 (H3) 34 1.3
	emb A1007494 A1007494 e9c09a1.rl Aspergillus nidulans 24hr asexu 34 1.3
15	emb AA787433 AA787433 n3d04a1.rl Aspergillus nidulans 24hr asexu 34 1.3
	emb X55548 ANH3GENE A.nidulans gene for core histone for H3. 34 1.3
	emb AQ396426 AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P 34 1.6
	emb AF262997 AF262997 Ricinus communis NADP-dependent malic prot 34 1.6
	gb[M19025]CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c 34 1.6
20	emb AF084888 AF084888 Neurospora crassa 656-2A mutant tryptophan 31 1.7
20	emb AF084887 AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta 31 1.7
	emb AW694774 AW694774 NF080A05ST1F1036 Developing stem Medicago 34 1.8
	emb Y18012 TVE18012 Trametes versicolor mRNA for laccase. 33 2.3
	emb AQ500614 AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc 33 2.5
25	emb AW187498 AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium 33 3.1
	emb AW187530 AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium 33 3.1
	emb AW694072 AW694072 NF072B12ST1F1096 Developing stem Medicago 33 3.1
	emb AW186883 AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium 33 3.1
	emb AW187537 AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium 33 3.1
30	emb AW187474 AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium 33 3.1
	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor 33 3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two 33 4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp 33 4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un 33 4.7
35	gb BE028433 BE028433 EtESTea78d07.yl Eimeria M5-6 Merozoite stag 32 5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li 32 5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom 32 5.9
	emb AW728623 AW728623 GA_Ea0017G06 Gossypium arboreum 7-10 dpa 32 5.9
40	gb BE027723 BE027723 EtESTea86c08.yl Eimeria M5-6 Merozoite stag 32 5.9
40	emb AI757375 AI757375 EtESTea32d03.yl Eimeria S5-2 Sporozoite st 32 5.9
	gb BE027843 BE027843 EtESTea88c05.yl Eimeria M5-6 Merozoite stag 32 5.9
	emb AI973878 AI973878 sd13a09.yl Gm-c1020 Glycine max cDNA clone 32 5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit 32 5.9
45	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit 32 5.9
43	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom 32 6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O 32 6.5
	emb AW707662 AW707662 832011E08.yl C. reinhardtii CC-125 nutrien 28 7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop 32 8.1
50	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two 32 8.1
50	emb AW703740 AW703740 sk23g09.yl Gm-c1028 Glycine max cDNA clone 32 8.1
	emb AW703739 AW703739 sk23g08.yl Gm-c1028 Glycine max cDNA clone 32 8.1 emb AV419698 AV419698 AV419698 Lotus japonicus young plants (two 32 8.1
55	43180.000.000.000.000.000.000.000.000.000.
-	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two 32 8.1 emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two 32 8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two 32 8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library 32 8.1
	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron. 32 8.1
60	

Query= TSB2 s at 14673 s at /id_source genbank /description gb|aaa32879.1| (m81620) tryptophan synthase beta-subunit [arabidopsis thaliana] thaliana] /blast_score 0 /ec_number /family /chip nova /gb link /ncgi 5 (1526 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching.....done Score E Sequences producing significant alignments: (bits) Value 15 emb|AF042320|AF042320 Camptotheca acuminata tryptophan synthase ... 858 0.0 emb|AF047024|AF047024 Chlamydomonas reinhardtii tryptophan synth... 712 0.0 gblJ04594[NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 473 e-140 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. emb|AW031813|AW031813 EST275267 tomato callus, TAMU Lycopersicon... 429 e-119 20 emb|AF121272|AF121272 Gracilaria gracilis putative NAD-myo-inosi... 426 e-118 dbj|D89113|D89113 Schizosaccharomyces pombe mRNA, partial cds, c... 310 e-114 emb|AI055312|AI055312 coau0003K07 Cotton Boll Abscission Zone cD... 404 e-112 emb|AF042321|AF042321 Camptotheca acuminata tryptophan synthase ... 346 e-109 gb|BE126222|BE126222 DG1_68_D09.b1_A002 Dark Grown 1 (DG1) Sorgh... 379 e-104 25 emb|AW650635|AW650635 EST329089 tomato germinating seedlings, TA... 372 e-102 emb|AI487343|AI487343 EST245665 tomato ovary, TAMU Lycopersicon ... 354 8e-97 emb|AI488733|AI488733 EST247072 tomato ovary, TAMU Lycopersicon ... 353 2e-96 emb|AA495663|AA495663 c313 Zhou and Ragan 1993 Gracilaria gracil... 350 1e-95 emb|AW160221|AW160221 EST290079 L. pennellii trichome, Cornell U... 327 1e-88 30 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 270 6e-88 emb|AI485149|AI485149 EST243453 tomato ovary, TAMU Lycopersicon ... 319 3e-86 emb|AI966766|AI966766 sc57f10.yl Gm-c1016 Glycine max cDNA clone... 306 3e-82 gb|M91659|CCITRP08 Coprinus cinereus tryptophan synthetase (TRP1... 302 4e-81 35 gb|BE058277|BE058277 sn13h12.yl Gm-c1016 Glycine max cDNA clone ... 259 6e-68 emb|AI488512|AI488512 EST246851 tomato ovary, TAMU Lycopersicon ... 237 2e-63 emb|AI487792|AI487792 EST246114 tomato ovary, TAMU Lycopersicon ... 232 8e-62 emb|AW696637|AW696637 NF109C11ST1F1085 Developing stem Medicago ... 213 2e-59 emb|AI898827|AI898827 EST268270 tomato ovary, TAMU Lycopersicon ... 228 7e-59 40 emb|AQ450225|AQ450225 500009D01.x1 CpIOWAM13mp18gDNA1 Cryptospor... 175 3eemb|AW160220|AW160220 EST290078 L. pennellii trichome, Cornell U... 223 3e-57 emb|AF084902|AF084902 Neurospora crassa TD2(4A-4A)2A mutant tryp... 214 2e-54 emb|AF084903|AF084903 Neurospora crassa TD71-19A mutant tryptoph... 213 3e-54 45 emb|AF084904|AF084904 Neurospora crassa TD54-6A mutant tryptopha... 210 3e-53 emb|AI779245|AI779245 EST260124 tomato susceptible, Cornell Lyco... 208 8e-53 emb|AI487088|AI487088 EST245410 tomato ovary, TAMU Lycopersicon ... 149 3e-51 emb|AQ876415|AQ876415 V99F5 mTn-3xHA/lacZ Insertion Library, str... 183 4e-50 emb|AL116518|CNS01D8U Botrytis cinerea strain T4 cDNA library un... 160 2e-47 50 emb|AW745773|AW745773 WS1_37_G06.b1_A002 Water-stressed 1 (WS1) ... 167_2e-40 emb|AF084893|AF084893 Neurospora crassa TD24-2A-28A mutant trypt... 130 8e-38 emb|AF084892|AF084892 Neurospora crassa 314-567-9A mutant trypto... 132 1e-37 emb|AF084891|AF084891 Neurospora crassa 314-616-2A mutant trypto... 132 1e-37 emb|AF084895|AF084895 Neurospora crassa TD10-8A mutant tryptopha... 130 1e-37 55 emb|AF084894|AF084894 Neurospora crassa TD7(13A-11A)13A mutant t... 130 1e-37 emblAF084901|AF084901 Neurospora crassa TD72-1-25A mutant trypto... 129 1e-37 emb|AF084900|AF084900 Neurospora crassa TD85-1-24A mutant trypto... 129 1e-37 emb|AF084899|AF084899 Neurospora crassa TD86-1-22A mutant trypto... 129 1e-37 emb|AF084898|AF084898 Neurospora crassa TD6(1-8A)22A mutant tryp... 129 1e-37 60 emb|AF084896|AF084896 Neurospora crassa NG29-3A mutant tryptopha... 129 1e-37 emb|AW745836|AW745836 WS1_37_G06.g1_A002 Water-stressed 1 (WS1) ... 157 2e-37

	emb AF084897 AF084897 Neurospora crassa TD3-32-16A mutant trypto 128 3e-37 emb AI399300 AI399300 NCW07F11T3 Westergaards Neurospora crassa 145 3e-37
	emb AF084906 AF084906 Neurospora crassa NG40-5A mutant tryptopha 152 8e-36
5	emb AF084905 AF084905 Neurospora crassa NG25-4A mutant tryptopha 152 8e-36
3	gb BE024522 BE024522 894003E01.yl C. reinhardtii CC-1690, normal 142 6e-33
	emb AJ229567 KLAJ9567 Kluyveromyces lactis DNA fragment for sequ 137 3e-31
	emb AQ449630 AQ449630 500002F12.x2 CpIOWAM13mp18gDNA1 Cryptospor 116 1e-27
• •	emb AW695848 AW695848 NF099D01ST1F1012 Developing stem Medicago 116 9e-27
10	emb AW098758 AW098758 ga01a03.yl Moss EST library CPU Ceratodon 118 1e-25
	gb M91658 CCITRP07 Coprinus cinereus tryptophan synthetase (TRP1 115 8e-25
	emb AW086510 AW086510 ga01a03.x1 Moss EST library CPU Ceratodon 103 4e-21
	emb AW221168 AW221168 EST297637 tomato fruit mature green, TAMU 96 5e-19
1.5	emb AW650217 AW650217 EST328671 tomato germinating seedlings, TA 95 1e-18
15	emb AV408265 AV408265 AV408265 Lotus japonicus young plants (two 77 4e-13
	emb AW688230 AW688230 NF005A01ST1F1000 Developing stem Medicago 72 1e-11
	emb AI488384 AI488384 EST246706 tomato ovary, TAMU Lycopersicon 70 4e-11
	emb AW032971 AW032971 EST276530 tomato callus, TAMU Lycopersicon 60 6e-08
20	emb AW755317 AW755317 sl01e06.yl Gm-c1036 Glycine max cDNA clone 57 4e-07
20	emb AW153250 AW153250 se37h08.yl Gm-c1015 Glycine max cDNA clone 56 1e-06 emb AQ450041 AQ450041 500007C05.xl CpIOWAM13mp18gDNA1 Cryptospor 37 2e-0-
	emb AQ450041 AQ450041 500007C05.x1 CpIOWAM13mp18gDNA1 Cryptospor 37 2e-0- emb AW625162 AW625162 EST319069 tomato radicle, 5 d post-imbibit 45 0.001
	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1 45 0.002
	emb AW926725 AW926725 HVSMEg0007P16 Hordeum vulgare pre-anthesis 42 0.013
25	emb X99652 ANG3PDEHY A.niger gpd gene. 35 0.084
	emb AV418759 AV418759 AV418759 Lotus japonicus young plants (two 38 0.17
	emb[AV417838]AV417838 AV417838 Lotus japonicus young plants (two 38 0.17
	emb AV414417 AV414417 AV414417 Lotus japonicus young plants (two 38 0.17
	emb AV419253 AV419253 AV419253 Lotus japonicus young plants (two 38 0.17
30	emb AV424994 AV424994 AV424994 Lotus japonicus young plants (two 38 0.17
	emb AA901537 AA901537 NCC2B7T7 Conidial Neurospora crassa cDNA c 38 0.23
	gb BE060085 BE060085 HVSMEg0011G11f Hordeum vulgare pre-anthesis 38 0.23
	gb U30626 SCU30626 Saccharomyces cerevisiae var. diastaticus glu 37 0.32
2.5	emb AJ010201 GMA010201 Glycine max mRNA for inosine monophosphat 37 0.32
35	emb AW185330 AW185330 se90b04.y1 Gm-c1027 Glycine max cDNA clone 37 0.32
	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168. 37 0.32
	emb AF160799 AF160799 Sporidiobolus salmonicolor aldehyde reduct 37 0.44
	emb AC016161 AC016161 Leishmania major chromosome 35 clone L8149 37 0.44 emb AW185636 AW185636 se80e06.yl Gm-c1023 Glycine max cDNA clone 37 0.44
40	emb AB030490 AB030490 Glycine max SG-05 gene for thiamin biosynt 36 0.60
-10	emb AW278827 AW278827 sf99b01.y1 Gm-c1019 Glycine max cDNA clone 36 0.60
	emb Z93048 SLZ93048 S.latifolia mRNA, clone CCLS 37.1. 30 0.72
	emb AV393412 AV393412 AV393412 Chlamydomonas reinhardtii C9 Chla 36 0.83
	emb AL035581 SPBC1677 S.pombe chromosome II cosmid c1677. 36 0.83
45	emb AV425767 AV425767 AV425767 Lotus japonicus young plants (two 36 0.83
	emb AI727538 AI727538 BNLGHi8343 Six-day Cotton fiber Gossypium 35 1.1
	gb BE053957 BE053957 GAEa0033K12f Gossypium arboreum 7-10 dpa 35 1.1
	emb AI731384 AI731384 BNLGHi8894 Six-day Cotton fiber Gossypium 35 1.1
	emb AW596016 AW596016 si96g09.yl Gm-c1032 Glycine max cDNA clone 35 1.1
50	emb AI730998 AI730998 BNLGHi8370 Six-day Cotton fiber Gossypium 35 1.1
	emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 28 1.3
	gb B13527 B13527 jd421 Trypanosome Shotgun M13 genomic Trypanoso 29 1.4
	gb U56698 CPU56698 Ceratodon purpureus phytochrome photoreceptor 35 2.2
55	emb AF079252 AF079252 Dichanthium aristatum granule-bound starch 35 2.2
55	emb AJ133604 TAE133604 Triticum aestivum mRNA for alpha-gliadin 34 4.1

Query= WT1012A_RC_i_at 14682_i_at /id_source genbank /description no hits found. /blast_score /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1012a| /ncgi

60

```
http://www.ncgr.org/cgi-bin/ff?wt1012a
            (257 letters)
       Database: plantfungal
 5
             661,018 sequences; 426,114,510 total letters
       Searching......done
                                           Score
       Sequences producing significant alignments:
10
                                                           (bits) Value
       emb|AL115243|CNS01C9F Botrytis cinerea strain T4 cDNA library un...
       gb|S69616|S69616 Ant18=dihydroflavonol-4-reductase [Hordeum vulg... 29 7.8
15
       Query= WT1096 at 14691 at /id source genbank /description no hits
       found. /blast score /ec number /family /chip nova /gb link
       http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1096|/ncgi
20.
      http://www.ncgr.org/cgi-bin/ff?wt1096
           (371 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
25
       Searching......done
                                           Score
                                                  Ε
       Sequences producing significant alignments:
                                                          (bits) Value
30
      emb|AW203566|AW203566 sf35f11.yl Gm-c1028 Glycine max cDNA clone... 36 0.099
      emb|AW776554|AW776554 EST335619 DSIL Medicago truncatula cDNA cl... 36 0.099
      emb|AW171733|AW171733 N100627e rootphos(-) Medicago truncatula c... 36 0.099
      emb|AW185514|AW185514 se80g03.y1 Gm-c1023 Glycine max cDNA clone... 36 0.099
35
      emb|AI777176|AI777176 EST258141 tomato resistant, Cornell Lycope... 35 0.26
      gb|C22084|C22084 C22084 Miyagawa-wase satsuma mandarin orange (M... 35 0.26
      emb|AW755041|AW755041 PC10A02 Pine TriplEx pollen cone library P... 35 0.26
      emb|AW218263|AW218263 EST303444 tomato radicle, 5 d post-imbibit... 35 0.26
      emb|AI488300|AI488300 EST246622 tomato ovary, TAMU Lycopersicon ... 35 0.26
40
      emb[AA557085]AA557085 927 Loblolly pine N Pinus taeda cDNA clone... 35 0.26
      emb|AW981718|AW981718 PC15H05 Pine TriplEx pollen cone library P... 35 0.26
      emb|AW982079|AW982079 PC23E11 Pine TriplEx pollen cone library P... 35 0.35
      emb|AF101786|AF101786 Pinus taeda clone PtaADH1 adhesive/proline... 35 0.35
      emb|AA785548|AA785548 g8e04a1.fl Aspergillus nidulans 24hr asexu... 35 0.35
45
      emb|AI812646|AI812646 17D5 Pine Lambda Zap Xylem library Pinus t... 35 0.35
      emb|AI776730|AI776730 EST257830 tomato resistant, Cornell Lycope... 34 0.49
      emb|AW040418|AW040418 EST283282 tomato mixed elicitor, BTI Lycop... 34 0.49
      emb|AI490164|AI490164 EST246756 tomato resistant, Cornell Lycope... 34 0.49
      emb|AA739624|AA739624 389 PtIFG2 Pinus taeda cDNA clone 8646M 3'... 34 0.49
50
      emb|AI490158|AI490158 EST246750 tomato resistant, Cornell Lycope... 34 0.49
      emb|AW625280|AW625280 EST319283 tomato radicle, 5 d post-imbibit... 34 0.49
      emb|AA740016|AA740016 781 PtIFG2 Pinus taeda cDNA clone 9242M 3'... 34 0.49
      emb|AW329045|AW329045 N200244e rootphos(-) Medicago truncatula c... 34 0.67
      emb|AA556671|AA556671 526 Loblolly pine CA Pinus taeda cDNA clon... 34 0.67
55
      emb|AI416531|AI416531 sa10c07.y1 Gm-c1003 Glycine max cDNA clone... 33 0.92
      emb|AI416664|AI416664 sa10c07.x1 Gm-c1003 Glycine max cDNA clone... 33 0.92
      gb|BE023931|BE023931 sm94c10.yl Gm-c1015 Glycine max cDNA clone ... 33 0.92
      emb|AW064558|AW064558 ST33A05 Pine TriplEx shoot tip library Pin... 33 1.3
      gb|BE033882|BE033882 MG01E10 MG Mesembryanthemum crystallinum cD... 33 1.3
      emb|AW011244|AW011244 ST18E01 Pine TriplEx shoot tip library Pin... 33 1.3
60
      gb|BE034004|BE034004 MG03C08 MG Mesembryanthemum crystallinum cD... 33 1.3
```

	emb AW043113 AW043113 ST29E06 Pine TriplEx shoot tip library Pin 33 1.3
	emb AA749493 AA749493 L30-34T3 Ice plant Lambda Uni-Zap XR expre 33 1.3
	emb AW042623 AW042623 ST24A10 Pine TriplEx shoot tip library Pin 33 1.3
	emb[AW216739]AW216739 EST295453 tomato callus, TAMU Lycopersicon 33 1.3
5	emb AA660660 AA660660 00548 MtRHE Medicago truncatula cDNA 5', m 33 1.3
	emb AW011516 AW011516 ST21G04 Pine TriplEx shoot tip library Pin 33 1.3
	emb AW310413 AW310413 sf35f11.x1 Gm-c1028 Glycine max cDNA clone 32 1.7
	4 1 4 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	4)) = = = = = 1) = = = = = = = = = = =
10	
10	emb AW255347 AW255347 ML358 peppermint glandular trichome Mentha 32 2.4
	emb AW349069 AW349069 GM210003B22D9R Gm-r1021 Glycine max cDNA 3 31 3.3
	emb AW597162 AW597162 sj74c10.yl Gm-c1034 Glycine max cDNA clone 31 3.3
	emb AI482974 AI482974 EST242297 tomato shoot, Cornell Lycopersic 31 3.3
1.5	emb AI482971 AI482971 EST242294 tomato shoot, Cornell Lycopersic 31 3.3
15	emb AW568662 AW568662 si60e08.yl Gm-r1030 Glycine max cDNA clone 31 3.3
	emb AI442234 AI442234 sa49d06.y1 Gm-c1004 Glycine max cDNA clone 31 3.3
	emb AI484234 AI484234 EST248461 tomato susceptible, Cornell Lyco 31 3.3
	emb AW568685 AW568685 si60g08.yl Gm-r1030 Glycine max cDNA clone 31 3.3
	emb AW218238 AW218238 EST303419 tomato radicle, 5 d post-imbibit 31 3.3
20	emb AW102024 AW102024 sd82b01.yl Gm-c1009 Glycine max cDNA clone 31 3.3
	emb AI484230 AI484230 EST248457 tomato susceptible, Cornell Lyco 31 3.3
	gb BE020040 BE020040 sm38c04.yl Gm-c1028 Glycine max cDNA clone 31 3.3
	emb AW064689 AW064689 ST34E09 Pine TriplEx shoot tip library Pin 31 4.5
	emb AI212169 AI212169 w9d03a1.fl Aspergillus nidulans 24hr asexu 31 4.5
25	emb AI938315 AI938315 sc42h10.y1 Gm-c1014 Glycine max cDNA clone 31 4.5
	emb AW010715 AW010715 ST11D03 Pine TriplEx shoot tip library Pin 31 4.5
	emb AW064688 AW064688 ST34E08 Pine TriplEx shoot tip library Pin 31 4.5
	emb AW705091 AW705091 sk57e09.yl Gm-c1019 Glycine max cDNA clone 30 6.2
	emb AW218605 AW218605 EST303788 tomato radicle, 5 d post-imbibit 30 6.2
30	emb AF039708 AF039708 Maackia amurensis early nodulin (ENOD2) mR 30 8.5
	emb AW747425 AW747425 WS1_68_B12.b1_A002 Water-stressed 1 (WS1) 30 8.5
	emb AW687627 AW687627 NF011F08RT1F1074 Developing root Medicago 30 8.5
	emb AW329000 AW329000 N200194e rootphos(-) Medicago truncatula c 30 8.5
	emb AW745895 AW745895 WS1_38_C08.b1_A002 Water-stressed 1 (WS1) 30 8.5
35	emb AW683985 AW683985 NF004G11NR1F1000 Nodulated root Medicago t 30 8.5
	emb AQ639472 AQ639472 927P1-2C7.TV 927P1 Trypanosoma brucei geno 30 8.5
	emb AW747471 AW747471 WS1_68_B12.g1_A002 Water-stressed 1 (WS1) 30 8.5
	emb AW208288 AW208288 M110945e GVSN Medicago truncatula cDNA clo 30 8.5
	the property and a second seco
40	Query= WT768 RC s at 14704 s at /id source genbank /description
•	gb aad15461.1 (ac006067) unknown protein [arabidopsis thaliana]
	/blast_score 1.00e-48 /ec number /family /chip nova /gb link /ncgi
	(315 letters)
	(5.5.10.10.10)
45	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	551,5 x 5 50quoisos, 120,111,510 total fottols
	Searchingdone
50	Score E
	Sequences producing significant alignments: (bits) Value
	(Oib) (uido
	emb AI771551 AI771551 EST252651 tomato ovary, TAMU Lycopersicon 105 1e-22
	emb AI896756 AI896756 EST266199 tomato callus, TAMU Lycopersicon 105 1e-22
55	emb AI778651 AI778651 EST259530 tomato susceptible, Cornell Lyco 105 1e-22
	emb AI898070 AI898070 EST267513 tomato ovary, TAMU Lycopersicon 105 1e-22
	emb AW030559 AW030559 EST273814 tomato callus, TAMU Lycopersicon 105 1e-22
	emb AW930095 AW930095 EST340552 tomato fruit mature green, TAMU 105 1e-22
	emb AI894447 AI894447 EST263902 tomato callus, TAMU Lycopersicon 105 1e-22
60	embla W2103091AW210309 ECT201076 Accessed and deal of the control
UV	emb AW219398 AW219398 EST301976 tomato root during/after fruit s 105 1e-22
	emb AW399345 AW399345 EST309845 L. pennellii trichome, Cornell U 104 2e-22

```
emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 104 2e-22
      emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycope... 104 3e-22
      gb|BE125244|BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh... 99 9e-21
      emb|AI736542|AI736542 sb30b04.yl Gm-c1009 Glycine max cDNA clone... 64 5e-17
 5
      emb|AI938176|AI938176 sc40e07.yl Gm-c1014 Glycine max cDNA clone... 84 2e-16
      emblAI938151lAI938151 sc40a07.yl Gm-c1014 Glycine max cDNA clone... 84 3e-16
      emb|AW133238|AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone... 84 3e-16
      emb|AW568464|AW568464 si59b03.yl Gm-r1030 Glycine max cDNA clone... 84 3e-16
      emb|AW832123|AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone... 84 5e-16
10
      emb|AI899328|AI899328 EST268771 tomato ovary, TAMU Lycopersicon ... 82 2e-15
      emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 80 6e-15
      emb|AI443600|AI443600 sa42b08.yl Gm-c1004 Glycine max cDNA clone... 72 1e-12
      gb|BE057559|BE057559 sn04a01.yl Gm-c1015 Glycine max cDNA clone ... 70 5e-12
      emb|AI896759|AI896759 EST266202 tomato callus, TAMU Lycopersicon... 61 3e-09
15
      gb|BE123900|BE123900 EST394025 DSIL Medicago truncatula cDNA clo... 58 2e-08
      emb|AW030966|AW030966 EST274273 tomato callus, TAMU Lycopersicon... 34 8e-05
      emb|AW185963|AW185963 se61h02.yl Gm-c1019 Glycine max cDNA clone... 40 0.004
      gb[T14912|T14912 crs394 lambdaZAPST Ricinus communis cDNA clone ... 40 0.004
      emb|AW184959|AW184959 se84d10.yl Gm-c1023 Glycine max cDNA clone... 40 0.004
20
      emb|AW217201|AW217201 EST295915 tomato callus, TAMU Lycopersicon... 29 0.010
      emb|AI487153|AI487153 EST245475 tomato ovary, TAMU Lycopersicon ... 35 0.14
      emb|AA556663|AA556663 518 Loblolly pine CA Pinus taeda cDNA clon... 35 0.26
      emb|AW472418|AW472418 si24h07.yl Gm-c1029 Glycine max cDNA clone... 29 0.37
      emb|AW831124|AW831124 sm09c06.yl Gm-c1027 Glycine max cDNA clone... 28 0.56
25
      gb|BE059192|BE059192 sn27d12.y1 Gm-c1016 Glycine max cDNA clone ... 32 1.3
      emb|AW101722|AW101722 sd69d02.y1 Gm-c1008 Glycine max cDNA clone... 32 1.3
      emb|AW395281|AW395281 sh46b07.yl Gm-c1017 Glycine max cDNA clone... 32 1.8
      emb|AW932541|AW932541 EST358384 tomato fruit mature green, TAMU ... 31 2.4
      emb|AV428275|AV428275 AV428275 Lotus japonicus young plants (two... 31 2.4
30
      emb|AV415030|AV415030 AV415030 Lotus japonicus young plants (two... 31 2.4
      emb|AW702436|AW702436 TgESTzz76b07.yl TgRH*-Tachyzoite cDNA Toxo... 31 2.4
      emb|AW621293|AW621293 EST312091 tomato root during/after fruit s... 31 2.4
      gb|BE036447|BE036447 MO24G12 MO Mesembryanthemum crystallinum cD... 31 2.4
      emb|AW509230|AW509230 sh92h07.yl Gm-c1016 Glycine max cDNA clone... 31 2.4
35
      emb|AW034791|AW034791 EST278827 tomato callus, TAMU Lycopersicon... 31 2.4
      emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 2,4
      gb|BE021558|BE021558 sm49e02.yl Gm-c1028 Glycine max cDNA clone ... 31 2.4
      emb|AW220250|AW220250 EST302733 tomato root during/after fruit s... 31 2.4
      emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop... 31 2.4
40
      emb|AW623982|AW623982 EST321927 tomato flower buds 3-8 mm, Corne... 29 2.5
      emb|AW719534|AW719534 LjNEST5c5rW Lotus japonicus nodule library... 31 3.3
      emb|AW926699|AW926699 HVSMEg0007O14 Hordeum vulgare pre-anthesis... 31 3.3
      emb|AL035264|LMFL8032 Leishmania major Friedlin chromosome 4 cos... 30 4.5
      emblAF015462|AF015462 Plasmodium falciparum microsatellite 14D s... 30 4.5
45
      emb|AQ989347|AQ989347 Gm_ISb001_080_I14R ISU Soybean BAC Library... 30 4.5
      emb|AL354553|LMFL232 Leishmania major Friedlin chromosome 14 cos... 30 6.2
      emb|AL049498|SPCC645 S.pombe chromosome III cosmid c645.
      emb|AI352775|AI352775 MB58-8A PZ204.BNlib Brassica napus cDNA cl... 30 6.2
      emb|AZ216688|AZ216688 Sheared DNA-84G11.TF Sheared DNA Trypanoso... 30 6.2
50
      emb|AQ160113|AQ160113 mgxb0003K19r CUGI Rice Blast BAC Library P... 30 6.2
      emb|AF105143|AF105143 Brassica napus chromosome N3 disease resis... 29 8.6
      emb|AV394954|AV394954 AV394954 Chlamydomonas reinhardtii C9 Chla...
      emb|AF162071|AF162071 Mortierella verticillata beta-tubulin 1 (b... 29 8.6
      emb|AV395268|AV395268 AV395268 Chlamydomonas reinhardtii C9 Chla... 29 8.6
55
      emb|AI960376|AI960376 sc82g12.y1 Gm-c1018 Glycine max cDNA clone... 29 8.6
      emb|AV393824|AV393824 AV393824 Chlamydomonas reinhardtii C9 Chla... 29 8.6
      emb|AW711896|AW711896 f6e11ne.r1 Neurospora crassa evening cDNA ... 29 8.6
      emb|AV396392|AV396392 AV396392 Chlamydomonas reinhardtii C9 Chla... 29 8.6
      emb|AQ659750|AQ659750 Sheared DNA-16J7.TF Sheared DNA Trypanosom... 29 8.6
60
      emb|AL163505|LMFL3640 Leishmania major Friedlin chromosome 21 co... 29 8.6
```

	Query= WT788_at 14709_at /id_source genbank /description no hits found less than or equal to 1e-15. /blast_score /ec_number /family /chip nova /gb_link
5	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb wt788 /ncgi
	http://www.ncgr.org/cgi-bin/ff?wt788
	(528 letters)
10	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
15	Score E
7.	Sequences producing significant alignments: (bits) Value
	emb AW156276 AW156276 se21h09.yl Gm-c1015 Glycine max cDNA clone 39 0:025
	emb AW688406 AW688406 NF007A07ST1F1000 Developing stem Medicago 35 0.59
20	emb AW729009 AW729009 GA_Ea0019F23 Gossypium arboreum 7-10 dpa 35 0.59
•	emb AI210929 AI210929 m0d12a1.rl Aspergillus nidulans 24hr asexu 34 0.81
	emb AI212271 AI212271 x1d11a1.rl Aspergillus nidulans 24hr asexu 34 0.81 emb AI210928 AI210928 m0d12a1.fl Aspergillus nidulans 24hr asexu 34 0.81
	emb AA783628 AA783628 c6ellal.rl Aspergillus nidulans 24hr asexu 34 0.81
25	emb AF093253 AF093253 Selaginella deflexa ribulose bisphosphate 34 1.1
	emb AW692476 AW692476 NF052A03ST1F1000 Developing stem Medicago 33 1.5
	emb AW756661 AW756661 sl25e12.yl Gm-c1027 Glycine max cDNA clone 33 1.5
	emb AW278522 AW278522 sf45e07.yl Gm-c1009 Glycine max cDNA clone 33 1.5
	emb AW424313 AW424313 sh63h04.yl Gm-c1015 Glycine max cDNA clone 33 1.5
30	emb AW696170 AW696170 NF103B07ST1F1060 Developing stem Medicago 33 1.5
	emb AW569414 AW569414 si86g10.yl Gm-c1031 Glycine max cDNA clone 33 1.5
	emb AW830833 AW830833 sm36c08.yl Gm-c1028 Glycine max cDNA clone 33 1.5
	emb AW831982 AW831982 sm18e08.yl Gm-c1027 Glycine max cDNA clone 33 1.5
0.5	emb AW734341 AW734341 sk81h11.yl Gm-c1016 Glycine max cDNA clone 33 1.5
35	emb Y07940 SSY07940 S.selaginoides chloroplast rbcL gene. 33 2.1
	emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 32 4.0
	emb AQ946352 AQ946352 Sheared DNA-45B22.TF Sheared DNA Trypanoso 31 5.5
	emb AW180477 AW180477 MgA0600f MgA Library Mycosphaerella gramin 31 5.5
40	emb AQ651798 AQ651798 Sheared DNA-20J13.TR Sheared DNA Trypanoso 31 5.5
-10	Query= af121356_f_at 15116 f at /id source genbank /description
	gb aad28243.1 af121356_1 (af121356) peroxiredoxin tpx2 [arabidopsis
	thaliana] /blast score 6.00e-81
	(647 letters)
45	
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
50	
	Score E
	Sequences producing significant alignments: (bits) Value
	emb AF133302 AF133302 Brassica rapa subsp. pekinensis type 2 per 331 2e-90
55	emb AW667697 AW667697 GA_Ea0010E14 Gossypium arboreum 7-10 dpa 287 6e-77
	emb AI778230 AI778230 EST259109 tomato susceptible, Cornell Lyco 287 6e-77
	emb AW218621 AW218621 EST303804 tomato radicle, 5 d post-imbibit 287 6e-77
•	emb AW668548 AW668548 GA_Ea0014I16 Gossypium arboreum 7-10 dpa 287 6e-77
C C	emb AW668413 AW668413 GA_Ea0013N18 Gossypium arboreum 7-10 dpa 287 6e-77
60	emb AI782495 AI782495 EST263374 tomato susceptible, Cornell Lyco 285 3e-76
	emblAI779421AI779421 EST260300 tomato susceptible. Cornell Lyco 285 3e-76

emb|AI775630|AI775630 EST256730 tomato resistant, Cornell Lycope... 285 3e-76 gb|BE055389|BE055389 GA_Ea0026N20f Gossypium arboreum 7-10 dpa ... 284 5e-76 emb|AI779420|AI779420 EST260299 tomato susceptible, Cornell Lyco... 282 2e-75 emb|AW349482|AW349482 GM210007A20G5R Gm-r1021 Glycine max cDNA 3... 282 2e-5 emblAW041006|AW041006 EST283870 tomato mixed elicitor, BTI Lycop... 279 2e-74 emb|AW597183|AW597183 sj74f03.y1 Gm-c1034 Glycine max cDNA clone... 278 3e-74 gb|BE055703|BE055703 GA Ea0033C16f Gossypium arboreum 7-10 dpa ... 275 2e-73 emb|AW567736|AW567736 si54c02.yl Gm-r1030 Glycine max cDNA clone... 275 2e-73 10 emb|AW569109|AW569109 si63e02.yl Gm-r1030 Glycine max cDNA clone... 275 2e-73 emb|AW472050|AW472050 si19d05.yl Gm-c1029 Glycine max cDNA clone... 273 8e-73 emb|AW568096|AW568096 si68d05.yl Gm-r1030 Glycine max cDNA clone... 273 1e-72 emb|AW568074|AW568074 si68b05.y1 Gm-r1030 Glycine max cDNA clone... 272 1e-72 emb|AW733947|AW733947 sk85e02.yl Gm-c1035 Glycine max cDNA clone... 271 4e-72 15 emb|AW508057|AW508057 si49e04.yl Gm-r1030 Glycine max cDNA clone... 271 4e-72 emb|AW573705|AW573705 EST316296 GVN Medicago truncatula cDNA clo... 271 4e-72 emb|AW508326|AW508326 si52e11.yl Gm-r1030 Glycine max cDNA clone... 270 7e-72 emb|AW980703|AW980703 EST391856 GVN Medicago truncatula cDNA clo... 269 1e-71 emb|AI930835|AI930835 sc47h06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71 20 emb|AI930828|AI930828 sc47g06.yl Gm-c1015 Glycine max cDNA clone... 269 1e-71 emb|AW035526|AW035526 EST281264 tomato callus, TAMU Lycopersicon... 266 1e-70 emb|AW568472|AW568472 si59c02.yl Gm-r1030 Glycine max cDNA clone... 262 2e-69 emb|AW729878|AW729878 GA _ Ea0026I18 Gossypium arboreum 7-10 dpa ... 261 4e-69 emb|AW101773|AW101773 sd70b02.yl Gm-c1008 Glycine max cDNA clone... 261 4e-69 25 emb|AW559683|AW559683 EST314795 DSIR Medicago truncatula cDNA cl... 260 6e-69 emb|AW317108|AW317108 sg44d09.yl Gm-c1025 Glycine max cDNA clone... 260 8e-69 emblAW397034|AW397034 sg66b12.yl Gm-c1007 Glycine max cDNA clone... 258 3e-68 emb|AW349372|AW349372 GM210004B12G2R Gm-r1021 Glycine max cDNA 3... 256 1e-30 emb|AW094638|AW094638 EST287806 tomato mixed elicitor, BTI Lycop... 255 3e-67 emb|AW585325|AW585325 EST306020 KV2 Medicago truncatula cDNA clo... 251 3e-66 emb|AW351217|AW351217 GM210010B20H5R Gm-r1021 Glycine max cDNA 3... 250 8eemb|AW666097|AW666097 sk32b07.yl Gm-c1028 Glycine max cDNA clone... 248 4e-65 35 emb|AW756544|AW756544 sl23d11.yl Gm-c1036 Glycine max cDNA clone... 247 6e-65 emb[AA556985]AA556985 827 Loblolly pine N Pinus taeda cDNA clone... 237 6e-62 emb|AW279163|AW279163 sf67b11.yl Gm-c1013 Glycine max cDNA clone... 237 8e-62 emb|AW201089|AW201089 se97f12.yl Gm-c1027 Glycine max cDNA clone... 236 1e-61 emb|AI162549|AI162549 A019P27U Hybrid aspen plasmid library Popu... 236 2e-61 emb|AW720300|AW720300 LjNEST20d9r Lotus japonicus nodule library... 236 2e-61 40 emb|AW065021|AW065021 ST38F08 Pine TriplEx shoot tip library Pin... 236 2e-61 emb|AI440757|AI440757 sa53g03.yl Gm-c1004 Glycine max cDNA clone... 234 6e-61 emb|AW043308|AW043308 ST31G09 Pine TriplEx shoot tip library Pin... 230 1e-59 emb|AW508348|AW508348 si52g09.y1 Gm-r1030 Glycine max cDNA clone... 229 2e-59 emb|AI774108|AI774108 EST255208 tomato resistant, Cornell Lycope... 227 7e-59 45 emb|AI163857|AI163857 A050p05u Hybrid aspen plasmid library Popu... 226 9e-59 emb|AW065077|AW065077 ST39D01 Pine TriplEx shoot tip library Pin... 225 2e-58 emb|AW704118|AW704118 sk16b03.yl Gm-c1028 Glycine max cDNA clone... 221 4e-57 emb|AI507795|AI507795 sb12g09.y1 Gm-c1004 Glycine max cDNA clone... 216 1e-55 50 emb|AW289649|AW289649 NXNV003G05F Nsf Xylem Normal wood Vertical... 215 2e-55 emb|AV422946|AV422946 AV422946 Lotus japonicus young plants (two... 122 3e-55 gb[T14824|T14824 crs266 lambdaZAPST Ricinus communis cDNA clone ... 212 2e-54 emblAW443507|AW443507 EST308437 tomato mixed elicitor, BTI Lycop... 207 6e-53 emb|AW226029|AW226029 ST76E07 Pine TriplEx shoot tip library Pin... 207 8e-53 55 emb[AW747461]AW747461 WSI 68 B01.g1 A002 Water-stressed 1 (WSI) ... 181 1e-51 emb|AI162776|AI162776 A023P56U Hybrid aspen plasmid library Popu... 132 7e-51 gb|BE054071|BE054071 GA Ea0035D19f Gossypium arboreum 7-10 dpa ... 93 4e-50 gb|C96251|C96251 C96251 Marchantia polymorpha immature sex organ... 98 5e-50 emb|AI442544|AI442544 sa32h03.y1 Gm-c1004 Glycine max cDNA clone... 196 2e-49 60 emb|AI164569|AI164569 A065P13U Hybrid aspen plasmid library Popu... 180 2e-48 emb|AW888188|AW888188 NXNV_105_F04_F Nsf Xylem Normal wood Verti... 183 1e-45

emb|AI855650|AI855650 sc32c06.yl Gm-c1014 Glycine max cDNA clone... 127 3e-45

emb|AI777234|AI777234 EST258199 tomato resistant, Cornell Lycope... 148 1e-44 emb|AI165310|AI165310 A081P03U Hybrid aspen plasmid library Popu... 152 7e-44 emb|AW870064|AW870064 NXNV_123_F09_F Nsf Xylem Normal wood Verti... 176_1e-43 emb|AI484178|AI484178 EST249331 tomato resistant, Cornell Lycope... 144 2e-43 emb|AI162101|AI162101 A012P21U Hybrid aspen plasmid library Popu... 164 3e-42 emb|AW255890|AW255890 ML976 peppermint glandular trichome Mentha... 143 7e-42 emb|AW733771|AW733771 sk84b01.yl Gm-c1035 Glycine max cDNA clone... 149 7e-42 emb|AW010084|AW010084 PC01E03 Pine TriplEx pollen cone library P... 160 7e-39 10 emb|AI161700|AI161700 A005P46U Hybrid aspen plasmid library Popu... 150 3e-38 emb|AW443795|AW443795 EST308725 tomato mixed elicitor, BTI Lycop... 157 6e-38 emb|AI774615|AI774615 EST255715 tomato resistant, Cornell Lycope... 157 6e-38 emb|AW651357|AW651357 EST329811 tomato germinating seedlings, TA... 157 6e-38 emb|AW623884|AW623884 EST321829 tomato flower buds 3-8 mm, Corne... 157 6e-38 15 emb|AI484189|AI484189 EST249342 tomato resistant, Cornell Lycope... 157 9e-38 gb|L37653|L37653 BNAESTGU Mustard flower buds Brassica rapa cDNA... 156 1e-37 emb|AW944894|AW944894 EST336944 tomato flower buds 3-8 mm, Corne... 154 8e-37 emb|AW726742|AW726742 GA Ea0022J15 Gossypium arboreum 7-10 dpa ... 152 2e-36 emb|AW694116|AW694116 NF072H11ST1F1095 Developing stem Medicago ... 150 2e-36 20 emb|AW649234|AW649234 EST327688 tomato germinating seedlings, TA... 151 5e-36 emb|AW725828|AW725828 GA_Ea0019N04 Gossypium arboreum 7-10 dpa ... 95 8e-36 emb|AI777997|AI777997 EST258876 tomato susceptible, Cornell Lyco... 149 3e-35 emb[AW317704]AW317704 sg56c06.y1 Gm-c1007 Glycine max cDNA clone... 148 4e-35 emb|AW432260|AW432260 sh71d04.y1 Gm-c1015 Glycine max cDNA clone... 143 2e-33 25 emb|AI165031|AI165031 A073p61u Hybrid aspen plasmid library Popu... 131 6e-32 emb|AI507718|AI507718 sb10g09.yl Gm-c1004 Glycine max cDNA clone... 131 2e-31 emb|AW756555|AW756555 sl23g03.yl Gm-c1036 Glycine max cDNA clone... 133 2e-30 emb|AI164114|AI164114 A055P05U Hybrid aspen plasmid library Popu... 89 2e-29 emb|AV428084|AV428084 AV428084 Lotus japonicus young plants (two... 127 1e-28 30 emb|AI899479|AI899479 EST268922 tomato susceptible, Cornell Lyco... 124 7e-28 emb|AI460396|AI460396 sa81a06.y1 Gm-c1004 Glycine max cDNA clone... 119 2e-26 emb|AT002745|AT002745 AT002745 POSLM01 Pleurotus ostreatus cDNA ... 116 9e-26 emb|AW508566|AW508566 si33e04.y1 Gm-r1030 Glycine max cDNA clone... 115 4e-25 emb|AI166161|AI166161 B00964U Hybrid aspen plasmid library Popul... 113 1e-24 35 Query= atu90522 s at 15161 s at /id source genbank /description gblaab53975.1 (u90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [arabidopsis thaliana] /blast score 0 (3267 letters) 40 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 45 Score Sequences producing significant alignments: (bits) Value emb|AI486200|AI486200 EST244521 tomato ovary, TAMU Lycopersicon ... 377 e-103 50 emb|AI894899|AI894899 EST264342 tomato callus, TAMU Lycopersicon... 357 4e-97 emb|AI488742|AI488742 EST247081 tomato ovary, TAMU Lycopersicon ... 347 2e-94 emb|AF042184|AF042184 Brassica napus lysine-ketoglutarate reduct... 334 1e-93 emb|AI054604|AI054604 coau0001I01 Cotton Boll Abscission Zone cD... 319 3e-92 emb|AW034280|AW034280 EST277851 tomato callus, TAMU Lycopersicon... 316 7e-85 emb|AI894874|AI894874 EST264317 tomato callus, TAMU Lycopersicon... 307 4e-82 emb|AW932187|AW932187 EST358030 tomato fruit mature green, TAMU ... 294 2e-78 emb|AW933092|AW933092 EST358935 tomato fruit mature green, TAMU ... 287 4e-76 emb|AW442160|AW442160 EST311556 tomato fruit red ripe, TAMU Lyco... 220 8e-74 emb|AW681014|AW681014 WS1_8 B05.b1 A002 Water-stressed 1 (WS1) S... 275 1e-72 60 emb|AW933411|AW933411 EST359350 tomato fruit mature green, TAMU ... 272 1e-71 emblAW931846|AW931846 EST357689 tomato fruit mature green, TAMU ... 264 3e-69

```
emb|AI485129|AI485129 EST243433 tomato ovary, TAMU Lycopersicon ... 253 8e-66
       emb|AW035300|AW035300 EST280663 tomato callus, TAMU Lycopersicon... 241 3e-62
       emb|AW934545|AW934545 EST353353 tomato flower buds 0-3 mm, Corne... 230 4e-59
       emb|AI771941|AI771941 EST253041 tomato ovary, TAMU Lycopersicon ... 228 2e-58
  5
       emb|AL022244|SPBC3B8 S.pombe chromosome II cosmid c3B8.
       emb|AW037965|AW037965 EST279609 tomato mixed elicitor, BTI Lycop... 211 2e-53
      emb|AW931630|AW931630 EST357473 tomato fruit mature green, TAMU ... 208 3e-52
      emb|AW035261|AW035261 EST280523 tomato callus, TAMU Lycopersicon... 142 4e-52
      emb|AI896768|AI896768 EST266211 tomato callus, TAMU Lycopersicon... 192 2e-47
 10
      emb|Z71665|SCYNR050C S.cerevisiae chromosome XIV reading frame O... 155 5e-47
      emb|X77363|SCLYS9 S.cerevisiae LYS9 gene.
      emb|AW224200|AW224200 EST301107 tomato fruit red ripe, TAMU Lyco... 188 2e-46
      emb|AW930672|AW930672 EST356515 tomato fruit mature green, TAMU ... 110 4e-45
      emb|AI771935|AI771935 EST253035 tomato ovary, TAMU Lycopersicon ... 173 6e-42
15
      emb|AI899372|AI899372 EST268815 tomato ovary, TAMU Lycopersicon ... 172 1e-41
      emb|AI486726|AI486726 EST245048 tomato ovary, TAMU Lycopersicon ... 110 2e-40
      emb|AI483615|AI483615 EST249479 tomato ovary, TAMU Lycopersicon ... 110 2e-40
      emb|AW441656|AW441656 EST311052 tomato fruit red ripe, TAMU Lyco... 110 2e-38
      emb|AI486762|AI486762 EST245084 tomato ovary, TAMU Lycopersicon ... 161 3e-38
20
      emb|AI488387|AI488387 EST246709 tomato ovary, TAMU Lycopersicon ... 160 6e-38
      emb|AW093830|AW093830 EST287010 tomato mixed elicitor, BTI Lycop... 98 4e-33
      emb|AV427683|AV427683 AV427683 Lotus japonicus young plants (two... 142 2e-32
      emb|AI782310|AI782310 EST263189 tomato susceptible, Cornell Lyco... 139 1e-31
      emb|AW432287|AW432287 sh71g03.y1 Gm-c1015 Glycine max cDNA clone... 82 6e-31
25
      emb|AL111972|CNS019QK Botrytis cinerea strain T4 cDNA library un... 136 1e-30
      emb|AU012735|AU012735 AU012735 Schizosaccharomyces pombe late lo... 125 5e-30
      emb|AI771382|AI771382 EST252482 tomato ovary, TAMU Lycopersicon ... 132 1e-29
      emb|AW681093|AW681093 WS1_8_B05.g1_A002 Water-stressed 1 (WS1) S... 127 7e-28
      emblAU010645|AU010645 AU010645 Schizosaccharomyces pombe late lo... 118 2e-25
30
      emb|AW038858|AW038858 EST280814 tomato mixed elicitor, BTI Lycop... 114 5e-24
      emb|AW201969|AW201969 sf09e01.yl Gm-c1027 Glycine max cDNA clone... 113 9e-24
      emb|AI487518|AI487518 EST245840 tomato ovary, TAMU Lycopersicon ... 110 6e-23
      emb|AI486763|AI486763 EST245085 tomato ovary, TAMU Lycopersicon ... 110 6e-23
      emb|AI399018|AI399018 NCW10A5T3 Westergaards Neurospora crassa c... 63 1e-21
35
      emb|AW031018|AW031018 EST274325 tomato callus, TAMU Lycopersicon... 101 4e-20
      emb|AW932183|AW932183 EST358026 tomato fruit mature green, TAMU ... 72 9e-13
      emb|AW096237|AW096237 EST289417 tomato mixed elicitor, BTI Lycop... 67 8e-10
      emb|AA577639|AA577639 EST213 Sugarcane leaf roll Saccharum sp. c... 65 3e-09
      emb|AW224318|AW224318 EST301045 tomato fruit red ripe, TAMU Lyco... 51 5e-05
40
      emb|AI900022|AI900022 sb97g03.yl Gm-c1012 Glycine max cDNA clone... 50 1e-04
      gb]M34929|YSJSACDHY Y.lipolytica saccharopine dehydrogenase (LYS... 46 0.002
      emb|Z38061|SC9168 S.cerevisiae chromosome IX cosmid 9168.
                                                                     45 0.004
      emb[X77362]SCLYS1 S.cerevisiae LYS1 gene.
                                                               45 0.004
      emb|AQ448181|AQ448181 mgxb0018C10r CUGI Rice Blast BAC Library P... 41 0.041
45
      gb|U13233|CAU13233 Candida albicans saccharopine dehydrogenase (... 40 0.078
      emb|AL110979|CNS018Z0 Botrytis cinerea strain T4 cDNA library un... 35 0.079
      emb|AL133156|SPAC227 S.pombe chromosome I cosmid c227.
                                                                      40 0.15
      emb|AF178855|AF178855 Candida albicans Crm1p (CRM1) gene, comple... 37 0.99
      emb|AI667978|AI667978 TENG0800 T. Cruzi epimastigote normalised ... 36 1.4
50
      emb|AW310192|AW310192 sf32e10.x1 Gm-c1028 Glycine max cDNA clone... 36 1.4
      emb|AW705872|AW705872 sk52a01.yl Gm-c1019 Glycine max cDNA clone... 35 2.6
      emblAL355930[NCB2O8 Neurospora crassa DNA linkage group II BAC c... 35 3.5
      gb|N82089|N82089 TgESTzy41f01.rl TgRH Tachyzoite cDNA Toxoplasma... 35 3.5
      emb|AW713255|AW713255 g6f04ne.fl Neurospora crassa evening cDNA ... 33 4.1
55
      emb|AW710105|AW710105 e1c07ne.fl Neurospora crassa evening cDNA ... 33 4.1
      emb|AW712320|AW712320 g1a02ne.f1 Neurospora crassa evening cDNA ... 33 4.2
      emb|AA451583|AA451583 AJK252 Onion seedling leaf cDNA library Al... 35 4.8
      emblAQ660868|AQ660868 Sheared DNA-27G4.TF Sheared DNA Trypanosom...
      emb|AI773473|AI773473 EST254573 tomato resistant, Cornell Lycope... 30 5.4
60
      emb|X99000|CS39KBCIV S.cerevisiae 39kb DNA segment of chromosome... 34 6.7
      gb|BE021261|BE021261 sm56g06.yl Gm-c1028 Glycine max cDNA clone ... 34 6.7
```

5	emb AA556567 AA556567 422 Loblolly pine C Pinus taeda cDNA clone 34 6.7 emb Z74265 SCYDL217C S.cerevisiae chromosome IV reading frame OR 34 6.7 emb Z73529 SCYPL173W S.cerevisiae chromosome XVI reading frame O 34 6.7 emb AI486066 AI486066 EST244387 tomato ovary, TAMU Lycopersicon 34 6.7 emb AV420631 AV420631 AV420631 Lotus japonicus young plants (two 34 6.7 emb AW759867 AW759867 sl55b07.yl Gm-c1027 Glycine max cDNA clone 34 6.7 emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai 34 9.2 emb AW278000 AW278000 sf89e04.yl Gm-c1019 Glycine max cDNA clone 34 9.2
10	emb AL033391 CAC20C1 C.albicans cosmid Ca20C1. 34 9.2 emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1 34 9.2 emb AW648458 AW648458 EST326912 tomato germinating seedlings, TA 34 9.2 emb AA051847 AA051847 Cn0025-5 Cryptococcus neoformans, Stratage 34 9.2 emb AI960767 AI960767 sc90b07.y1 Gm-c1019 Glycine max cDNA clone 34 9.2 emb Z49384 SCYJL109C S.cerevisiae chromosome X reading frame ORF 34 9.2
15	emb AF106954 AF106954 Brassica napus galactinol synthase (GS) mR 34 9.2 emb AW164589 AW164589 se73h03.y1 Gm-c1023 Glycine max cDNA clone 34 9.2 emb AW731148 AW731148 GA_Ea0010C07 Gossypium arboreum 7-10 dpa 34 9.2 emb AW308914 AW308914 sf91g02.y1 Gm-c1019 Glycine max cDNA clone 34 9.2 emb X85021 SCXLTORFS S.cerevisiae DNA from left arm of chromosom 34 9.2
20	emb AV423166 AV423166 AV423166 Lotus japonicus young plants (two 34 9.2 emb Z99164 SPAC29B12 S.pombe chromosome I cosmid c29B12. 29 9.4
25	Query= athpro25a_s_at 15616_s_at /id_source genbank /description emb caa08794.1 (aj009696) wall-associated kinase 1 [arabidopsis thaliana] /blast_score 0 (2138 letters)
30	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
35	Score E Sequences producing significant alignments: (bits) Value
40	emb AW565461 AW565461 LG1_344_F11.g1_A002 Light Grown 1 (LG1) So 269 7e-71 emb AW455238 AW455238 EST311898 tomato root during/after fruit s 229 1e-63 emb AW568861 AW568861 si73b10.y1 Gm-c1031 Glycine max cDNA clone 139 3e-61 emb AI487264 AI487264 EST245586 tomato ovary, TAMU Lycopersicon 205 1e-55 emb AI485585 AI485585 EST243906 tomato ovary, TAMU Lycopersicon 205 1e-54 emb AW667985 AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa 128 4e-54
45	emb AI485223 AI485223 EST243527 tomato ovary, TAMU Lycopersicon 203 5e-54 emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon 205 7e-54 gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK 162 1e-53 emb AI486547 AI486547 EST244868 tomato ovary, TAMU Lycopersicon 150 1e-53 gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine 165 1e-53
50	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon 205 3e-53 emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k 168 5e-53 emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc 163 9e-53 gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp 170 8e-52
55	emb AI485022 AI485022 EST243302 tomato ovary, TAMU Lycopersicon 205 1e-51 emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon 205 1e-51 emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon 205 1e-51 emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti 160 2e-51 emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei 144 2e-51 emb AW616916 AW616916 EST323327 L. hirsutum trichome, Cornell Un 145 3e-51
60	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds. 165 1e-50 emb AI487456 AI487456 EST245778 tomato ovary, TAMU Lycopersicon 139 3e-50 gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR 154 7e-50 gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase 164 7e-50

```
emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7...
                                                                        96 2e-49
       emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein.
                                                                       156 le-48
       emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 153 3e-48
       emb|AW266297|AW266297 L30-3030T3 Ice plant Lambda Uni-Zap XR exp... 169 3e-48
  5
       emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 154 4e-48
       emb|Al898374|Al898374 EST267817 tomato ovary, TAMU Lycopersicon ... 192 1e-47
       emb|Al484550|Al484550 EST242780 tomato ovary, TAMU Lycopersicon ... 191 2e-47
      emb|AI967314|AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two... 89 3e-47
      dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 127 5e-47
10
      emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 153 7e-47
      emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 152 7e-47
      emb|AI483733|AI483733 EST249604 tomato ovary, TAMU Lycopersicon ... 188 1e-46
      emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 127 1e-46
      emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 150 1e-46
15
      gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 126 2e-46
      gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 151 3e-46
      emb|AW597214|AW597214 si71g06.y1 Gm-c1031 Glycine max cDNA clone... 187 4e-46
      emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 156 6e-46
      emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 185 9e-46
20
      emb[Y14286]BOY14286 Brassica oleracea SFR3 gene, partial.
                                                                    91 le-45
      emb|AW774582|AW774582 EST333733 KV3 Medicago truncatula cDNA clo... 81 1e-45
      emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 81 1e-45
      dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 127 2e-45
      dbi|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 134 2e-45
25
      emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 145 2e-45
      emb|A1898918|A1898918 EST268361 tomato ovary, TAMU Lycopersicon ... 183 5e-45
      emb|AF131222|AF131222 Lophopyrum elongatum protein serine/threon... 138 2e-44
      emb|AW756743|AW756743 sl26f10.yl Gm-c1027 Glycine max cDNA clone... 181 2e-44
      emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 96 2e-44
30
      emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 132 3e-44
      emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 151 4e-44
      emb|AI489009|AI489009 EST247348 tomato ovary, TAMU Lycopersicon ... 117 7e-44
      emb|AI483732|AI483732 EST249603 tomato ovary, TAMU Lycopersicon ... 177 4e-43
      emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 153 6e-43
      gb|U59315|LPU59315 Lycopersicon pimpinellifolium serine/threonin... 88 1e-42
      gb|U02271|LEU02271 Lycopersicon pimpinellifolium Rio Grande-PtoR... 88 1e-42
      emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 80 2e-42
      emb|AI490032|AI490032 EST248371 tomato ovary, TAMU Lycopersicon ... 149 2e-42
      emb|AW220490|AW220490 EST297043 tomato fruit mature green, TAMU ... 116 2e-42
40
      gb|U28007|LEU28007 Lycopersicon esculentum Pto kinase interactor... 83 3e-42
      emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 143 4e-42
      emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 149 6e-42
      emb|AW684940|AW684940 NF023C12NR1F1000 Nodulated root Medicago t... 113 6e-42
      emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 78 8e-42
45
      gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 87 1e-41
      emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 93 1e-41
      emb|AW220491|AW220491 EST297044 tomato fruit mature green, TAMU ... 116 2e-41
      dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 81 2e-41
      dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 81 2e-41
50
      emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 77 3e-41
      emb|AW220489|AW220489 EST297042 tomato fruit mature green, TAMU ... 112 3e-41
      emb|AI937984|AI937984 sc06e07.yl Gm-c1012 Glycine max cDNA clone... 170 5e-41
      emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 75 1e-40
      emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 127 1e-40
55
      emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 122 1e-40
      emb|AW672145|AW672145 LG1_357_A10.b1_A002 Light Grown 1 (LG1) So... 167 2e-40
      gb|U59317|LPU59317 Lycopersicon pimpinellifolium serine/threonin... 93 3e-40
      gb|U13923|LEU13923 Lycopersicon pimpinellifolium serine/threonin... 93 3e-40
      emb|Z73295|CRPK1 C.roseus mRNA for receptor-like protein kinase.
60
      gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 92 6e-40
```

emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 129 1e-39. emb|A67797|A67797 Sequence 2 from Patent WO9743427. gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 125 1e-39 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 72 2e-39 emb|AW284352|AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So... 165 2e-39 emb[Y14600]SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 123 2e-39 emb|AW222552|AW222552 EST299363 tomato fruit red ripe, TAMU Lyco... 82 2e-39 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 70 4e-39 emb|AI901283|AI901283 sc31d08.yl Gm-c1014 Glycine max cDNA clone... 163 5e-39 10 emblAB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 71 5e-39 emblAW223870|AW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 99 6e-39 gb|BE053916|BE053916 GA_Ea0031D03f Gossypium arboreum 7-10 dpa ... 77 le-38 emb|AW760240|AW760240 sl59g07.yl Gm-c1027 Glycine max cDNA clone... 130 2e-38 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 73 3e-38 15 Query= ab003280 s at 15629 s at /id source genbank /description dbj|baa24440.1| (ab010407) phosphoglycerate dehydrogenase [arabidopsis thaliana]/blast score 0 20 (2127 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 25 Searching.....done E Score Sequences producing significant alignments: (bits) Value 30 emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 403 e-111 emb|AW625643|AW625643 EST319550 tomato radicle, 5 d post-imbibit... 377 e-103 emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 367 e-100 emb|AW666282|AW666282 sk34f11.yl Gm-c1028 Glycine max cDNA clone... 360 2e-98 emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 332 5e-96 , 35 gb|BE055044|BE055044 GA_ Ea0031H08f Gossypium arboreum 7-10 dpa ... 332 9e-95 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 347 3e-94 emb|AW926942|AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... 295 6e-89 emb|AW737130|AW737130 EST338557 tomato flower buds, anthesis, Co... 325 1e-87 emb|AW689358|AW689358 NF018C09ST1F1000 Developing stem Medicago ... 281 3e-85 40 emb|AW650696|AW650696 EST329150 tomato germinating seedlings, TA... 179 2e-84 emb|AW625020|AW625020 EST313849 tomato radicle, 5 d post-imbibit... 301 1e-80 emblAI813214|AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... 297 2e-80 emb|AW692700|AW692700 NF054C07ST1F1000 Developing stem Medicago ... 279 6e-80 gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 258 2e-79 45 gb|BE020170|BE020170 sm39e05.yl Gm-c1028 Glycine max cDNA clone ... 293 3e-78 emb|AW423801|AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone... 293 4e-78 gb|BE052354|BE052354 GA Ea0034P16f Gossypium arboreum 7-10 dpa ... 282 5e-75 emb|AW687344|AW687344 NF008F03RT1F1029 Developing root Medicago ... 269 5e-71 50 emb|AW926887|AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... 264 1e-69 emb|AW944677|AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two... 248 1e-64 emb|AW755716|AW755716 sl08b12.yl Gm-c1036 Glycine max cDNA clone... 234 2e-60 emb|AW923236|AW923236 DG1_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg... 233 3e-60 55 gb|BE060782|BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... 226 7e-58 emb|AW203801|AW203801 sf38d05.y1 Gm-c1028 Glycine max cDNA clone... 215 1e-54 emb|AW317181|AW317181 sf38d05.x1 Gm-c1028 Glycine max cDNA clone... 200 4e-50 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 177 2e-43 emb|AW650818|AW650818 EST329272 tomato germinating seedlings, TA... 148 2e-42

emb|AW697347|AW697347 NF115F08ST1F1074 Developing stem Medicago ... 168 2e-40 emb|AW428657|AW428657 Ljirnpest22-731-a5 Ljirnp Lambda HybriZap ... 168 2e-40

60

	emb AW695961 AW695961 NF101A09ST1F1068 Developing stem Medicago 168 2e-40
	emb AV395160 AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla 164 2e-39
	ambit W00700418 W007004 EST242221 and the other field at the Committee Commi
	emb AW907004 AW907004 EST343231 potato stolon, Cornell Universit 163 5e-39
_	emb AW736943 AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti 161 1e-38
5	gb BE123645 BE123645 NXNV_150_D07_F Nsf Xylem Normal wood Vertic 158 1e-37
	gb LA7851 LA7851 BNAF1389 Mustard flower buds Brassica rapa cDNA 155 le-36
	gb BE058285 BE058285 sn14b01.yl Gm-c1016 Glycine max cDNA clone 152 8e-36
	gb BE055879 BE055879 GA_Ea0026P04f Gossypium arboreum 7-10 dpa 149 5e-35
	amble 4.66000714 4.66007 0.0004 1.60117 1.41 0.000711111 atooleum 7-10 dpa 149 36-33
10	emb AA660997 AA660997 00894 MtRHE Medicago truncatula cDNA 5' si 72 2e-34
10	emb AW693956 AW693956 NF071B03ST1F1027 Developing stem Medicago 92 8e-33
	emb AI165568 AI165568 A086P59U Hybrid aspen plasmid library Popu 137 1e-31
	emb AV428639 AV428639 AV428639 Lotus japonicus young plants (two 133 7e-30
	emb AV408249 AV408249 AV408249 Lotus japonicus young plants (two 133 7e-30
	emb Z97052 SPCC4G3 S.pombe chromosome III cosmid c4G3. 82 7e-30
15	gb BE060772 BE060772 HVSMEg0013F04f Hordeum vulgare pre-anthesis 99 2e-29
, ,	dbiE12500E12500 Nucleotide comment of the control o
	dbj E12500 E12500 Nucleotide sequence of eta gene of cephalospor 78 2e-29
	emb AJ273311 AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575 77 4e-28
	emb AA840711 AA840711 CAN22 Anther cDNA library of Hot pepper Ca 93 5e-28
	emb AW688606 AW688606 NF009E07ST1F1000 Developing stem Medicago 124 2e-27
20	emb AC005761 AC005761 Leishmania major chromosome 3 clone L952 s 78 5e-27
	emb AL157811 SPAC186 S.pombe chromosome I cosmid c186. 90 2e-26
	gb U18839 SCE9747 Saccharomyces cerevisiae chromosome V cosmids 80 2e-23
	emb AL033389 SPBC1773 S.pombe chromosome II cosmid c1773. 106 1e-22
^~	emb Z37997 SC9877 S.cerevisiae chromosome IX cosmid 9877. 80 2e-22
25	emb AW689996 AW689996 NF026G01ST1F1000 Developing stem Medicago 91 7e-20
	emb AL031180 SPUNK4 S.pombe chromosome I cosmid c2E11. 99 2e-19
	dbj D89185 D89185 Schizosaccharomyces pombe mRNA, partial cds, c 99 2e-19
	emb AF079881 AF079881 Entodinium caudatum D-3-phosphoglycerate d 53 2e-19
	emb AW736063 AW736063 EST332049 KV3 Medicago truncatula cDNA clo 93 9e-18
30	gb BE054038 BE054038 GA_Ea0008F24f Gossypium arboreum 7-10 dpa 88 2e-16
	11177770000711777700007 1 0 0 0 0 0 0 0
	gb[U43503 SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi 84 3e-15
	emb AW283359 AW283359 LG1_223_C04.g1_A002 Light Grown 1 (LG1) So 84 5e-15
25	emb AW625680 AW625680 EST319587 tomato radicle, 5 d post-imbibit 83 le-14
35	emb AI486949 AI486949 EST245271 tomato ovary, TAMU Lycopersicon 83 1e-14
	emb Z71550 SCYNL274C S.cerevisiae chromosome XIV reading frame O 83 1e-14
	emb AW442114 AW442114 EST311510 tomato fruit red ripe, TAMU Lyco 83 1e-14
	emb AW030822 AW030822 EST274077 tomato callus, TAMU Lycopersicon 83 1e-14
	emb AI484846 AI484846 EST243107 tomato ovary, TAMU Lycopersicon 83 1e-14
40	emb AW442123 AW442123 EST311519 tomato fruit red ripe, TAMU Lyco 83 1e-14
	emb AW651324 AW651324 EST329778 tomato germinating seedlings, TA 83 1e-14
	1143776400711437764004450000000000000000000000000000000
	1 1701 4000 (7000007777 0 . 4
	emb ZZ1493 MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 83 1e-14
15	emb AI822999 AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr 82 1e-14
45	emb AW693443 AW693443 NF065D03ST1F1000 Developing stem Medicago 71 2e-14
	emb AI488120 AI488120 EST246442 tomato ovary, TAMU Lycopersicon 80 5e-14
	emb AT000538 AT000538 AT000538 Brassica rapa guard cell Brassica 80 7e-14
	emb AI490350 AI490350 EST248676 tomato ovary, TAMU Lycopersicon 79 9e-14
	emb AQ874261 AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st 79 1e-13
50	emb AI490396 AI490396 EST248734 tomato ovary, TAMU Lycopersicon 78 2e-13
	dbj D88272 D88272 Hordeum vulgare mRNA for formate dehydrogenase 78 3e-13
	emb AW266848 AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr 74 3e-12
c	emb AI897727 AI897727 EST267170 tomato ovary, TAMU Lycopersicon 74 4e-12
55	emb AI898003 AI898003 EST267446 tomato ovary, TAMU Lycopersicon 74 4e-12
	emb AI898454 AI898454 EST267897 tomato ovary, TAMU Lycopersicon 74 4e-12
	emb AI898267 AI898267 EST267710 tomato ovary, TAMU Lycopersicon 74 4e-12
	emb AW278707 AW278707 sf96b06.yl Gm-c1019 Glycine max cDNA clone 73 6e-12
	emb AI483926 AI483926 EST249797 tomato ovary, TAMU Lycopersicon 73 8e-12
60	emb AW930862 AW930862 EST356705 tomato fruit mature green, TAMU 73 1e-11
•	emblA18990381A1899038 FST268481 tomato overy TAMILI yeonemican 73 lo 11

gb|BE055276|BE055276 GA_Ea0034L16f Gossypium arboreum 7-10 dpa ... 57 2e-11 emb|AI488243|AI488243 EST246565 tomato ovary, TAMU Lycopersicon ... 72 2e-11 emb|AW153099|AW153099 se34h11.yl Gm-c1015 Glycine max cDNA clone... 71 4e-11 emb|AI940852|AI940852 sb80b11.y1 Gm-c1010 Glycine max cDNA clone... 71 4e-11 5 emb|AW100275|AW100275 sd22a06.y2 Gm-c1012 Glycine max cDNA clone... 71 4e-11 emb|AW164250|AW164250 se23h05.yl Gm-c1015 Glycine max cDNA clone... 70 5e-11 emb|AW981354|AW981354 EST392507 DSIL Medicago truncatula cDNA cl... 69 1e-10 10 Query= afl 17063 s at 15641 s at /id source genbank /description gb|aad10829.1| (af117063) putative inositol polyphosphate 5-phosphatase at5p2 [arabidopsis thaliana] /blast score 0 (2458 letters) 15 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 20 Score E Sequences producing significant alignments: (bits) Value emb|AI898446|AI898446 EST267889 tomato ovary, TAMU Lycopersicon ... 209 e-108 emb|AW217248|AW217248 EST295962 tomato callus, TAMU Lycopersicon... 245 3e-89 25 emb|AI485780|AI485780 EST244101 tomato ovary, TAMU Lycopersicon ... 242 2e-86 emb|AI485695|AI485695 EST244016 tomato ovary, TAMU Lycopersicon ... 261 5e-86 emb|AI899197|AI899197 EST268640 tomato ovary, TAMU Lycopersicon ... 161 2e-78 emb|AI485239|AI485239 EST243543 tomato ovary, TAMU Lycopersicon ... 291 1e-77 emb|AW034573|AW034573 EST278257 tomato callus, TAMU Lycopersicon... 272 9e-72 30 emb|AI488812|AI488812 EST247151 tomato ovary, TAMU Lycopersicon ... 251 1e-65 emb|AW687082|AW687082 NF005G09RT1F1071 Developing root Medicago ... 182 7e-65 emb|AI898248|AI898248 EST267691 tomato ovary, TAMU Lycopersicon ... 206 2e-64 emb|AI483614|AI483614 EST249464 tomato ovary, TAMU Lycopersicon ... 238 1e-61 emb|AI897089|AI897089 EST266532 tomato ovary, TAMU Lycopersicon ... 226 8e-58 35 emb|AW774994|AW774994 EST334145 KV3 Medicago truncatula cDNA clo... 182 3e-56 emb|AW559604|AW559604 EST314652 DSIR Medicago truncatula cDNA cl... 177 4e-53 emb|AI485284|AI485284 EST243588 tomato ovary, TAMU Lycopersicon ... 206 5e-52 emb|AI485664|AI485664 EST243985 tomato ovary, TAMU Lycopersicon ... 198 2e-49 emb[AW774741]AW774741 EST333892 KV3 Medicago truncatula cDNA clo... 90 2e-48 40 emb|AI487608|AI487608 EST245930 tomato ovary, TAMU Lycopersicon ... 187 3e-46 emb|AI483438|AI483438 EST249259 tomato ovary, TAMU Lycopersicon ... 169 7e-41 emb|AI485008|AI485008 EST243271 tomato ovary, TAMU Lycopersicon ... 157 3e-37 emb|AI938737|AI938737 sb58c06.y1 Gm-c1018 Glycine max cDNA clone... 151 2e-35 emb|AI967736|AI967736 Ljirnpest11-837-a7 Ljirnp Lambda HybriZap ... 147 4e-34 45 emb|AW775688|AW775688 EST334753 DSIL Medicago truncatula cDNA cl... 108 8e-34 emb|Z50161|SCC14ORFS S.cerevisiae orfs and LEU4, MET4, POL1, RAS... 60 1e-33 emb|Z71382|SCYNL106C S.cerevisiae chromosome XIV reading frame O... 60 1e-33 emb|AI973618|AI973618 sd07d04.y1 Gm-c1020 Glycine max cDNA clone... 141 3e-32 emb|AI485392|AI485392 EST243713 tomato ovary, TAMU Lycopersicon ... 138 2e-31 50 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 51 1e-29 emb|Z75017|SCYOR109W S.cerevisiae chromosome XV reading frame OR... 51 1e-29 emb|AL022103|SPBC2G2 S.pombe chromosome II cosmid c2G2. 78 3e-27 emb|X79743|SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes. 72 3e-27 emb|Z38062|SC9687 S.cerevisiae chromosome IX cosmid 9687. emb|AI488810|AI488810 EST247149 tomato ovary, TAMU Lycopersicon ... 121 3e-26 gb|BE020060|BE020060 sm38e06.yl Gm-c1028 Glycine max cDNA clone ... 118 2e-25 emb|AW685248|AW685248 NF028A10NR1F1000 Nodulated root Medicago t... 116 2e-24 emb|AW257207|AW257207 EST305344 KV2 Medicago truncatula cDNA clo... 75 2e-24 emb|AV406995|AV406995 AV406995 Lotus japonicus young plants (two... 67 2e-23 60 emb|AW034093|AW034093 EST277588 tomato callus, TAMU Lycopersicon... 111 3e-23 emb|Z98763|SPAC9G1 S.pombe chromosome I cosmid c9G1.

```
emb|AQ502761|AQ502761 V84A11 mTn-3xHA/lacZ Insertion Library Sac... 52 2e-22
      emb|AI897134|AI897134 EST266577 tomato ovary, TAMU Lycopersicon ... 107 4e-22
      emb|AI771644|AI771644 EST252744 tomato ovary, TAMU Lycopersicon ... 104 4e-21
      emb|AW731056|AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ... 100 5e-20
      emb|AV413397|AV413397 AV413397 Lotus japonicus young plants (two... 100 9e-20
      emb|AW616540|AW616540 EST322951 L. hirsutum trichome, Cornell Un... 98 2e-19
      emb|AL110506|SPBC577 S.pombe chromosome II cosmid c577.
      emb|AW126841|AW126841 ga16f04.yl Moss EST library PPU Physcomitr... 94 4e-18
      emb|AI780067|AI780067 EST260946 tomato susceptible, Cornell Lyco... 94 6e-18
10
      emb|AW687035|AW687035 NF005C05RT1F1037 Developing root Medicago ... 73 2e-17
      emb|AW685930|AW685930 NF036F03NR1F1000 Nodulated root Medicago t... 73 2e-17
      emb|AV415287|AV415287 AV415287 Lotus japonicus young plants (two... 90 5e-17
      gb|BE124605|BE124605 EST393640 GVN Medicago truncatula cDNA clon... 65 6e-15
      emb|AW220291|AW220291 EST302774 tomato root during/after fruit s... 68 le-14
15
      emblAQ644913|AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso... 53 2e-13
      emb|AA495505|AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil... 49 5e-13
      emb|AW830613|AW830613 sm04c07.yl Gm-c1027 Glycine max cDNA clone... 77 5e-13
      emb|AW666237|AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone... 77 5e-13
      emb|AW285758|AW285758 LG1 223 C03.b1 A002 Light Grown 1 (LG1) So... 74 5e-12
      emb|AQ658256|AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom... 73 1e-11
      emb|AW704333|AW704333 sk18a03.y1 Gm-c1028 Glycine max cDNA clone... 71 5e-11
      emb|AV390446|AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla... 70 6e-11
      emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 64 8e-11
      emb|AW695904|AW695904 NF099H04ST1F1043 Developing stem Medicago ... 49 2e-10
25
      emb|AZ048449|AZ048449 PSB67 Barley PstI genomic clones Hordeum v... 67 8e-10
      emb|AW760518|AW760518 sl51d02.yl Gm-c1027 Glycine max cDNA clone... 66 1e-09
      emb|AW332143|AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car... 36 1e-09
      emb|AW687790|AW687790 NF013E04RT1F1034 Developing root Medicago ... 65 3e-09
      emb|AI486692|AI486692 EST245014 tomato ovary, TAMU Lycopersicon ... 54 3e-09
30
      emb|AW333870|AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c... 36 5e-09
      emb|AQ850639|AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra... 44 6e-09
      emb|AW127178|AW127178 M110117 GVN Medicago truncatula cDNA clone... 63 1e-08
      emb|AW616547|AW616547 EST322958 L. hirsutum trichome, Cornell Un... 62 2e-08
      emb|AW399291|AW399291 EST309791 L. pennellii trichome, Cornell U... 62 2e-08
35
      emb|AW693686|AW693686 NF068A05ST1F1036 Developing stem Medicago ... 62 3e-08
      emb|AW208046|AW208046 M111077e DSIR Medicago truncatula cDNA clo... 61 5e-08
      emb|AQ642482|AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos... 53 7e-08
      emb|AW686583|AW686583 NF039G02NR1F1000 Nodulated root Medicago t... 45 5e-07
      emb|AQ849089|AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra... 44 6e-06
40
      emb|AI781410|AI781410 EST262277 tomato susceptible, Cornell Lyco... 52 2e-05
      emb|AW617564|AW617564 EST323975 L. hirsutum trichome, Cornell Un... 49 2e-04
      emb|AQ946427|AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom... 47 Se-04
      emb|AW099113|AW099113 sd34f04.yl Gm-c1012 Glycine max cDNA clone... 46 0.002
      emb|Z74807|SCYOL065C S.cerevisiae chromosome XV reading frame OR... 29 0.003
45
      emb|AQ655271|AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso... 38 0.004
      emb|AW685854|AW685854 NF031A06NR1F1000 Nodulated root Medicago t... 43 0.009
      emb|AW437996|AW437996 ST83C09 Pine TriplEx shoot tip library Pin... 42 0.016
      emb|AI440709|AI440709 sa62e11.yl Gm-c1004 Glycine max cDNA clone... 31 0.045
      emb|AW979881|AW979881 EST341528 tomato root deficiency, Cornell ... 37 0.54
50
      emblAF263282|AF263282 Filobasidiella neoformans var. neoformans ... 34 0.64
      emb|AW702543|AW702543 TgESTzz85a12.yl TgRH*-Tachyzoite cDNA Toxo... 32 0.69
      emb|AZ214873|AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso... 37 0.74
      emb|AQ939979|AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso... 37 0.74
      emb|AQ651205|AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso... 37 0.74
      emb|AQ945454|AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso... 37 0.74
      emb|AW774740|AW774740 EST333891 KV3 Medicago truncatula cDNA clo... 36 1.4
      emb|Z38060|SC5610 S.cerevisiae chromosome IX sequence derived fr... 36 1.4
      emb|AL049183|PFMAL13P6 Plasmodium falciparum chromosome 13 strai... 35 2.6
      gb|M28064|PFAHRKP Plasmodium brasilianum DNA homologous to the h... 35 2.6
60
      emb|AI482770|AI482770 EST242093 tomato shoot, Cornell Lycopersic... 35 2.6
      emb|AQ653909|AQ653909 Sheared DNA-1G20.TR Sheared DNA Trypanosom... 35 2.6
```

Query= af022658 s at 15665 s at /id source genbank /description

gb|aab80922.1| (af022658) putative c2h2 zinc finger transcription 5 factor [arabidopsis thaliana] /blast score 3.00e-94 (938 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching......done Score Sequences producing significant alignments: (bits) Value 15 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 71 1e-35 emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 71 3e-35 emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 70 3e-33 20 emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 70 7e-31 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 68 3e-30 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 68 8e-30 emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 70 1e-29 gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 70 1e-29 25 emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 70 9e-29 emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 64 1e-28 dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 69 1e-28 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 68 4e-28 emb|AI988290|AI988290 sc98f10.yl Gm-c1020 Glycine max cDNA clone... 64 3e-27 30 emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 69 2e-26 emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 69 3e-26 emb|AW616587|AW616587 EST322998 L. hirsutum trichome, Cornell Un... 68 5e-26 gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 69 5e-26 emb|AW278572|AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone... 65 8e-26 35 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 68 9e-26 dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 60 1e-25 emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 68 1e-25 emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 67 2e-25 emb|AW164639|AW164639 se74f02.yl Gm-c1023 Glycine max cDNA clone... 67 2e-25 40 emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 71 2e-25 gb[BE059872]BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ... 71 4e-25 gb|U76554|BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR... 63 9e-25 gb[U76555]BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA... 62 3e-24 emb|AI966679|AI966679 sc55a11.yl Gm-c1015 Glycine max cDNA clone... 64 4e-24 45 emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 62 6e-24 emb|AI488218|AI488218 EST246540 tomato ovary, TAMU Lycopersicon ... 62 9e-24 emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 59 4e-23 emb[Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 67 8e-23 emb|AW030858|AW030858 EST274148 tomato callus, TAMU Lycopersicon... 66 9e-23 50 emb|AW032112|AW032112 EST275566 tomato callus, TAMU Lycopersicon... 68 5e-22 emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 59 8e-21 emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 66 2e-20 emb|AI485651|AI485651 EST243972 tomato ovary, TAMU Lycopersicon ... 62 2e-20 emb|AW033574|AW033574 EST277145 tomato callus, TAMU Lycopersicon... 66 2e-20 55 emb|AI896031|AI896031 EST265474 tomato callus, TAMU Lycopersicon... 66 3e-20 emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 66 3e-20 emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 66 3e-20 emb|AW219736|AW219736 EST302218 tomato root during/after fruit s... 59 1e-19 emb|AW219517|AW219517 EST301915 tomato root during/after fruit s... 59 2e-19 60 emb|AW706014|AW706014 sk64g01.y1 Gm-c1016 Glycine max cDNA clone... 69 1e-18

emb|AV426673|AV426673 AV426673 Lotus japonicus young plants (two... 60 5e-18

```
emblAV423639lAV423639 AV423639 Lotus japonicus young plants (two... 66 7e-18
       gb|BE021759|BE021759 sm62a09.yl Gm-c1028 Glycine max cDNA clone ... 71 3e-17
       emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 55 4e-17
      emb|AW720367|AW720367 LjNEST21g11r Lotus japonicus nodule librar... 64 6e-17
  5
      emb|AW648971|AW648971 EST327425 tomato germinating seedlings, TA... 59 9e-17
      emb|AB000455|AB000455 Petunia hybrida mRNA for PEThy; ZPT4-1, com... 60 1e-16
      gb|BE058334|BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ... 62 le-16
      emb|AW035987|AW035987 EST282846 tomato callus, TAMU Lycopersicon... 55 2e-16
      emb|AV422432|AV422432 AV422432 Lotus japonicus young plants (two... 66 3e-16
10
      emb|AW277333|AW277333 sf80a11.yl Gm-c1019 Glycine max cDNA clone... 64 4e-16
      emb|AI900061|AI900061 sb98d02.yl Gm-c1012 Glycine max cDNA clone... 64 5e-16
      emb|AW684558|AW684558 NF018C10NR1F1000 Nodulated root Medicago t... 63 6e-16
      emb|AI960244|AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone... 64 7e-16
      emb|AI055219|AI055219 coau0003G03 Cotton Boll Abscission Zone cD... 62 1e-15
15
      emb|AI736394|AI736394 sb28a06.yl Gm-c1009 Glycine max cDNA clone... 67 5e-15
      emb|AI894999|AI894999 EST264442 tomato callus, TAMU Lycopersicon... 68 9e-15
      emb|AW622660|AW622660 EST313460 tomato root during/after fruit s... 68 9e-15
      emb|AW755973|AW755973 sl11h06.yl Gm-c1036 Glycine max cDNA clone... 64 4e-14
      emb|AI938565|AI938565 sb55e03.yl Gm-c1018 Glycine max cDNA clone... 64 4e-14
20
      emb|AB035133|AB035133 Petunia x hybrida gene for C2H2 zinc-finge... 52 1e-13
      emb|AB006605|AB006605 Petunia x hybrida mRNA for ZPT3-3, complet... 52 1e-13
      emb|AB035132|AB035132 Petunia x hybrida gene for C2H2 zinc-finge... 50 4e-13
      emblAB006597|AB006597 Petunia x hybrida mRNA for ZPT2-10, comple... 50 4e-13
      emb|AB006606|AB006606 Petunia x hybrida mRNA for ZPT4-4, complet... 51 8e-13
25
      emb|AW684455|AW684455 NF017B06NR1F1000 Nodulated root Medicago t... 54 8e-13
      emb|AW776204|AW776204 EST335269 DSIL Medicago truncatula cDNA cl... 65 1e-12
      emb|AB000451|AB000451 Petunia hybrida mRNA for PEThy; ZPT2-5, com... 50 2e-12
      emb|AI485306|AI485306 EST243610 tomato ovary, TAMU Lycopersicon ... 66 2e-12
      emb|AW216968|AW216968 EST295682 tomato callus, TAMU Lycopersicon... 55 2e-12
30
      emb|AV422972|AV422972 AV422972 Lotus japonicus young plants (two... 60 3e-12
      emb|AV423707|AV423707 AV423707 Lotus japonicus young plants (two... 60 3e-12
      emb|AV424707|AV424707 AV424707 Lotus japonicus young plants (two... 60 3e-12
      emb|AV411009|AV411009 AV411009 Lotus japonicus young plants (two... 60 3e-12
      emb|AV413230|AV413230 AV413230 Lotus japonicus young plants (two... 60 3e-12
35
      emb|AV418453|AV418453 AV418453 Lotus japonicus young plants (two... 60 3e-12
      emb|AV412443|AV412443 AV412443 Lotus japonicus young plants (two... 60 3e-12
      emb|AV411580|AV411580 AV411580 Lotus japonicus young plants (two...
      emb|AV412455|AV412455 AV412455 Lotus japonicus young plants (two...
      emb|AB006600|AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...
40
      emb|AW687462|AW687462 NF009H03RT1F1031 Developing root Medicago ... 50 4e-12
      emblAB006603|AB006603 Petunia x hybrida mRNA for ZPT2-8, complet... 49 5e-12
      emb|AB006601|AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...
      emb|AI442517|AI442517 sa32e09.y1 Gm-c1004 Glycine max cDNA clone...
      gb|BE023156|BE023156 sm79a08.yl Gm-c1015 Glycine max cDNA clone ...
                                                                           69 le-11
45
      dbj|D16415|WHTWZF1A Wheat gene for WZF1, complete cds.
                                                                      56 le-11
      dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds.
                                                                        56 le-11
      emb|AB006599|AB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 48 1e-11
      emb|AW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 48 1e-11
      emb|AV424248|AV424248 AV424248 Lotus japonicus young plants (two... 58 1e-11
50
      emb|AI775063|AI775063 EST256163 tomato resistant, Cornell Lycope... 59 2e-11
      emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 59 2e-11
      emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 59 2e-11
      emb|AB006602|AB006602 Petunia x hybrida mRNA for ZPT2-7, complet... 49 2e-11
      emb|AI959966|AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone...
55
```

Query= ab004796_s_at 16061_s_at /id_source genbank /description gb|aab97145.1| (af000977) mek1 [arabidopsis thaliana] thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1352 letters)

60

WO 02/22675

Database: plantfungal

```
661,018 sequences; 426,114,510 total letters
       Searching.....done
  5
                                          Score E
       Sequences producing significant alignments:
                                                         (bits) Value
       emblAJ000728 LEAJ728 Lycopersicon esculentum mRNA for MAP kinase... 555 e-157
10
       emb|AF165186|AF165186 Nicotiana tabacum MAP kinase kinase mRNA, ... 540 e-153
       emb|AW945105|AW945105 EST337156 tomato flower buds 3-8 mm, Corne... 318 6e-86
       emb|AW756736|AW756736 sl26f02.yl Gm-c1027 Glycine max cDNA clone... 174 9e-75
       dbj|D31964|TOBNPK2 Tobacco mRNA for protein kinase (NPK2), compl... 183 8e-65
       15
      emb|AW220008|AW220008 EST302491 tomato root during/after fruit s... 228 6e-59
      emb|AW624623|AW624623 EST322568 tomato flower buds 3-8 mm, Corne... 215 9e-55
      emb|AI438023|AI438023 sa34h10.y1 Gm-c1004 Glycine max cDNA clone... 208 7e-53
       emb|AW617901|AW617901 EST296829 L. hirsutum trichome, Cornell Un... 203 2e-51
      emb|AJ007393|YLI7393 Yarrowia lipolytica ste7 gene.
                                                                92 4e-49
20
      emb|AW931392|AW931392 EST357235 tomato fruit mature green, TAMU ... 189 3e-47
      emb|AW039087|AW039087 EST281060 tomato mixed elicitor, BTI Lycop... 183 2e-45
      emb|Z99259|SPAC2C4 S.pombe chromosome I cosmid c2C4.
      emb|AW032808|AW032808 EST276367 tomato callus, TAMU Lycopersicon... 175 9e-43
      gb|U07801|UMU07801 Ustilago maydis serine/threonine/tyrosine kin... 121 2e-42
25
      emb|AJ009609|BNA9609 Brassica napus mRNA for MAP4K alpha2 protein. 87 1e-41
      dbi|D13001|YSCSSP32 Yeast Mkk1/SSP32 gene for Mkk1 protein kinas... 72 3e-41
      emb|Z75139|SCYOR231W S.cerevisiae chromosome XV reading frame OR... 72 3e-41
      emb|AF169644|AF169644 Glomerella cingulata MAP kinase kinase (EM... 82 7e-41
      emb|AJ009608|BNA9608 Brassica napus mRNA for MAP4K alpha 1 protein. 82 8e-41
30
      emb|AW127406|AW127406 M110589 DSIL Medicago truncatula cDNA clon... 94 2e-39
      emb|AJ225532|AJ225532 AJ225532 Abscisic acid-treated protonemata... 162 5e-39
      emb|AZ215495|AZ215495 Sheared DNA-56D6.TR Sheared DNA Trypanosom... 113 3e-38
      dbj|D13785|YSCMKK2 S.cerevisiae gene for Mkk2 protein kinase, co... 68 1e-37
      gb|U72980|CAU72980 Candida albicans Map kinase kinase (STE7) gen... 128 2e-37
35
      gb|L19195|YSASTKIN Candida albicans (clone pKB66) serine/threoni... 128 2e-37
      emb|AL109822|SPBC409 S.pombe chromosome II cosmid c409.
      gb|U43703|SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi... 68 2e-37
      emb[X62631|SPWIS1 S.pombe wis1 gene for protein kinase.
                                                                  68 3e-37
      emb|AW625928|AW625928 EST319823 tomato radicle, 5 d post-imbibit... 90 8e-37
40
      emb|AW348493|AW348493 GM210002B12A8R Gm-r1021 Glycine max cDNA 3... 154 1e-
      36
      emb|AZ213240|AZ213240 Sheared DNA-102E10.TF Sheared DNA Trypanos... 140 3e-36
      emb|AW497308|AW497308 ga57h06.y1 Moss EST library PPU Physcomitr... 150 2e-35
      emb|Z49403|SCYJL128C S.cerevisiae chromosome X reading frame ORF... 78 5e-35
45
      gb|U12237|SCU12237 Saccharomyces cerevisiae suppressor of fluori... 78 5e-35
      gb|J02946|YSCPBS2 Saccharomyces cerevisiae putative protein kina... 78 5e-35
      emblAJ243184LIN243184 Leishmania infantum mkk gene for putative... 78 2e-34
      emb|AW032663|AW032663 EST276222 tomato callus, TAMU Lycopersicon... 82 2e-34
      emb|AJ243118|LME243118 Leishmania mexicana mkk gene for putative... 78 3e-34
50
      emb|AJ243187|LTR243187 Leishmania tropica mkk gene for putative ... 78 3e-34
      emb|AJ243188|LMA243188 Leishmania major mkk gene for putative mi... 78 3e-34
      emb|AJ243183|LAM243183 Leishmania amazonensis mkk gene for putat... 78 3e-34
      emb|AJ243186|LAE243186 Leishmania aethiopica mkk gene for putati... 78 3e-34
      emb|AW185502|AW185502 se80e12.yl Gm-c1023 Glycine max cDNA clone... 85 6e-34
      gb|U16029|U16029 Leishmania donovani protein kinase (lpk) mRNA, ... 78 1e-33
55
      emb|AJ243185|LDO243185 Leishmania donovani mkk gene for putative... 78 1e-33
      emb|AI781759|AI781759 EST262638 tomato susceptible, Cornell Lyco... 97 3e-33
      gb|BE059041|BE059041 sn24d08.y1 Gm-c1016 Glycine max cDNA clone ... 143 3e-33
      emb|AW929787|AW929787 EST354057 tomato flower buds 8 mm to pre-a... 102 9e-32
60
      emb|AW981083|AW981083 EST392236 GVN Medicago truncatula cDNA clo... 88 3e-31
      gb|BE036317|BE036317 MO23C02 MO Mesembryanthemum crystallinum cD... 82 1e-30
```

	emb AF069777 AF069777 Cryphonectria parasitica mitogen-activated 66 2e-30
	emb AW099876 AW099876 sd17g06.y2 Gm-c1012 Glycine max cDNA clone 80 3e-30
	emb AF249887 AF249887 Pneumocystis carinii map kinase kinase (mk 72 6e-30
	emb AW622016 AW622016 EST312814 tomato root during/after fruit s 97 7e-29
5	emb Z69239 SPAC1D4 S.pombe chromosome I cosmid c1D4. 116 2e-28
	emb X07445 SPBYR1 Fission yeast byr1 gene. 116 2e-28
	emb Z67750 SC41KCIV S.cerevisiae DNA (cosmid 31A2; chromosome IV 77 7e-28
	emb X97751 SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RPC 77 7e-28
	emb Z74207 SCYDL159W S.cerevisiae chromosome IV reading frame OR 77 8e-28
10	gb M14097 YSCSTE7 Yeast (S. cerevisiae) regulatory gene STE7, com 77 8e-28
	dbj D26601 TOBPK Tobacco mRNA for protein kinase, complete cds. 54 1e-27
	dbj E05289 E05289 DNA encoding a protein kinase that is homologo 54 1e-27
	emb AL358652 LMFP1408 Leishmania major Friedlin chromosome 14 PA 100 3e-27
	emb AW349565 AW349565 GM210005A21F10R Gm-r1021 Glycine max cDNA 85 4e-27
15	
13	emb AF169643 AF169643 Glomerella cingulata MAP kinase kinase (EM 74 5e-27
	emb AQ849880 AQ849880 LMAJFV1_lm51a11.x1 Leishmania major FV1 ra 104 1e-26
	emb AW564378 AW564378 LG1_292_H08.b1_A002 Light Grown 1 (LG1) So 121 1e-26
	emb AC005140 AC005140 Plasmodium falciparum chromosome 12 clone 88 2e-26
20	emb AW030150 AW030150 EST273405 tomato callus, TAMU Lycopersicon 120 3e-26
20	emb Z28126 SCYKL126W S.cerevisiae chromosome XI reading frame OR 84 5e-26
	gb M21307 YSCPKN Yeast (S.cerevisiae) protein kinase (YPK1) gene 84 7e-26
	emb AW676925 AW676925 DG1_2_B05.b1_A002 Dark Grown 1 (DG1) Sorgh 89 9e-26
	emb Z49702 SC9718 S.cerevisiae chromosome XIII cosmid 9718. 85 9e-26
0.5	gb M24929 YSCYKR2A Saccharomyces cerevisiae protein kinase (YKR2 85 9e-26
25	emb AI779511 AI779511 EST260390 tomato susceptible, Cornell Lyco 118 1e-25
	emb AZ048376 AZ048376 LMAJFV1_lm77f10.x1 Leishmania major FV1 ra 100 1e-25
	gb U11581 YSCHL5018 Saccharomyces cerevisiae chromosome VIII cos 86 2e-25
	gb M94719 YSCSTE20P Saccharomyces cerevisiae protein kinase (Ste 86 2e-25
	gb L04655 YSCSERKIN Saccharomyces cerevisiae serine/threonine ki 86 2e-25
30	emb AW922296 AW922296 DG1_17_G11.g1_A002 Dark Grown 1 (DG1) Sorg 116 4e-25
	emb Z98763 SPAC9G1 S.pombe chromosome I cosmid c9G1. 92 4e-25
	emb AE001376 AE001376 Plasmodium falciparum chromosome 2, sectio 49 6e-25
	emb Z97211 SPBC2F12 S.pombe chromosome II cosmid c2F12. 56 2e-24
0.5	emb Z98270 SPBC1D7 S.pombe chromosome II cosmid c1D7. 56 2e-24
35	emb AW351150 AW351150 GM210011A20C11R Gm-r1021 Glycine max cDNA 78 2e-24
	gb M74293 YSPBYR2 Schizosaccharomyces pombe byr2 gene, complete 56 2e-24
	emb X68851 SPSTE8A S.pombe ste8 gene encoding protein kinase. 56 2e-24
	emb AJ238845 BNA238845 Brassica napus mRNA for MAP3K epsilon 1 p 78 3e-24
40	gb L47210 YSASTPK Candida albicans serine/threonine protein kina 86 8e-24
40	gb U73457 CAU73457 Candida albicans Cst20p (CST20) gene, complet 86 8e-24
	emb AJ005079 AJKL5079 Kluyveromyces lactis BCK1 gene, complete CDS. 51 8e-24
	emb AF157632 AF157632 Schizosaccharomyces pombe MAPK kinase Skh1 73 2e-23
	dbj D82023 D82023 Schizosaccharomyces pombe mkkl+ gene for MAP k 73 2e-23
	emb AF034090 AF034090 Neurospora crassa MAPKK kinase (nrc-1) gen 58 2e-23
45	emb AQ501953 AQ501953 V11H7 mTn-3xHA/lacZ Insertion Library Sacc 72 2e-23
	emb AL034433 SPBC1604 S.pombe chromosome II cosmid c1604. 87 4e-23
	gb[U22371 SPU22371 Schizosaccharomyces pombe Paklp (PAK1) mRNA, 87 5e-23
	gb[L41552 YSPSHK1A Schizosaccharomyces pombe Ste20 homologous pr 87 5e-23
50	
	Query= af153283_s_at 16083_s_at /id_source genbank /description
	gb aad34615.1 af153283_1 (af153283) putative progesterone-binding
	protein homolog [arabidopsis thaliana] /blast_score 1.00e-116
	(930 letters)
55	
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
60	Searchingdone
60	

Score E

Sequences producing significant alignments:

(bits) Value

gb|BE052137|BE052137 GA Ea0031L11f Gossypium arboreum 7-10 dpa ... 257 8e-77 emb|AW727234|AW727234 GA__Ea0011E21 Gossypium arboreum 7-10 dpa ... 257 1e-76 5 emb|AW737982|AW737982 EST339409 tomato flower buds, anthesis, Co... 287 2e-76 emb|AW626347|AW626347 EST320254 tomato radicle, 5 d post-imbibit... 287 2e-76 emb|AW622517|AW622517 EST313317 tomato root during/after fruit s... 287 2e-76 emb|AW623663|AW623663 EST321608 tomato flower buds 3-8 mm, Corne... 287 2e-76 10 emb|AW622008|AW622008 EST312806 tomato root during/after fruit s... 287 2e-76 emb|AI777165|AI777165 EST258130 tomato resistant, Cornell Lycope... 287 2e-76 emb|AW730733|AW730733 GA_Ea0027113 Gossypium arboreum 7-10 dpa ... 254 7e-76 emb|AW705652|AW705652 sk50g08.yl Gm-c1019 Glycine max cDNA clone... 248 1e-74 emb|AW755296|AW755296 sl01c07.yl Gm-c1036 Glycine max cDNA clone... 245 6e-74 emb|AW775898|AW775898 EST334963 DSIL Medicago truncatula cDNA cl... 243 2e-71 15 emb|AW774377|AW774377 EST333528 KV3 Medicago truncatula cDNA clo... 242 4e-71 emb|AW620616|AW620616 sj07e05.yl Gm-c1032 Glycine max cDNA clone... 230 3e-69 emb|AW398755|AW398755 EST309255 L. pennellii trichome, Cornell U... 251 3e-68emb|AW559353|AW559353 EST314401 DSIR Medicago truncatula cDNA cl... 231 6e-68 20 emblAI727590|AI727590 BNLGHi8481 Six-day Cotton fiber Gossypium ... 226 2e-67 emb|AW696709|AW696709 NF109H10ST1F1091 Developing stem Medicago ... 211 7e-67 gb|T24185|T24185 crs173 lambdaZAPST Ricinus communis cDNA clone ... 254 2e-66 emb|AW255061|AW255061 ML1356 peppermint glandular trichome Menth... 219 4e-64 emb|AW678629|AW678629 WS1 1 D02.b1 A002 Water-stressed 1 (WS1) S... 245 1e-63 emb|AW672535|AW672535 LG1 360_B02.b1_A002 Light Grown 1 (LG1) So... 245 1e-63 25 emb|AW678699|AW678699 WS1_1_D02.b2_A002 Water-stressed 1 (WS1) S... 245_1e-63 emb|AI776227|AI776227 EST257327 tomato resistant, Cornell Lycope... 244 3e-63 emb|AI899451|AI899451 EST268894 tomato susceptible, Cornell Lyco... 242 9e-63 gb|BE125791|BE125791 DG1_57_D06.b1_A002 Dark Grown 1 (DG1) Sorgh... 241 2e-62 30 emb|AI482787|AI482787 EST242110 tomato shoot, Cornell Lycopersic... 241 2e-62 gb|BE123902|BE123902 EST394027 DSIL Medicago truncatula cDNA clo... 231 2e-62 emb|AW704889|AW704889 sk40g12.yl Gm-c1019 Glycine max cDNA clone... 241 2e-62 emb|AW185657|AW185657 se81h10.yl Gm-c1023 Glycine max cDNA clone... 238 1e-61 emb|AW254869|AW254869 ML1292 peppermint glandular trichome Menth... 211 1e-61 35 emb[AW255550]AW255550 ML584 peppermint glandular trichome Mentha... 237 4e-61 emb|AW704813|AW704813 sk55h01.yl Gm-c1019 Glycine max cDNA clone... 236 5e-61 emb|AI895103|AI895103 EST264546 tomato callus, TAMU Lycopersicon... 232 7e-60 gb|BE059713|BE059713 sn35h07.yl Gm-c1016 Glycine max cDNA clone ... 232 7e-60 emb|AW705371|AW705371 sk48b10.y1 Gm-c1019 Glycine max cDNA clone... 228 2e-58 40 emb|AW755523|AW755523 s105a05.y1 Gm-c1036 Glycine max cDNA clone... 223 4e-57 emb|AW201709|AW201709 sf06d02.yl Gm-c1027 Glycine max cDNA clone... 216 6e-55 emb|AW203472|AW203472 sf30f04.yl Gm-c1028 Glycine max cDNA clone... 216 6e-55 emb|AI161953|AI161953 A010P20U Hybrid aspen plasmid library Popu... 149 2e-54 emb|AI162696|AI162696 A022P09U Hybrid aspen plasmid library Popu... 152 2e-54 45 emb|AV410373|AV410373 AV410373 Lotus japonicus young plants (two... 186 4e-54 emb|AW217074|AW217074 EST295788 tomato callus, TAMU Lycopersicon... 213 5e-54 emb|AI441526|AI441526 sa67a03.yl Gm-c1004 Glycine max cDNA clone... 177 2e-53 emb|AW678831|AW678831 WS1 _1 _D02.g1 A002 Water-stressed 1 (WS1) S... 208 2e-52 50 emb|AW100277|AW100277 sd22a12.y2 Gm-c1012 Glycine max cDNA clone... 192 2e-52 emblAW745340lAW745340 WS1 33 H02.b1 A002 Water-stressed 1 (WS1) ... 154 4e-48 emb|AW185605|AW185605 se79h09.yl Gm-c1023 Glycine max cDNA clone... 193 6e-48 emb|AW278821|AW278821 sf99a06.y1 Gm-c1019 Glycine max cDNA clone... 192 8e-48 gb|BE035142|BE035142 MM03H05 MM Mesembryanthemum crystallinum cD... 178 1e-47 emb|AW255911|AW255911 ML998 peppermint glandular trichome Mentha... 124 2e-47 55 emb|AW683421|AW683421 NF011G07LF1F1055 Developing leaf Medicago ... 190 4e-47 emb|AI778919|AI778919 EST259798 tomato susceptible, Cornell Lyco... 188 1e-46 emb|AI938231|AI938231 sc41d07.yl Gm-c1014 Glycine max cDNA clone... 184 2e-45 emb|AW677289|AW677289 DG1_7_D03.b1_A002 Dark Grown 1 (DG1) Sorgh... 182 1e-44 60 emb|AW287668|AW287668 LG1_244_H12.b1_A002 Light Grown 1 (LG1) So... 180 4e-44 emb|AW625474|AW625474 EST319381 tomato radicle, 5 d post-imbibit... 156 1e-41

	emb AI729205 AI729205 BNLGHi12887 Six-day Cotton fiber Gossypium 171 1e-41 emb AI941012 AI941012 sb83c05.yl Gm-c1010 Glycine max cDNA clone 168 1e-40 emb AI855517 AI855517 sc20b06.yl Gm-c1013 Glycine max cDNA clone 168 1e-40
	emb AV429287 AV429287 AV429287 Lotus japonicus young plants (two 163 3e-39
5	emb AW255564 AW255564 ML599 peppermint glandular trichome Mentha 137 7e-39
	emb AW677432 AW677432 DG1_7_F03.b1_A002 Dark Grown 1 (DG1) Sorgh 157 3e-37
	emb AV426850 AV426850 AV426850 Lotus japonicus young plants (two 126 3e-37
	gb BE125876 BE125876 DG1_59_A12.b1_A002 Dark Grown 1 (DG1) Sorgh 155 1e-36
	gb BE125862 BE125862 DG1_58_G08.b1_A002 Dark Grown 1 (DG1) Sorgh 155 1e-36
10	emb AV417826 AV417826 AV417826 Lotus japonicus young plants (two 121 7e-36
	emb AV426599 AV426599 AV426599 Lotus japonicus young plants (two 121 7e-36
	emb AI812547 AI812547 12F5 Pine Lambda Zap Xylem library Pinus t 150 2e-35
	emb AW145544 AW145544 ga26e09.y1 Moss EST library PPN Physcomitr 149 6e-35
15	emb AW156347 AW156347 se22h07.yl Gm-c1015 Glycine max cDNA clone 147 3e-34
13	emb AI482794 AI482794 EST242117 tomato shoot, Cornell Lycopersic 146 5e-34
	gb BE125045 BE125045 DG1_14_A09.b1_A002 Dark Grown 1 (DG1) Sorgh 144 1e-33 emb AW092409 AW092409 EST285589 tomato mixed elicitor, BTI Lycop 141 2e-32
	emb AI774296 AI774296 EST255312 tomato resistant, Cornell Lycope 141 2e-32
	emb AW037498 AW037498 EST276719 tomato mixed elicitor, BTI Lycop 141 2e-32
20	emb AW037272 AW037272 EST274122 tomato mixed elicitor, BTI Lycop 141 2e-32
	emb[AW094681]AW094681 EST287849 tomato mixed elicitor, BTI Lycop 141 2e-32
	emb AW649965 AW649965 EST328419 tomato germinating seedlings, TA 141 2e-32
	emb AW041262 AW041262 EST284126 tomato mixed elicitor, BTI Lycop 139 4e-32
	gb BE022031 BE022031 sm65f07.yl Gm-c1028 Glycine max cDNA clone 139 6e-32
25	emb AW093288 AW093288 EST286468 tomato mixed elicitor, BTI Lycop 136 4e-31
	emb AW596364 AW596364 sj02e02.yl Gm-c1032 Glycine max cDNA clone 80 6e-31
	emb AW981553 AW981553 PC14A01 Pine TriplEx pollen cone library P 135 8e-31
	emb AW832150 AW832150 sm20d11.yl Gm-c1027 Glycine max cDNA clone 135 1e-30
20	emb AI440919 AI440919 sa56f12.yl Gm-c1004 Glycine max cDNA clone 135 1e-30
30	emb AW349246 AW349246 GM210004B21F9R Gm-r1021 Glycine max cDNA 3 134 1e-30
	emb AW759979 AW759979 sl56e07.yl Gm-c1027 Glycine max cDNA clone 134 2e-30
	emb AW782208 AW782208 sm02h06.y1 Gm-c1027 Glycine max cDNA clone 134 2e-30
	emb AW832627 AW832627 sm14h06.y1 Gm-c1027 Glycine max cDNA clone 134 2e-30 emb AW666184 AW666184 sk33d03.y1 Gm-c1028 Glycine max cDNA clone 121 3e-30
35	emb AW925882 AW925882 HVSMEg0005M05 Hordeum vulgare pre-anthesis 133 3e-30
55	emb AW559445 AW559445 EST314493 DSIR Medicago truncatula cDNA cl 132 7e-30
	emb AW761414 AW761414 sl67b12.y1 Gm-c1027 Glycine max cDNA clone 130 2e-29
	emb AW754652 AW754652 PC04G03 Pine TriplEx pollen cone library P 130 3e-29
	emb AW679942 AW679942 WS1_33 H02.gl A002 Water-stressed 1 (WS1) 129 5e-29
40	emb AW754728 AW754728 PC07B03 Pine TriplEx pollen cone library P 127 3e-28
	emb AW756987 AW756987 sk82g11.yl Gm-c1016 Glycine max cDNA clone 126 4e-28
15	Query= athlsp83_s_at 16091_s_at /id_source
45	/description gb aaa32822.1 (m62984) heat shock protein 83
	[arabidopsis thaliana] /blast_score 0 (2390 letters)
	(2590 letters)
	Database: plantfungal
50	661,018 sequences; 426,114,510 total letters
•	Searchingdone
	Score E
55	Sequences producing significant alignments: (bits) Value
	1 B (00 42 1 B) TO TO DO A D1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2
	gb M99431 PHNHSP83A Pharbitis nil heat shock protein 83 (Hsp83) 597 0.0
	gb M96549 TOMHSC80P Tomato heat shock cognate protein 80 gene, 3 577 0.0
60	gb U55859 TAU55859 Triticum aestivum heat shock protein 80 mRNA, 575 0.0 emb X98582 TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0
00	emb[X63195]NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0

	emb AF123259 AF123259 Lycopersicon esculentum heat shock protein 483 0.0
	emb AF165818 AF165818 Guillardia theta nucleomorph 5S ribosomal 505 0.0 emb AF042329 AF042329 Eimeria tenella heat shock protein 90 (hsp 514 0.0
	gb M57386 THEHSP90 T.parva heat shock protein 90 (hsp90) mRNA, c 500 0.0
5	emb Z29667 PFHESHPR P.falciparum (7) mRNA for heat-shock protein. 507 0.0
	gb U45449 EBU45449 Eimeria bovis heat shock protein 90 (hsp90) m 495 0.0
	emb AF151114 AF151114 Tetrahymena thermophila strain B2086 hsp82 486 0.0
	emb AF136649 AF136649 Babesia bovis heat shock protein 90 (HSP90 487 0.0
	gb M15346 TRBHSC T.cruzi tandemly repeated gene encoding an 85 k 457 0.0
10	emb X14176 TBHSP83 Trypanosoma brucei HSP83 gene. 452 0.0
	gb M73492 LEIHSP90 Leishmania donovani heat shock protein 90 mRN 456 0.0
	emb X87770 LIHSP83GN L.infantum hsp83 gene. 454 0.0
	gb[M92926]LEIHSP01 Leishmania amazonensis heat shock protein 83 449 0.0
	gb U92465 AFU92465 Aspergillus fumigatus heat shock protein (Hsp 458 e-165
15	emb AF212996 AF212996 Neurospora crassa heat shock protein 80 ge 473 e-165
	emb AL110469 SPAC926 S.pombe chromosome I cosmid c926. 460 e-165
•	gb L35550 YSPHSP90X Schizosaccharomyces pombe heat shock protein 460 e-162
	gb U81165 PAU81165 Podospora anserina suppressor of vegetative i 292 e-161
	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb). 448 e-159
20	emb Z73596 SCYPL240C S.cerevisiae chromosome XVI reading frame O 448 e-159
-	gb K01387 YSCHSP82A Yeast (S.cerevisiae) HSP82 (heat shock-induc 448 e-159
	emb X81025 CAHSP90 C.albicans hsp90 gene. 451 e-159
	emb AF251005 AF251005 Candida tropicalis heat shock protein 90 g 444 e-158
25	emb Z49808 SC8010 S.cerevisiae chromosome XIII cosmid 8010. 447 e-158
23	emb AF221856 AF221856 Euphorbia esula heat-shock protein 80 mRNA 292 e-158
	gb M26044 YSCHSC82 S. cerevisiae HSC82 gene encoding hsc82, the 447 e-157 emb AW729825 AW729825 GAEa0026E04 Gossypium arboreum 7-10 dpa 473 e-134
	emb AW727612 AW727612 GA_Ea0026E04 Gossypium arboreum 7-10 dpa 473 e-134 emb AW727612 AW727612 GA_Ea0015C16 Gossypium arboreum 7-10 dpa 454 e-132
	emb AI489832 AI489832 EST248171 tomato ovary, TAMU Lycopersicon 471 e-132
30	emb AW982575 AW982575 HVSMEg0003K07f Hordeum vulgare pre-anthesi 471 e-131
-	emb AW774793 AW774793 EST333944 KV3 Medicago truncatula cDNA clo 459 e-128
	emb AW221746 AW221746 EST298557 tomato fruit red ripe, TAMU Lyco 350 e-128
	emb AW728021 AW728021 GAEa0029G22 Gossypium arboreum 7-10 dpa 315 e-127
	gb BE035845 BE035845 MO11A12 MO Mesembryanthemum crystallinum cD 455 e-127
35	emb AW650299 AW650299 EST328753 tomato germinating seedlings, TA 455 e-127
	emb AW982497 AW982497 HVSMEg0003G20f Hordeum vulgare pre-anthesi 439 e-126
	emb AF078070 AF078070 Griffithsia japonica heat-shock protein 90 245 e-126
	emb AW218188 AW218188 EST303369 tomato radicle, 5 d post-imbibit 452 e-126
40	emb AW731352 AW731352 GA_Ea0030E22 Gossypium arboreum 7-10 dpa 449 e-125
40	emb AW621485 AW621485 EST312283 tomato root during/after fruit s 445 e-124
	emb AW905909 AW905909 EST342082 potato stolon, Cornell Universit 331 e-124
	emb AW618647 AW618647 EST320633 L. pennellii trichome, Cornell U 439 e-122
	emb AI730385 AI730385 BNLGHi6770 Six-day Cotton fiber Gossypium 439 e-122 emb AW931002 AW931002 EST356845 tomato fruit mature green, TAMU 436 e-121
45	emb AW186517 AW186517 se68g12.yl Gm-c1019 Glycine max cDNA clone 432 e-120
	gb BE055051 BE055051 GA_Ea0031H10f Gossypium arboreum 7-10 dpa 381 e-118
	emb AW217359 AW217359 EST296010 tomato flower buds 0-3 mm, Corne 427 e-118
	emb AW216642 AW216642 EST295356 tomato callus, TAMU Lycopersicon 423 e-117
	emb AW217696 AW217696 EST296410 tomato flower buds 8 mm to pre-a 422 e-117
50	emb AW011081 AW011081 ST16E03 Pine TriplEx shoot tip library Pin 421 e-116
	emb AI730419 AI730419 BNLGHi7100 Six-day Cotton fiber Gossypium 417 e-115
	emb AW907064 AW907064 EST343096 potato stolon, Cornell Universit 413 e-114
	emb AW696590 AW696590 NF108G11ST1F1087 Developing stem Medicago 413 e-114
	emb AW738699 AW738699 EST340126 tomato flower buds, anthesis, Co 412 e-114
55	emb AI442468 AI442468 sa27d08.y1 Gm-c1004 Glycine max cDNA clone 412 e-114
	emb AW684853 AW684853 NF022C08NR1F1000 Nodulated root Medicago t 403 e-114
	emb AW693965 AW693965 NF071A06ST1F1040 Developing stem Medicago 408 e-113
	emb AW690869 AW690869 NF036A07ST1F1000 Developing stem Medicago 390 e-113
60	emb AW030608 AW030608 EST273863 tomato callus, TAMU Lycopersicon 407 e-112
UU	emb AW983321 AW983321 HVSMEg0010D10f Hordeum vulgare pre-anthesi 354 e-112
	emb AI726426 AI726426 BNLGHi5602 Six-day Cotton fiber Gossypium 407 e-112

emb|AW930252|AW930252 EST340709 tomato fruit mature green, TAMU ... 406 e-112 emb|AW979717|AW979717 EST341337 tomato root deficiency, Cornell ... 404 e-111 emb|AW695561|AW695561 NF096B09ST1F1076 Developing stem Medicago ... 404 e-111 emb|AW691505|AW691505 NF045G02ST1F1000 Developing stem Medicago ... 361 e-111 5 emb[AW735801]AW735801 EST336569 tomato flower buds 0-3 mm, Corne... 402 e-111 emb|AW737406|AW737406 EST338749 tomato flower buds, anthesis, Co... 402 e-111 emb|AL112936|CNS01AHC Botrytis cinerea strain T4 cDNA library un... 400 e-110 emb|AW217697|AW217697 EST296411 tomato flower buds 8 mm to pre-a... 400 e-110 emb|AW218948|AW218948 EST301430 tomato root during/after fruit s... 396 e-110 10 emb|AW220869|AW220869 EST297338 tomato fruit mature green, TAMU ... 398 e-109 emb|AW616417|AW616417 EST322828 L. hirsutum trichome, Cornell Un... 397 e-109 emb|AW688548|AW688548 NF008H04ST1F1000 Developing stem Medicago ... 396 e-109 emb|AW738535|AW738535 EST339962 tomato flower buds, anthesis, Co... 242 e-109 emb|AW649397|AW649397 EST327851 tomato germinating seedlings, TA... 394 e-108 15 emb|AW693115|AW693115 NF060C10ST1F1081 Developing stem Medicago ... 226 e-107 emb|AI488065|AI488065 EST246387 tomato ovary, TAMU Lycopersicon ... 390 e-107 emb|AI726157|AI726157 BNLGHi5098 Six-day Cotton fiber Gossypium ... 226 e-107 gb|BE060856|BE060856 HVSMEg0013J20f Hordeum vulgare pre-anthesis... 388 e-107 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107 20 emb|AL111751|CNS019KF Botrytis cinerea strain T4 cDNA library un... 389 e-107 emb|AW092845|AW092845 EST286025 tomato mixed elicitor, BTI Lycop... 386 e-106 emb]AW983154|AW983154 HVSMEg0008G17f Hordeum vulgare pre-anthesi... 224 e-106 emb|AI780272|AI780272 EST261151 tomato susceptible, Cornell Lyco... 215 e-106 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106 25 emb|AW690804|AW690804 NF035B11ST1F1000 Developing stem Medicago ... 375 e-106 emb|AW154860|AW154860 EST290253 tomato root deficiency, Cornell ... 385 e-105 emb|AI780075|AI780075 EST260954 tomato susceptible, Cornell Lyco... 383 e-105 emb|AW928471|AW928471 EST337259 tomato flower buds 8 mm to pre-a... 382 e-105 gb|L34028|PFAHSP86B Plasmodium falciparum (clone HB3) heat shock... 382 e-105 30 emb|AF030694|AF030694 Plasmodium falciparum strain Dd2 heat shoc... 382 e-105 gb|L34027|PFAHSP86A Plasmodium falciparum (clone Dd2) heat shock... 382 e-105 emb|AW737397|AW737397 EST338740 tomato flower buds, anthesis, Co... 381 e-104 emb|AW334905|AW334905 S40F8 AGS-1 Pneumocystis carinii f. sp. ca... 381 e-104 emb|AW035244|AW035244 EST280506 tomato callus, TAMU Lycopersicon... 380 e-104. 35

Query= atu68017_s_at 16105_s_at /id_source /description gb|aac31756.1| (u68017) heat shock transcription factor 4 [arabidopsis thaliana] /blast_score 1.00e-113 (1422 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

45 Searching.....done

40

Score E

Sequences producing significant alignments:

(bits) Value

emb|AB014483|AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho... 213 2e-62 emb|X55347|LPHSF24 Tomato mRNA for heat stress transcription fac... 210 2e-53 emb|AI900223|AI900223 sc02f05.y1 Gm-c1012 Glycine max cDNA clone... 205 3e-53 emb|Z46953|GMHSF34 G.max mRNA for heat shock transcription facto... 203 6e-53 emb|AV408054|AV408054 AV408054 Lotus japonicus young plants (two... 203 3e-51 emb|AV415115|AV415115 AV415115 Lotus japonicus young plants (two... 197 2e-49 emb|AW774951|AW774951 EST334102 KV3 Medicago truncatula cDNA clo... 194 1e-48 emb|AW689532|AW689532 NF021G10ST1F1000 Developing stem Medicago ... 194 1e-48 emb|AI728175|AI728175 BNLGHi10028 Six-day Cotton fiber Gossypium... 192 5e-48 emb|AI055366|AI055366 coau0003M17 Cotton Boll Abscission Zone cD... 191 1e-47 emb|AW428882|AW428882|Ljirnpest25-001-b9 Ljirnp Lambda HybriZap ... 190 2e-47

emb|AW931781|AW931781 EST357624 tomato fruit mature green, TAMU ... 189 3e-47 emb|AW686121|AW686121 NF033H01NR1F1000 Nodulated root Medicago t... 188 1e-46 emb|Z46956|GMHSF5 G.max mRNA for heat shock transcription factor 5. 185 6e-46 emb|AW109013|AW109013 gate0002O16f Gossypium arboreum 7-10 dpa f... 179 4e-44 5 gb|BE054274|BE054274 GA Ea0002O16f Gossypium arboreum 7-10 dpa ... 179 4e-44 gb|BE020791|BE020791 sm52h09.y1 Gm-c1028 Glycine max cDNA clone ... 178 1e-43 emb|AW696868|AW696868 NF111F05ST1F1046 Developing stem Medicago ... 166 3e-43 emb|AW686271|AW686271 NF039H06NR1F1000 Nodulated root Medicago t... 171 5e-42 emb|AW931176|AW931176 EST357019 tomato fruit mature green, TAMU ... 168 8e-41 gblC95479|C95479 C95479 Citrus unshiu Miyagawa-wase maturation s... 166 5e-40 10 emblAW033421|AW033421 EST276992 tomato callus, TAMU Lycopersicon... 165 1e-39 emb|AW030725|AW030725 EST273980 tomato callus, TAMU Lycopersicon... 165 1e-39 emb|AW041695|AW041695 EST284559 tomato mixed elicitor, BTI Lycop... 165 1e-39 emb|AW217982|AW217982 EST296697 tomato flower buds, anthesis, Co... 165 1e-39 15 emb|X67600|LPHSF8 L.peruvianum Lp-hsf8 mRNA for heat stress tran... 161 1e-38 emb|AW774397|AW774397 EST333548 KV3 Medicago truncatula cDNA clo... 160 2e-38 emb|AW686582|AW686582 NF042H04NR1F1000 Nodulated root Medicago t... 155 6e-37 emb|AW776460|AW776460 EST335525 DSIL Medicago truncatula cDNA cl... 152 7e-36 emb|AW738023|AW738023 EST339450 tomato flower buds, anthesis, Co... 150 3e-35 20 emb|AW036683|AW036683 EST278726 tomato fruit mature green, TAMU ... 149 5e-35 emb|AI729182|AI729182 BNLGHi12855 Six-day Cotton fiber Gossypium... 149 5e-35 emb|AI489721|AI489721 EST248060 tomato ovary, TAMU Lycopersicon ... 149 5e-35 emb|AW034402|AW034402 EST277973 tomato callus, TAMU Lycopersicon... 148 7e-35 emb|X67601|LPHSF30 L.peruvianum Lp-hsf30 mRNA for heat stress tr... 148 9e-35 25 emb|AW906822|AW906822 EST342945 potato stolon, Cornell Universit... 147 2e-34 emb|AW164509|AW164509 se74f12.yl Gm-c1023 Glycine max cDNA clone... 147 2e-34 emb|AW034874|AW034874 EST279103 tomato callus, TAMU Lycopersicon... 147 2e-34 emb|Z46952|GMHSF21 G.max mRNA for heat shock transcription facto... 145 8e-34 emb|AF235958|AF235958 Medicago sativa heat shock transcription f... 145 8e-34 30 emb|AW559623|AW559623 EST314671 DSIR Medicago truncatula cDNA cl... 144 2e-33 emb|AW222011|AW222011 EST298822 tomato fruit red ripe, TAMU Lyco... 144 2e-33 emb|AW930998|AW930998 EST356841 tomato fruit mature green, TAMU ... 143 4e-33 emb|AW906840|AW906840 EST342963 potato stolon, Cornell Universit... 140 2e-32 emb|AB014484|AB014484 Nicotiana tabacum NtHSF2 mRNA for heat sho... 140 3e-32 35 emb|AF208544|AF208544 Lycopersicon peruvianum heat stress transc... 139 4e-32 emb|AW738534|AW738534 EST339961 tomato flower buds, anthesis, Co... 139 5e-32 emb|AI725043|AI725043 942 PtIFG2 Pinus taeda cDNA clone 8824r, m... 139 5e-32 emb|AW596493|AW596493 sj13a09.yl Gm-c1032 Glycine max cDNA clone... 138 1e-31 emb|AW874988|AW874988 00109 leafy spurge Lambda HybriZAP 2.1 two... 138 1e-31 40 emb|AV415736|AV415736 AV415736 Lotus japonicus young plants (two... 138 1e-31 emblAW979619|AW979619 EST341218 tomato root deficiency, Cornell ... 137 2e-31 emb|AW932142|AW932142 EST357985 tomato fruit mature green, TAMU ... 136 3e-31 emb|Z46954|GMHSF33 G.max mRNA for heat shock transcription facto... 135 9e-31 emb|AW569138|AW569138 si63g09.yl Gm-r1030 Glycine max cDNA clone... 134 1e-30 45 emb|AW569256|AW569256 si64g09.yl Gm-r1030 Glycine max cDNA clone... 134 1e-30 emb|AW203851|AW203851 sf38h11.yl Gm-c1028 Glycine max cDNA clone... 133 3e-30 emb|AW220758|AW220758 EST297227 tomato fruit mature green, TAMU ... 132 6e-30 emblAI728806|AI728806 BNLGHi11701 Six-day Cotton fiber Gossypium... 108 2e-28 emb|AW736596|AW736596 EST333088 KV3 Medicago truncatula cDNA clo... 103 3e-28 50 emb|AI895934|AI895934 EST265377 tomato callus, TAMU Lycopersicon... 123 3e-27 emb|Z46951|GMHSF29 G.max mRNA for heat shock transcription facto... 120 2e-26 gb|BE019974|BE019974 sm38b12.yl Gm-c1028 Glycine max cDNA clone ... 119 6e-26 emb|Z46955|GMHSF31 G.max mRNA for heat shock transcription facto... 115 8e-25 emb|X67599|LEHSF8 L.esculentum Le-hsf8 gene for heat stress tran... 114 2e-24 55 emb|AQ579554|AQ579554 T135016b shotgun sub-library of BAC clone ... 113 4e-24 emb|AW775388|AW775388 EST334453 DSIL Medicago truncatula cDNA cl... 66 1e-23 emb|AW931892|AW931892 EST357735 tomato fruit mature green, TAMU ... 104 2e-21 emb|AQ579623|AQ579623 T135087b shotgun sub-library of BAC clone ... 103 4e-21 emb|AW736595|AW736595 EST333087 KV3 Medicago truncatula cDNA clo... 103 4e-21 60 emb|AW697097|AW697097 NF112C08ST1F1065 Developing stem Medicago ... 103 4e-21 emb|AV420766|AV420766 AV420766 Lotus japonicus young plants (two... 102 8e-21

5	emb AV413314 AV413314 AV413314 Lotus japonicus young plants (two 102 8e-21 emb AW693546 AW693546 NF067D12ST1F1101 Developing stem Medicago 101 1e-20 emb AI895294 AI895294 EST264737 tomato callus, TAMU Lycopersicon 101 1e-20 emb AJ010644 PSA010643 Pisum sativum hsfA gene, exons 1 to 2, pa 99 7e-20 emb AW924303 AW924303 WS1_52_H11.b1_A002 Water-stressed 1 (WS1) 99 7e-20 emb AI895834 AI895834 EST265277 tomato callus, TAMU Lycopersicon 95 9e-19 emb AW756148 AW756148 sl16e07.yl Gm-c1036 Glycine max cDNA clone 93 4e-18 gb M94683 YSPHSF Schizosaccharomyces pombe heat shock transcript 93 6e-18
10	emb AW132703 AW132703 se09a08.yl Gm-c1013 Glycine max cDNA clone 93 6e-18 emb X55149 KLHSFG K. lactis HSF gene for heat shock transcriptio 76 2e-17 emb AW933448 AW933448 EST359387 tomato fruit mature green, TAMU 89 8e-17 emb AI896906 AI896906 EST266349 tomato callus, TAMU Lycopersicon 89 1e-16 emb AZ045432 AZ045432 T234030b shotgun sub-library of BAC clone 84 3e-15 gb U00485 YSCSKN7 Saccharomyces cerevisiae putative transcriptio 83 5e-15
15	emb X83031 SCPOS9 S.cerevisiae POS9 gene. 83 5e-15 gb U00029 YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm 83 5e-15 emb Z69726 SPAC2E12 S.pombe chromosome I cosmid c2E12. 83 7e-15 gb M22040 YSCHSF1A S.cerevisiae heat shock transcription factor 81 2e-14 gb J03139 YSCHSF S.cerevisiae heat shock factor gene (HSF), comp 81 2e-14
20	emb Z72596 SCYGL074C S.cerevisiae chromosome VII reading frame O 81 2e-14 emb AI212342 AI212342 x3c12a1.rl Aspergillus nidulans 24hr asexu 73 8e-14 emb AW686674 AW686674 NF040F05NR1F1000 Nodulated root Medicago t 79 8e-14 emb AZ048458 AZ048458 PSB119 Barley PstI genomic clones Hordeum 78 2e-13 emb AW034135 AW034135 EST277706 tomato callus, TAMU Lycopersicon 57 9e-13
25	emb AW933529 AW933529 EST359288 tomato fruit mature green, TAMU 72 1e-11 emb AW307441 AW307441 sf57a06.y1 Gm-c1009 Glycine max cDNA clone 70 5e-11 emb AW620962 AW620962 sj98b03.y1 Gm-c1023 Glycine max cDNA clone 70 5e-11
30	Query= athpear_s_at 16150_s_at /id_source genbank /description emb cab41718.1 (al049730) pearli 1 [arabidopsis thaliana] /blast_score 5.00e-43 (810 letters)
35	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
40	Score E Sequences producing significant alignments: (bits) Value
45	emb AI352845 AI352845 MB69-3F PZ204.BNlib Brassica napus cDNA cl 161 2e-55 emb AI352927 AI352927 MB74-12D PZ204.BNlib Brassica napus cDNA c 169 8e-43 gb S68113 S68113 proline-rich SAC51 [Brassica napus=oilseed rape 163 1e-42 emb X71618 BNPRPPDA B.napus proline-rich mRNA accumulating durin 163 1e-42 emb AF109654 AF109654 AF109654 Capsicum annuum root susceptible 169 3e-41 emb AI352937 AI352937 MB74-5H PZ204.BNlib Brassica napus cDNA cl 115 5e-40
50	emb AW621250 AW621250 EST312048 tomato root during/after fruit s 162 6e-40 emb AW626221 AW626221 EST320128 tomato radicle, 5 d post-imbibit 162 6e-40 emb AI779211 AI779211 EST260090 tomato susceptible, Cornell Lyco 162 6e-40 emb AW443140 AW443140 EST308070 tomato mixed elicitor, BTI Lycop 162 6e-40
55	emb AI776056 AI776056 EST257156 tomato resistant, Cornell Lycope 162 6e-40 emb AW032764 AW032764 EST276323 tomato callus, TAMU Lycopersicon 162 6e-40 emb AW217082 AW217082 EST295796 tomato callus, TAMU Lycopersicon 162 6e-40 emb AW035571 AW035571 EST281309 tomato callus, TAMU Lycopersicon 162 6e-40 emb AV413531 AV413531 AV413531 Lotus japonicus young plants (two 163 1e-39
60	gb BE124752 BE124752 EST393787 GVN Medicago truncatula cDNA clon 163 2e-39 emb AW980687 AW980687 EST391840 GVN Medicago truncatula cDNA clo 163 2e-39 gb BE124520 BE124520 EST393555 GVN Medicago truncatula cDNA clon 163 2e-39 emb AW980826 AW980826 EST391979 GVN Medicago truncatula cDNA clo 163 2e-39

```
emb|AW980547|AW980547 EST391700 GVN Medicago truncatula cDNA clo... 163 2e-39
      gb[BE124445]BE124445 EST393480 GVN Medicago truncatula cDNA clon... 163 2e-39
      gb|BE124789|BE124789 EST393824 GVN Medicago truncatula cDNA clon... 163 2e-39
      emblAW725519lAW725519 GA Ea0018G20 Gossypium arboreum 7-10 dpa ... 163 2e-39
      emb|AW685869|AW685869 NF031B09NR1F1000 Nodulated root Medicago t... 163 2e-39
      emb|AW287846|AW287846 N100689e rootphos(-) Medicago truncatula c... 163 2e-39
      gb|BE124744|BE124744 EST393779 GVN Medicago truncatula cDNA clon... 163 2e-39
      emb|AW560894|AW560894 EST315942 DSIR Medicago truncatula cDNA cl... 163 2e-39
      emb|AW684629|AW684629 NF019B05NR1F1000 Nodulated root Medicago t... 163 2e-39
10
      emb|AW329233|AW329233 N200445e rootphos(-) Medicago truncatula c... 163 2e-39
      emb|AW034083|AW034083 EST277578 tomato callus, TAMU Lycopersicon... 162 2e-39
      emb|AW094444|AW094444 EST287624 tomato mixed elicitor, BTI Lycop... 162 2e-39
      emb|AW907202|AW907202 EST343325 potato stolon, Cornell Universit... 160 1e-38
      emb|AW125962|AW125962 N100157e rootphos(-) Medicago truncatula c... 160 2e-38
15
      emb|AW217088|AW217088 EST295802 tomato callus, TAMU Lycopersicon... 159 3e-38
      emb|AW685279|AW685279 NF025G02NR1F1000 Nodulated root Medicago t... 158 4e-38
      emblAF026382|AF026382 Fragaria x ananassa HyPRP mRNA, complete cds. 158 6e-38
      emb|AI779212|AI779212 EST260091 tomato susceptible, Cornell Lyco... 158 6e-38
      emb|AW257148|AW257148 EST305285 KV2 Medicago truncatula cDNA clo... 158 6e-38
20
      emb|AW349572|AW349572 GM210005A21F12R Gm-r1021 Glycine max cDNA ... 157 8e-38
      dbj|D83227|POPELPG Populus nigra gene for extensin like protein,... 157 1e-37
      dbj|D83226|POPELP Populus nigra mRNA for extensin like protein, ... 157 le-37
      emb|AW624937|AW624937 EST313766 tomato radicle, 5 d post-imbibit... 156 2e-37
      emb|AW622601|AW622601 EST313401 tomato root during/after fruit s... 156 2e-37
25
      emb|AW287985|AW287985 N100829e rootphos(-) Medicago truncatula c... 153 2e-36
      emb|AW625740|AW625740 EST319647 tomato radicle, 5 d post-imbibit... 152 4e-36
      emb|X85206|CRRNAHPRP C.roseus mRNA for hybrid proline-rich protein. 152 4e-36
      emb|AW622645|AW622645 EST313445 tomato root during/after fruit s... 151 7e-36
      gb|BE021488|BE021488 sm59b04.yl Gm-c1028 Glycine max cDNA clone ... 150 1e-35
30
      emb|Z26880|CR14KDPP C.roseus mRNA for 14 kDa polypeptide.
      emb|AW309747|AW309747 sf24c01.x1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
      emb|AW309357|AW309357 sf16d03.x1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
      gb|BE022318|BE022318 sm73d03.y1 Gm-c1028 Glycine max cDNA clone ... 131 3e-34
      emb|AW234182|AW234182 sf22b12.yl Gm-c1028 Glycine max cDNA clone... 131 3e-34
35
      emb[AW704401]AW704401 sk30f03.y1 Gm-c1028 Glycine max cDNA clone... 131 3e-34
      emb|AI736342|AI736342 sb27c03.yl Gm-c1009 Glycine max cDNA clone... 129 4e-34
      gb|BE022083|BE022083 sm68c08.yl Gm-c1028 Glycine max cDNA clone ... 130 4e-34
      dbj|D86629|D86629 Nicotiana tabacum mRNA for NT16 polypeptide, c... 144 1e-33
      emb|AI442014|AI442014 sa66e07.yl Gm-c1004 Glycine max cDNA clone... 128 2e-33
40
      emb|AW306872|AW306872 sf49g05.yl Gm-c1009 Glycine max cDNA clone... 128 2e-33
      emb|AW597518|AW597518 sj48b01.yl Gm-c1033 Glycine max cDNA clone... 128 2e-33
      emb|AW597680|AW597680 sj49e04.yl Gm-c1033 Glycine max cDNA clone... 128 2e-33
      emb|AW307412|AW307412 sf56f11.yl Gm-c1009 Glycine max cDNA clone... 128 2e-33
      emb|AI441411|AI441411 sa59e12.yl Gm-c1004 Glycine max cDNA clone... 128 2e-33
45
      emb|AI776903|AI776903 EST258003 tomato resistant, Cornell Lycope... 127 3e-33
      emb|AW092951|AW092951 EST286131 tomato mixed elicitor, BTI Lycop... 127 3e-33
      emb|AW650542|AW650542 EST328996 tomato germinating seedlings, TA... 127 3e-33
      emblAI772831|AI772831 EST253931 tomato resistant, Cornell Lycope... 127 3e-33
      dbi|D86721|D86721 Nicotiana tabacum DNA for glycine-rich polypep... 142 3e-33
50
      emb|AW163963|AW163963 Ljirnpest17-382-g10 Ljirnp Lambda HybriZap... 142 3e-33
      gb|BE022257|BE022257 sm72g11.yl Gm-c1028 Glycine max cDNA clone ... 127 4e-33
      emb|AW666281|AW666281 sk34f10.y1 Gm-c1028 Glycine max cDNA clone... 127 4e-33
      emb|AW706178|AW706178 sj52g11.yl Gm-c1033 Glycine max cDNA clone... 127 4e-33
      emb|AB035125|AB035125 Nicotiana tabacum mRNA for glycine-rich pr... 140 1e-32
55
      dbi|D26454|TOBTID23 Nicotiana glauca X Nicotiana langsdorffii mR... 140 1e-32
      emb|AW443491|AW443491 EST308421 tomato mixed elicitor, BTI Lycop... 125 1e-32
      emb[X15436]DC215G Carrot DC 2.15 mRNA for 14 kD protein.
      emb|AW622484|AW622484 EST313272 tomato root during/after fruit s... 124 3e-32
      emb|AW906384|AW906384 EST342506 potato stolon, Cornell Universit... 126 3e-32
60
      emb|AW093202|AW093202 EST286382 tomato mixed elicitor, BTI Lycop... 123 3e-32
      emblAW649092|AW649092 EST327546 tomato germinating seedlings, TA... 123 3e-32
```

```
emb|AV411071|AV411071 AV411071 Lotus japonicus young plants (two... 135 3e-31
      emblAW719418|AW719418 LjNEST4c12r Lotus japonicus nodule library... 126 4e-31
      emb|AV423170|AV423170 AV423170 Lotus japonicus young plants (two... 126 4e-31
      emb|AV422321|AV422321 AV422321 Lotus japonicus young plants (two... 125 6e-31
 5
      emb|AV416097|AV416097 AV416097 Lotus japonicus young plants (two... 125 6e-31
      emb|AV413898|AV413898 AV413898 Lotus japonicus young plants (two... 125 6e-31
      emb|AV415427|AV415427 AV415427 Lotus japonicus young plants (two... 125 6e-31
      emb|AW309629|AW309629 sf22b12.x1 Gm-c1028 Glycine max cDNA clone... 123 1e-30
      emb|AW570545|AW570545 sj63d10.yl Gm-c1033 Glycine max cDNA clone... 125 2e-30
10
      emb|AW152920|AW152920 se32g01.yl Gm-c1015 Glycine max cDNA clone... 125 2e-30
      emb|AW830131|AW830131 sm23c07.yl Gm-c1028 Glycine max cDNA clone... 125 2e-30
      emb|AI736269|AI736269 sb26b02.yl Gm-c1008 Glycine max cDNA clone... 125 2e-30
      emb|AI442516|AI442516 sa32e08.yl Gm-c1004 Glycine max cDNA clone... 125 2e-30
      emb|AW203388|AW203388 sf29f06.yl Gm-c1028 Glycine max cDNA clone... 125 4e-30
15
      emb|AW309693|AW309693 sf23c12.x1 Gm-c1028 Glycine max cDNA clone... 123 4e-30
      emb|AW597294|AW597294 si71c07.yl Gm-c1031 Glycine max cDNA clone... 125 4e-30
      emb|AW707234|AW707234 sk22d10.yl Gm-c1028 Glycine max cDNA clone... 125 4e-30
      emb|AW568746|AW568746 si72e11.yl Gm-c1031 Glycine max cDNA clone... 125 4e-30
      emb|AW568382|AW568382 si70b03.yl Gm-c1031 Glycine max cDNA clone... 125 4e-30
20
      emb|AW830420|AW830420 sm26e07.yl Gm-c1028 Glycine max cDNA clone... 125 4e-30
      Query= ab008107 s at 16536 s at /id source genbank /description
      dbj|baa32422.1| (ab008107) ethylene responsive element binding factor
25
      5 [arabidopsis thaliana] /blast_score 1.00e-117 /ec_number /family
      /chip nova /gb link /ncgi
           (1059 letters)
      Database: plantfungal
30
            661,018 sequences; 426,114,510 total letters
      Searching.....done
                                         Score E
35
      Sequences producing significant alignments:
                                                         (bits) Value
      emb|AW396250|AW396250 sh26c01.yl Gm-c1016 Glycine max cDNA clone... 141 4e-37
      emb|AW200919|AW200919 se95c12.yl Gm-c1027 Glycine max cDNA clone... 149 5e-35
      emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 94 5e-33
40
      emb|AW776671|AW776671 EST335736 DSIL Medicago truncatula cDNA cl... 111 2e-32
      emb|AI897834|AI897834 EST267277 tomato ovary, TAMU Lycopersicon ... 132 2e-30
      emb|AW349516|AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ... 130 2e-
      29
      emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 125 2e-29
45
      emb|AI899000|AI899000 EST268443 tomato ovary, TAMU Lycopersicon ... 128 3e-29
      emb|AW458901|AW458901 sh16c12.yl Gm-c1016 Glycine max cDNA clone... 108 8e-29
      dbi|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds.
      emb|AI486689|AI486689 EST245011 tomato ovary, TAMU Lycopersicon ... 127 2e-28
      gb|BE023264|BE023264 sm80a11.yl Gm-c1015 Glycine max cDNA clone ... 103 5e-28
50
      emb|AI897797|AI897797 EST267240 tomato ovary, TAMU Lycopersicon ... 124 1e-27
      emb|AI794657|AI794657 sb67b03.y1 Gm-c1019 Glycine max cDNA clone... 124 1e-27
      emb|AW507860|AW507860 si45h05.yl Gm-r1030 Glycine max cDNA clone... 123 2e-27
      emb|AW775819|AW775819 EST334884 DSIL Medicago truncatula cDNA cl... 95 5e-27.
      emb|AW685077|AW685077 NF024H04NR1F1000 Nodulated root Medicago t... 93 8e-27
55
      emb|AW573782|AW573782 EST316373 GVN Medicago truncatula cDNA clo... 93 9e-27
      emb|AW620490|AW620490 sj05h02.yl Gm-c1032 Glycine max cDNA clone... 121 1e-26
      emb|AW759181|AW759181 sl38a09.yl Gm-c1027 Glycine max cDNA clone... 121 1e-26
      emb|AI778693|AI778693 EST259572 tomato susceptible, Cornell Lyco... 120 2e-26
      emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 118 6e-26
60
      emb|AW776668|AW776668 EST335733 DSIL Medicago truncatula cDNA cl... 118 6e-26
      emb|AW574222|AW574222 EST316813 GVN Medicago truncatula cDNA clo... 118 6e-26
```

emb|AI899889|AI899889 sb94g05.yl Gm-c1017 Glycine max cDNA clone... 117 1e-25 emb|AW185128|AW185128 se87b10.yl Gm-c1023 Glycine max cDNA clone... 116 2e-25 emb|AW688546|AW688546 NF008H02ST1F1000 Developing stem Medicago ... 89 2e-25 emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 115 5e-25 5 emb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 115 5e-25 emblAI782381|AI782381 EST263260 tomato susceptible, Cornell Lyco... 115 8e-25 emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 114 1e-24 emb|AW781602|AW781602 sl82d06.yl Gm-c1037 Glycine max cDNA clone... 114 1e-24 emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 113 2e-24 10 emb|AI965917|AI965917 sc79f12.yl Gm-c1018 Glycine max cDNA clone... 113 3e-24 emb|AI484961|AI484961 EST243224 tomato ovary, TAMU Lycopersicon ... 112 5e-24 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 111 1e-23 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 110 2e-23 emb|AV421566|AV421566 AV421566 Lotus japonicus young plants (two... 109 3e-23 15 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. emb|AW101306|AW101306 sd77c11.yl Gm-c1009 Glycine max cDNA clone... 89 5e-23 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 107 2e-22 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 107 2e-22 20 gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 107 2e-22 emb|AW596384|AW596384 sj02f12.y1 Gm-c1032 Glycine max cDNA clone... 107 2e-22 dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. emb|AV417552|AV417552 AV417552 Lotus japonicus young plants (two... 103 2e-21 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 103 2e-21 25 emb|AW278190|AW278190 sf40g11.yl Gm-c1009 Glycine max cDNA clone... 103 2e-21 emblAJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 102 4e-21 emb|AI973653|AI973653 sd07h05.yl Gm-c1020 Glycine max cDNA clone... 102 4e-21 emb|AW690929|AW690929 NF034G08ST1F1000 Developing stem Medicago ... 73 9e-21 emb|AW233956|AW233956 sf32e02.y1 Gm-c1028 Glycine max cDNA clone... 101 1e-20 30 emb|AW736415|AW736415 EST332429 KV3 Medicago truncatula cDNA clo... 73 2e-20 emb|AI440657|AI440657 sa63d09.yl Gm-c1004 Glycine max cDNA clone... 100 2e-20 emb|AV422393|AV422393 AV422393 Lotus japonicus young plants (two... 100 2e-20 emb|AI967551|AI967551 Ljirnpest05-400-d11 Ljirnp Lambda HybriZap... 100 2e-20 emb|AI731242|AI731242 BNLGHi9002 Six-day Cotton fiber Gossypium ... 100 3e-20 35 gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 99 5e-20 emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 99 5e-20 emb|AI894873|AI894873 EST264316 tomato callus, TAMU Lycopersicon... 99 5e-20 emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 99 5e-20 emb|AW729466|AW729466 GA_Ea0025B11 Gossypium arboreum 7-10 dpa ... 98 1e-19 40 emb|AW507898|AW507898 si46f03.y1 Gm-r1030 Glycine max cDNA clone... 98 1e-19 emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 98 1e-19 emb|AW840611|AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two... 97 2e-19 emb|AI736796|AI736796 sb33f06.y1 Gm-c1012 Glycine max cDNA clone... 97 2e-19 emb|AI966559|AI966559 sc52a04.yl Gm-c1015 Glycine max cDNA clone... 97 2e-19 45 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 96 3e-19 emb|AI896308|AI896308 EST265751 tomato callus, TAMU Lycopersicon... 96 5e-19 emb|AI898992|AI898992 EST268435 tomato ovary, TAMU Lycopersicon ... 95 6e-19 emb|AW980654|AW980654 EST391807 GVN Medicago truncatula cDNA clo... 95 6e-19 emb|AI495036|AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone... 94 2e-18 50 gblU81157INTU81157 Nicotiana tabacum S25-XP1 DNA binding protein... 94 2e-18 emb|AW706628|AW706628 sj62g05.yl Gm-c1033 Glycine max cDNA clone... 70 3e-18 emb|AI442716|AI442716 sa85d10.yl Gm-c1004 Glycine max cDNA clone... 93 4e-18 emb|AW559315|AW559315 EST306358 DSIR Medicago truncatula cDNA cl... 93 4e-18 emb|AW035119|AW035119 EST280381 tomato callus, TAMU Lycopersicon... 91 1e-17 55 emb|AI490591|AI490591 EST249145 tomato ovary, TAMU Lycopersicon ... 91 1e-17 emb|AI489147|AI489147 EST247486 tomato ovary, TAMU Lycopersicon ... 91 1e-17 emb|AW782252|AW782252 sm03d11.yl Gm-c1027 Glycine max cDNA clone... 63 1e-17 emb|AW348322|AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3... 90 2e-17 emb|AW759236|AW759236 s138f08.y1 Gm-c1027 Glycine max cDNA clone... 90 2e-17 60 emb|AW686013|AW686013 NF033D04NR1F1000 Nodulated root Medicago t... 90 2e-17 emb|AI776626|AI776626 EST257726 tomato resistant, Cornell Lycope... 89 4e-17

	emb AW443265 AW443265 EST308195 tomato mixed elicitor, BTI Lycop 89 5e-17
	emb AW308784 AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone 89 5e-17 emb AF211541 AF211541 AF211541 34.1B Nicotiana tabacum cDNA clon 87 2e-16
5	emb AW621700 AW621700 EST312498 tomato root during/after fruit s 87 2e-16 emb AI489709 AI489709 EST248048 tomato ovary, TAMU Lycopersicon 62 2e-16
,	emb AW560968 AW560968 EST316016 DSIR Medicago truncatula cDNA cl 60 4e-16
•	emb AW560196 AW560196 EST315244 DSIR Medicago truncatula cDNA cl 60 4e-16 emb AW185802 AW185802 se59h01.y1 Gm-c1019 Glycine max cDNA clone 71 5e-16
10	emb AW734757 AW734757 sk88d02.y1 Gm-c1035 Glycine max cDNA clone 85 1e-15 emb AV417624 AV417624 AV417624 Lotus japonicus young plants (two 58 1e-15
10	emb AV407462 AV407462 AV407462 Lotus japonicus young plants (two 58 1e-15
	emb AW256448 AW256448 EST304585 KV2 Medicago truncatula cDNA clo 59 1e-15 emb AW560135 AW560135 EST315183 DSIR Medicago truncatula cDNA cl 59 2e-15
15	emb AW267756 AW267756 EST305884 DSIR Medicago truncatula cDNA cl 59 2e-15 emb AW560134 AW560134 EST315182 DSIR Medicago truncatula cDNA cl 59 2e-15
13	emb AW574073 AW574073 EST316664 GVN Medicago truncatula cDNA clo 61 2e-13
20	Query= athrprp1b_s_at 16578_s_at /id_source /description "emb cab68132.1 (al137080) beta-1, 3-glucanase
-	2 (bg2) [arabidopsis thaliana]" /blast_score 0
	(1181 letters)
25	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
	Score E
30	Sequences producing significant alignments: (bits) Value
30 35	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prumus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100
	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 289 1e-98
35	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VV1277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 289 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 99 2e-98 gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95
35 40	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VV1277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 db E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 db E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 289 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 99 2e-98 gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-gluc 262 1e-94
35 40 45	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 glucanase 289 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94
35 40 45	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VV1277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3-glucanase 210 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase 208 9e-94 emb A26453 A26453 Recombinant soya beta-1,3-glucanase cDNA. 244 3e-93 emb A26449 A26449 Soya mutant beta-1,3-glucanase cDNA.
35 40 45	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 289 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 99 2e-98 gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase 208 9e-94 emb A26453 A26453 Recombinant soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 244 3e-93 emb A26454 GHBGLUCS G.hirsutum mRNA for 1,3-beta-glucanase. 174 3e-93
35 40 45	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 glucanase 210 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase 208 9e-94 emb A26445 A26449 Soya mutant beta-1,3-glucanase cDNA 244 3e-93 emb A26449 A26449 Soya mutant beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 244 3e-93 emb A26403 TOBGLB13B Nicotiana tabacum glucan beta-1,3-glucosidas 207 3e-93
35 40 45	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 289 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 99 2e-98 gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 106 3e-95 emb AF067863 AF067863 Solanum tuberosum Datura endo-1,3-beta-glucan glucanoh 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94 emb A26449 A26449 Soya mutant beta-1,3-glucanase cDNA. 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 144 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 144 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 144 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA. 244 3e-93 emb A54742 NPB13GG Nicotiana plumbaginifolia beta-(1,3)-gl
35 40 45	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 265 e-106 gb U49454 PPU49454 Prumus persica beta-1,3-glucanase (Gns1) gene 292 e-106 gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 265 e-105 emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 284 e-104 dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 226 e-100 dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 226 e-100 gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 226 e-100 gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 171 e-100 emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. 133 1e-99 gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 209 8e-99 gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 210 1e-98 emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 289 1e-98 emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase (HGN1) 265 1e-95 emb X54456 NTEC32139 N. tabacum mRNA for beta-1,3-glucanase (HGN1) 265 1e-95 emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 210 6e-95 gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 8e-95 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94 emb X53600 NTGLN2G Tobacco gln2 gene for beta-1,3-glucanase 208 9e-94 emb A26449 A26449 Soya mutant beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A26447 Soya beta-1,3-glucanase cDNA 244 3e-93 emb A26447 A2644

	emb[X74905]LEQA L.esculentum TomQ'a mRNA for beta(1,3)glucanase. 105 2e-90
	emb X89717 PVB13GLUC P.vulgaris beta-1,3-glucanase gene. 243 3e-89
	gb[U01902[U01902 Solanum tuberosum Datura endo-1,3-beta-D-glucan 210 2e-88
	emb AJ131047 CAR131047 Cicer arietinum mRNA for glucan-endo-1,3 188 5e-88
5	emb X74906 LEQB L.esculentum TomQ'b mRNA for beta(1,3)glucanase. 110 1e-86
	emb AF227953 AF227953 Capsicum annuum basic beta-1,3-glucanase (252 3e-86
	emb AF001523 AF001523 Musa acuminata beta-1, 3-glucananse mRNA, 148 5e-86
	embla F004929la F004929 a ferra since the table 1.2 of the footing for the footing footing for the footing footing for the footing footing for the footing footing for the foo
	emb AF004838 AF004838 Musa acuminata beta-1,3-glucanase mRNA, pa 148 7e-86
10	gb L02212 PEABETAGLU Pea beta-1,3-glucanase gene, complete cds. 180 1e-85
10	gb S51479 S51479 beta-1,3-glucanase [Pisum sativum=peas, cultiva 180 2e-85
	emb AF186083 AF186083 AF186083 Populus alba x Populus tremula ba 218 5e-85
	gb M20620 TOBGLUBC N.tabacum beta-1,3-glucanase mRNA, clone pGL43. 207 4e-84
	gb U27179 MSU27179 Medicago sativa acidic glucanase mRNA, comple 138 7e-79
	gb M60463 TOBGL153A Tobacco GL153 protein mRNA, complete cds. 99 3e-77
15	emb AF141654 AF141654 Nicotiana tabacum beta-1,3-glucanase (GGL4 99 5e-77
	gb M60460 TOBPR2A Tobacco PR2 protein mRNA, complete cds. 100 3e-76
•	gb M59443 TOBGLUCB N.tabacum acidic beta-1,3-glucanase gene, com 100 1e-75
	emb A16120 A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID 100 1e-75
•	gb M63634 TOBGCBREG Nicotiana plumbaginifolia beta(1,3)-glucanas 268 2e-75
20	emb X54431 NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 100 1e-74
	emb X81560 NTSP41AGN N,tabacum Sp41a gene. 100 2e-74
	emb X54430 NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 100 2e-74
	gb[M96941]BLYGCNHVI Hordeum vulgare glucan endo-1,3-beta-glucosi 93 8e-74
	emb AJ012751 CAR012751 Cicer arietinum mRNA for glucan endo-beta 140 4e-73
25	gb M20618 TOBGLUBA N.tabacum beta-1,3-glucanase mRNA, clones pGL 207 9e-73
2.5	
	emb Z15131 ASBGLUCAN A.sativa mRNA for beta glucanase. 158 le-70
	gb M62740 BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan 158 2e-70
	emb Z22874 TABETGLUB T.aestivum (1,3;1,4) beta glucanase mRNA, c 158 2e-70
30	emb Z22873 TABETGLUA T.aestivum beta glucanase mRNA, complete CDS. 158 3e-70
30	emb X52572 HVBDG Barley DNA for (1-3,1-4)-beta-D-glucanase (EC 3 158 1e-69
	emb X56775 HVGLB1,H.vulgare Glb 1 gene for 1-3,1-4-beta-D-glucan 158 1e-69
	emb X56260 HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC 158 1e-69
	gb M80604 TOMB13GLUA Lycopersicon esculentum beta-1,3-glucanase 94 2e-69
35	emb AJ009932 STAJ9932 Solanum tuberosum mRNA for beta-1,3-glucan 95 6e-69
33	emb AF034107 AF034107 Glycine max beta-1,3-glucanase 2 (SGlu2) g 122 2e-67
	emb AF112965 AF112965 Triticum aestivum beta-1,3-glucanase precu 166 2e-66
	gb]M60462]TOBPRNA Tobacco PRN protein mRNA, 3' end. 100 5e-65
	emb AW030776 AW030776 EST274031 tomato callus, TAMU Lycopersicon 210 2e-64
40	emb AF112967 AF112967 Triticum aestivum beta-1,3-glucanase precu 175 2e-64
40	emb AW216754 AW216754 EST295468 tomato callus, TAMU Lycopersicon 202 7e-64
	emb AI895131 AI895131 EST264574 tomato callus, TAMU Lycopersicon 202 7e-64
	gb U96096 HVU96096 Hordeum vulgare endo-1,3-beta-glucanase (Hv34 72 3e-62
	gb M13237 BLYGLUCB Barley beta glucanase mRNA. 158 4e-62
4	emb AW625790 AW625790 EST319697 tomato radicle, 5 d post-imbibit 193 2e-61
45	gb M96939 BLYGLCNHV Hordeum vulgare glucan endo-1,3-beta-glucosi 121 3e-61
	emb AJ271367 HVU271367 Hordeum vulgare mRNA for beta-1,3-glucanase. 92 7e-61
	gb M23548 BLYGEH Barley (1->3)-beta-glucan endohydrolase mRNA, c 92 7e-61
	emb[Y18212 TAY18212 Triticum aestivum mRNA for beta-1,3-endogluc 93 9e-61
	emb AF030771 AF030771 Hordeum vulgare beta-1,3-glucanase 2 (BGL3 92 2e-60
50	gb M62907 BLYCBGL32 H.vulgare L. (1-3)-beta-glucanase mRNA, comp 92 2e-60
	emb A37992 A37992 Sequence 11 from Patent EP0616035. 92 2e-60
	gb M91814 BLYGLU2X Barley beta-1,3-glucanase (GLU2) gene, exons 116 3e-60
	emb AW649248 AW649248 EST327702 tomato germinating seedlings, TA 200 2e-59
•	emb AF034109 AF034109 Glycine max beta-1,3-glucanase 4 (SGlu4) g 139 2e-59
55	emb AW033770 AW033770 EST277341 tomato callus, TAMU Lycopersicon 122 3e-59
	emb AW830464 AW830464 sm27f06.yl Gm-c1028 Glycine max cDNA clone 221 4e-59
	emb AW034001 AW034001 EST277663 tomato callus, TAMU Lycopersicon 202 8e-58
-	emb X67099 HV13GEIII H.vulgare gene for 1,3-glucan endohydrolase 153 2e-57
	emb AW034584 AW034584 EST278268 tomato callus, TAMU Lycopersicon 164 2e-57
60	emb AI894452 AI894452 EST263907 tomato callus, TAMU Lycopersicon 210 4e-57
	emb AW034632 AW034632 EST278316 tomato callus, TAMU Lycopersicon 124 4e-57
	, and the second

emb|AW034478|AW034478 EST278049 tomato callus, TAMU Lycopersicon... 162 9e-57 emb|AW216963|AW216963 EST295677 tomato callus, TAMU Lycopersicon... 202 1e-56 gb|BE020030|BE020030 sm41c02.y1 Gm-c1028 Glycine max cDNA clone ... 220 2e-56 emb|AW032447|AW032447 EST276006 tomato callus, TAMU Lycopersicon... 166 6e-56 5 emblAW031387lAW031387 EST274841 tomato callus, TAMU Lycopersicon... 191 6e-56 emb|AW036009|AW036009 EST282868 tomato callus, TAMU Lycopersicon... 207 1e-55 emb|AW031078|AW031078 EST274385 tomato callus, TAMU Lycopersicon... 109 2e-55 emb|AW035366|AW035366 EST280928 tomato callus, TAMU Lycopersicon... 191 6e-55 emb]AI780513|AI780513 EST261392 tomato susceptible, Cornell Lyco... 110 6e-55 10 Query= ab008104_s_at 16609_s_at /id_source genbank /description dbj/baa32419.1 (ab008104) ethylene responsive element binding factor 2 [arabidopsis thaliana] /blast score 1.00e-112 15 (921 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 20 Searching.....done Score E Sequences producing significant alignments: (bits) Value 25 dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44 emb|AW220395|AW220395 EST302878 tomato root during/after fruit s... 132 9e-43 dbj|D38123|TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds. 134 6e-41 emb|AF245119|AF245119 Mesembryanthemum crystallinum AP2-related ... 161 5e-39 emb|AW267820|AW267820 EST305948 DSIR Medicago truncatula cDNA cl... 160 1e-38 30 emb|AB035270|AB035270 Matricaria chamomilla McEREBP1 mRNA for et... 155 5e-37 gb|U89255|LEU89255 Lycopersicon esculentum DNA-binding protein P... 138 3e-32 emb|AI771213|AI771213 EST252409 tomato ovary, TAMU Lycopersicon ... 135 1e-31 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 134 1e-30 35 emb|AF057373|AF057373 Nicotiana tabacum ethylene response elemen... 125 4e-28 emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 124 8e-28 emb|AW396250|AW396250 sh26c01.yl Gm-c1016 Glycine max cDNA clone... 116 2e-25 emb|AW233956|AW233956 sf32e02.yl Gm-c1028 Glycine max cDNA clone... 115 5e-25 emb|AW185128|AW185128 se87b10.yl Gm-c1023 Glycine max cDNA clone... 114 1e-24 40 emb|AI897834|AI897834 EST267277 tomato ovary, TAMU Lycopersicon ... 113 2e-24 emb|AW349516|AW349516 GM210007B10A12R Gm-r1021 Glycine max cDNA ... 113 2eemb|AV423260|AV423260 AV423260 Lotus japonicus young plants (two... 111 6e-24 emb|AV425560|AV425560 AV425560 Lotus japonicus young plants (two... 111 6e-24 45 emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 89 6e-24 emb|AI899000|AI899000 EST268443 tomato ovary, TAMU Lycopersicon ... 110 2e-23 emb|AI965917|AI965917 sc79f12.y1 Gm-c1018 Glycine max cDNA clone... 110 2e-23 emb|AI794657|AI794657 sb67b03.yl Gm-c1019 Glycine max cDNA clone... 110 2e-23 emb|AW200919|AW200919 se95c12.yl Gm-c1027 Glycine max cDNA clone... 109 3e-23 50 emb|AW507860|AW507860 si45h05.y1 Gm-r1030 Glycine max cDNA clone... 109 3e-23 emb|AW507898|AW507898 si46f03.yl Gm-r1030 Glycine max cDNA clone... 97 3e-23 dbj|D38125|TOBBY4C Tobacco mRNA for EREBP-4, complete cds. 109 4e-23 emb|AW349638|AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3... 109 4e-55 emb|AW278190|AW278190 sf40g11.yl Gm-c1009 Glycine max cDNA clone... 109 4e-23 emb|AI486689|AI486689 EST245011 tomato ovary, TAMU Lycopersicon ... 108 5e-23 emb|AW618245|AW618245 EST314295 L. pennellii trichome, Cornell U... 108 8e-23 emb|AW776671|AW776671 EST335736 DSIL Medicago truncatula cDNA cl... 108 8e-23 emb|AW759181|AW759181 sl38a09.yl Gm-c1027 Glycine max cDNA clone... 107 1e-22 60 emb|AW596384|AW596384 sj02f12.yl Gm-c1032 Glycine max cDNA clone... 107 le-22 emb|AI897797|AI897797 EST267240 tomato ovary, TAMU Lycopersicon ... 107 1e-22

	emb AI973653 AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone 107 1e-22 emb AW620490 AW620490 sj05h02.y1 Gm-c1032 Glycine max cDNA clone 106 2e-22 emb AI899889 AI899889 sb94g05.y1 Gm-c1017 Glycine max cDNA clone 105 4e-22
5	emb AW574222 AW574222 EST316813 GVN Medicago truncatula cDNA clo 105 4e-22 emb AI778693 AI778693 EST259572 tomato susceptible, Cornell Lyco 105 4e-22
	emb AW776668 AW776668 EST335733 DSIL Medicago truncatula cDNA cl 105 4e-22 emb AW774176 AW774176 EST333259 KV3 Medicago truncatula cDNA clo 105 4e-22
	emb AI894873 AI894873 EST264316 tomato callus, TAMU Lycopersicon 103 2e-21 gb U89256 LEU89256 Lycopersicon esculentum DNA-binding protein P 103 2e-21
10	emb AW030386 AW030386 EST273641 tomato callus, TAMU Lycopersicon 103 2e-21 emb AW030009 AW030009 EST273264 tomato callus, TAMU Lycopersicon 103 2e-21
	emb AI782381 AI782381 EST263260 tomato susceptible, Cornell Lyco 100 1e-20 emb AW980654 AW980654 EST391807 GVN Medicago truncatula cDNA clo 100 2e-20
1.5	emb AV422393 AV422393 AV422393 Lotus japonicus young plants (two 100 2e-20
15	emb AI484961 AI484961 EST243224 tomato ovary, TAMU Lycopersicon 100 3e-20 emb AW781602 AW781602 sl82d06.y1 Gm-c1037 Glycine max cDNA clone 100 3e-20
•	emb AW443265 AW443265 EST308195 tomato mixed elicitor, BTI Lycop 100 3e-20
	emb AI440657 AI440657 sa63d09.yl Gm-c1004 Glycine max cDNA clone 99 4e-20 gb U81157 NTU81157 Nicotiana tabacum S25-XP1 DNA binding protein 98 8e-20
20	emb[AJ238740]CRO238740 Catharanthus roseus mRNA for AP2-domain D 98 8e-20
	emb AW840611 AW840611 00057 leafy spurge Lambda HybriZAP 2.1 two 97 1e-19
	emb AW559315 AW559315 EST306358 DSIR Medicago truncatula cDNA cl 97 2e-19
	emb AV421566 AV421566 AV421566 Lotus japonicus young plants (two 97 2e-19
25	emb AI966559 AI966559 sc52a04.y1 Gm-c1015 Glycine max cDNA clone 97 2e-19 emb AI495036 AI495036 sa90a09.y1 Gm-c1004 Glycine max cDNA clone 95 5e-19
23	emb AI442716 AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone 95 5e-19
	emb AI055252 AI055252 coau0003H16 Cotton Boll Abscission Zone cD 67 8e-19
	emb AI967551 AI967551 Ljimpest05-400-d11 Ljimp Lambda HybriZap 95 1e-18
	emb A1896308 A1896308 EST265751 tomato callus, TAMU Lycopersicon 94 1e-18
30	emb AI776626 AI776626 EST257726 tomato resistant, Cornell Lycope 93 3e-18
	emb AW686013 AW686013 NF033D04NR1F1000 Nodulated root Medicago t 92 5e-18
	emb AW981323 AW981323 EST392476 DSIL Medicago truncatula cDNA cl 92 5e-18 emb AV417552 AV417552 AV417552 Lotus japonicus young plants (two 92 5e-18
	emb AW618246 AW618246 EST314296 L. pennellii trichome, Cornell U 92 5e-18
35	emb AW685077 AW685077 NF024H04NR1F1000 Nodulated root Medicago t 90 2e-17
	emb AW573782 AW573782 EST316373 GVN Medicago truncatula cDNA clo 90 2e-17
	emb AW308784 AW308784 sf71h01.yl Gm-c1013 Glycine max cDNA clone 88 1e-16
	emb AW782252 AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone 59 1e-16 emb AW980481 AW980481 EST391634 GVN Medicago truncatula cDNA clo 87 2e-16
40	gb BE023264 BE023264 sm80all.yl Gm-c1015 Glycine max cDNA clone 87 2e-16
. •	emb AW458901 AW458901 sh16c12.y1 Gm-c1016 Glycine max cDNA clone 86 4e-16
	emb AW348322 AW348322 GM210001B23F6R Gm-r1021 Glycine max cDNA 3 85 8e-16
	emb AW685799 AW685799 NF030D09NR1F1000 Nodulated root Medicago t 53 1e-15
45	emb AW775819 AW775819 EST334884 DSIL Medicago truncatula cDNA cl 84 2e-15
40	emb AI731242 AI731242 BNLGHi9002 Six-day Cotton fiber Gossypium 84 2e-15 emb AI898992 AI898992 EST268435 tomato ovary, TAMU Lycopersicon 84 2e-15
ļ.	emb AI736796 AI736796 sb33f06.yl Gm-c1012 Glycine max cDNA clone 83 3e-15
	emb AW560968 AW560968 EST316016 DSIR Medicago truncatula cDNA cl 57 4e-15
	emb AW560196 AW560196 EST315244 DSIR Medicago truncatula cDNA cl 57 4e-15
50	emb AI489709 AI489709 EST248048 tomato ovary, TAMU Lycopersicon 56 6e-15
	emb AW759236 AW759236 sl38f08.y1 Gm-c1027 Glycine max cDNA clone 80 2e-14
	gb BE057468 BE057468 sm58e08.y1 Gm-c1028 Glycine max cDNA clone 55 7e-14 gb T14923 T14923 crs406 lambdaZAPST Ricinus communis cDNA clone 56 9e-14
	emb AI489199 AI489199 EST247538 tomato ovary, TAMU Lycopersicon 52 1e-13
55	emb AI486929 AI486929 EST245251 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AI483636 AI483636 EST249507 tomato ovary, TAMU Lycopersicon 52 1e-13
	emb AW033743 AW033743 EST277314 tomato callus, TAMU Lycopersicon 52 1e-13
	emb AI483510 AI483510 EST249359 tomato ovary, TAMU Lycopersicon 52 1e-13
60	emb AI771755 AI771755 EST252855 tomato ovary, TAMU Lycopersicon 52 1e-13
υU	emb AI485175 AI485175 EST243479 tomato ovary, TAMU Lycopersicon 52 1e-13

emb|AI897787|AI897787 EST267230 tomato ovary, TAMU Lycopersicon ...

```
emb|AI771834|AI771834 EST252934 tomato ovary, TAMU Lycopersicon ...
      emb|AI485460|AI485460 EST243781 tomato ovary, TAMU Lycopersicon ...
                                                                            52 le-13
      emb|AI771795|AI771795 EST252895 tomato ovary, TAMU Lycopersicon ...
      Query= athorf s at 16649 s at /id source
      description gb|aaf16576.1|ac012563 29 (ac012563) putative
      s-adenosyl-l-methionine:trans-caffeoyl-coenzyme a
10
      3-o-methyltransferase [arabidopsis thaliana] /blast score 1.00e-121
      /ec number /family /chip nova /gb link /ncgi
           (965 letters)
      Database: plantfungal
15
            661,018 sequences; 426,114,510 total letters
      Searching.....done
                                           Score
20
      Sequences producing significant alignments:
                                                           (bits) Value
      emb|AB000408|AB000408 Populus kitakamiensis mRNA for caffeoyl-Co... 215 3e-73
      gb[U20736]MSU20736 Medicago sativa S-adenosyl-L-methionine:trans... 142 2e-68
      emb|AW624860|AW624860 EST313689 tomato radicle, 5 d post-imbibit... 139 2e-67
25
      emb|AF022775|AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methylt... 138 2e-67
      emb|Z54233|VVCCOAOMT V.vinifera mRNA for caffeoyl-CoA O-methyltr... 136 9e-67
      gb|M69184|PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl... 133 2e-66
      gb|U27116|PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr... 135 3e-66
      emb|AJ224894|PBTAJ4894 Populus balsamifera subsp. trichocarpa mR... 135 3e-66
30
      gb[U13151|ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-... 136 4e-66
      emb|AI489305|AI489305 EST247644 tomato ovary, TAMU Lycopersicon ... 139 4e-66
      emb|AJ224895|PBTAJ4895 Populus balsamifera subsp. trichocarpa mR... 136 6e-66
      emb|AJ224896|PBTAJ4896 Populus balsamifera subsp. trichocarpa mR... 136 6e-66
      emb|AF168780|AF168780 Eucalyptus globulus caffeoyl-CoA O-methylt... 133 8e-66
35
      emb|AF053553|AF053553 Mesembryanthemum crystallinum caffeoyl-CoA... 132 1e-65
      emb|AF240466|AF240466 Populus tomentosa caffeoyl-CoA O-methyltra... 135 1e-65
      emb|A22706|A22706 Caffeoyl-CoA-3-O-Methyltransferase gene.
      gb|U62734|NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 5e-65
      emb|Z56282|NTCCOAOMT N.tabacum mRNA for caffeoyl-CoA O-methyltra... 132 5e-65
40
      gb|U62736|NTU62736 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 136 5e-65
      gb|U38612|NTU38612 Nicotiana tabacum caffeoyl-coenzymeA O-methyl... 136 5e-65
      emb|Y12228|EG12228 E.gunnii mRNA for caffeoyl-CoA O-methyltransf... 133 7e-65
      gb|L22203|SLASADEN Stellaria longipes S-adenosyl-L-methionine:tr... 124 8e-65
      emb|AF046122|AF046122 Eucalyptus globulus caffeoyl-CoA 3-O-methy... 133 9e-65
45
      gb[U62735]NTU62735 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 3e-64
      emb|AF036095|AF036095 Pinus taeda caffeoyl-CoA O-methyltransfera... 130 6e-64
      emb|AF060180|AF060180 Nicotiana tabacum caffeoyl-coenzyme A trun... 90 9e-60
      emb|AW102353|AW102353 sd86f04.y1 Gm-c1009 Glycine max cDNA clone... 139 5e-58
      emb|AJ130841|PBA130841 Populus balsamifera subsp. trichocarpa mR... 133 2e-57
50
      emb|AJ001447|FVAJ1447 Fragaria vesca mRNA for putative caffeoyl-... 137 3e-57
      gb|BE124003|BE124003 EST394128 DSIL Medicago truncatula cDNA clo... 127 9e-57
      emb|AW775400|AW775400 EST334465 DSIL Medicago truncatula cDNA cl... 142 2e-56
      emb|AW030189|AW030189 EST273444 tomato callus, TAMU Lycopersicon... 133 4e-56
      emb|AW695080|AW695080 NF091D11ST1F1093 Developing stem Medicago ... 142 6e-56
55
      emb|AW348485|AW348485 GM210002B12A10R Gm-r1021 Glycine max cDNA ... 131 2e-
      emb|AI486500|AI486500 EST244821 tomato ovary, TAMU Lycopersicon ... 139 2e-55
      emb|AI166541|AI166541 xylem.est.363 Poplar xylem Lambda ZAPII li... 135 7e-55
      gb|BE034896|BE034896 ML05H01 ML Mesembryanthemum crystallinum cD... 132 1e-54
60
      emb|AW306951|AW306951 sf50h03.y1 Gm-c1009 Glycine max cDNA clone... 133 2e-54
      emb|AW278810|AW278810 sf98g06.y1 Gm-c1019 Glycine max cDNA clone... 135 3e-54
```

```
emb|AI939180|AI939180 sc67h02.yl Gm-c1016 Glycine max cDNA clone... 125 3e-54
      emb|AW102461|AW102461 sd88d11.y1 Gm-c1009 Glycine max cDNA clone... 133 3e-54
      emb|AW776700|AW776700 EST335765 DSIL Medicago truncatula cDNA cl... 127 4e-54
      emb|AW757356|AW757356 sl32c10.yl Gm-c1027 Glycine max cDNA clone... 133 2e-53
 5
      emb|AW030736|AW030736 EST273991 tomato callus, TAMU Lycopersicon... 133 8e-53
      emb|AI898029|AI898029 EST267472 tomato ovary, TAMU Lycopersicon ... 133 8e-53
      emb|AW625527|AW625527 EST319434 tomato radicle, 5 d post-imbibit... 133 8e-53
      emb|AW218547|AW218547 EST303730 tomato radicle, 5 d post-imbibit... 133 8e-53
      emb[AW733300]AW733300 sk71f10.yl Gm-c1016 Glycine max cDNA clone... 134 1e-52
10
      emb|AW442463|AW442463 EST307393 tomato mixed elicitor, BTI Lycop... 133 1e-52
      emb|AW094365|AW094365 EST287545 tomato mixed elicitor, BTI Lycop... 133 1e-52
      gb|BE021597|BE021597 sm60a04.y1 Gm-c1028 Glycine max cDNA clone ... 135 1e-52
      emblAW034347|AW034347 EST277918 tomato callus, TAMU Lycopersicon... 133 2e-52
      emb|AI443130|AI443130 sa84g01.yl Gm-c1004 Glycine max cDNA clone... 131 2e-51
15
      emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51
      emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51'
      emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
      emb|AI899227|AI899227 EST268670 tomato ovary, TAMU Lycopersicon ... 139 3e-50
      emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50
20
      emblAW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
      emblAW690185|AW690185 NF029D09ST1F1000 Developing stem Medicago ... 142 1e-49
      emb|AI895091|AI895091 EST264534 tomato callus, TAMU Lycopersicon... 99 3e-49
      emb|AW306980|AW306980 sf51c05.y1 Gm-c1009 Glycine max cDNA clone... 135 8e-48
      emb|AW695176|AW695176 NF092D12ST1F1101 Developing stem Medicago ... 142 1e-47
25
      emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
      emb|AA660318|AA660318 00189 MtRHE Medicago truncatula cDNA 5' si... 144 2e-47
      emb[AW703717]AW703717 sk23e07.yl Gm-c1028 Glycine max cDNA clone... 132 4e-47
      emb|AW776435|AW776435 EST335500 DSIL Medicago truncatula cDNA cl... 142 5e-47
      emb|AI486948|AI486948 EST245270 tomato ovary, TAMU Lycopersicon ... 100 1e-46
30
      emb|AW620537|AW620537 sj06d09.yl Gm-c1032 Glycine max cDNA clone... 133 le-46
      emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycope... 139 2e-46
      gb|BE124333|BE124333 EST393368 GVN Medicago truncatula cDNA clon... 125 3e-46
      emb|AW704578|AW704578 sk38h08.y1 Gm-c1028 Glycine max cDNA clone... 140 3e-46
      emb|AW350997|AW350997 GM210010A10C11R Gm-r1021 Glycine max cDNA ... 97 6e-46
35
      emb|AW707224|AW707224 sk22c12.y1 Gm-c1028 Glycine max cDNA clone... 140 9e-46
      emb|AW625126|AW625126 EST313943 tomato radicle, 5 d post-imbibit... 133 6e-45
      emb|AI974778|AI974778 T113251e KV2 Medicago truncatula cDNA clon... 142 6e-45
      emb|AI898101|AI898101 EST267544 tomato ovary, TAMU Lycopersicon ... 98 8e-45
      gb|BE124175|BE124175 EST394300 DSIL Medicago truncatula cDNA clo... 127 1e-44
40
      emb|AW686370|AW686370 NF040G10NR1F1000 Nodulated root Medicago t... 127 4e-44
      emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44
      emb|AW256836|AW256836 EST304973 KV2 Medicago truncatula cDNA clo... 144 5e-44
      emb|AW559274|AW559274 EST306110 DSIR Medicago truncatula cDNA cl... 142 5e-44
      emb|AW278618|AW278618 sf46h04.yl Gm-c1009 Glycine max cDNA clone... 139 1e-43
45
      gb|BE059325|BE059325 sn31c09.yl Gm-c1016 Glycine max cDNA clone ... 140 3e-43
      emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43
      emb|AI938893|AI938893 sc62d08.yl Gm-c1016 Glycine max cDNA clone... 134 2e-42
      emb|AW257069|AW257069 EST305206 KV2 Medicago truncatula cDNA clo... 142 2e-42
      emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42
50
      emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
      emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
      emb|AW152892|AW152892 se32d04.y1 Gm-c1015 Glycine max cDNA clone... 82 2e-41
      gb|BE125749|BE125749 DG1 55 H11.b1 A002 Dark Grown 1 (DG1) Sorgh... 127 2e-41
      gb|BE022002|BE022002 sm65c10.y1 Gm-c1028 Glycine max cDNA clone ... 137 3e-41
55
      emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41
      emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
      emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
      emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
      emb|AI960196|AI960196 sc80a08.yl Gm-c1018 Glycine max cDNA clone... 132 5e-40
60
      emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
      emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39
```

Query= atu05206_s_at 17014_s_at /id_source genbank /description gb|aac48925.1| (u05206) ribonuclease [arabidopsis thaliana] /blast_score 1.00e-115 /ec_number /family /chip nova /gb_link /ncgi

(925 letters)

5

```
Database: plantfungal
10
            661,018 sequences; 426,114,510 total letters
      Searching......done
                                          Score E
15
      Sequences producing significant alignments:
                                                          (bits) Value
      emb|AJ012689|CAR012689 Cicer arietinum mRNA for ribonuclease T2.
                                                                        384 e-106
      gb|U13256|NAU13256 Nicotiana alata RNase NE mRNA, complete cds.
                                                                         361 4e-99
      gb|U19924|ZEU19924 Zinnia elegans wounding-induced ribonuclease ... 358 4e-98
20
      emb|AB034638|AB034638 Nicotiana tabacum mRNA for RNase, complete... 353 1e-96
      emb|X79337|LERNALE L.esculentum mRNA for ribonuclease le.
                                                                      212 2e-93
      dbi|D49529|D49529 Pyrus pyrifolia mRNA for ribonuclease, complet... 335 4e-91
      emb|AI486253|AI486253 EST244574 tomato ovary, TAMU Lycopersicon ... 212 2e-89
      emb|AI485206|AI485206 EST243510 tomato ovary, TAMU Lycopersicon ... 212 1e-81
25
      gb|U19923|ZEU19923 Zinnia elegans ribonuclease mRNA, complete cds. 232 3e-80
      emb|X79338|LERNALX L.esculentum mRNA for ribonuclease lx.
      emb|AB032257|AB032257 Nicotiana glutinosa NGR3 mRNA for RNase NG... 176 7e-70
      emb|AI484830|AI484830 EST243091 tomato ovary, TAMU Lycopersicon ... 212 7e-70
      emb|AW684365|AW684365 NF016B03NR1F1000 Nodulated root Medicago t... 251 7e-66
30
      emb|AI489460|AI489460 EST247799 tomato ovary, TAMU Lycopersicon ... 212 3e-63
      emb|Y17444|LES17444 Lycopersicon esculentum RNALE gene, exons 1 ... 152 2e-57
      emb|AI772676|AI772676 EST253776 tomato resistant, Cornell Lycope... 152 2e-57
      emb|AI775352|AI775352 EST256452 tomato resistant, Cornell Lycope... 212 3e-56
      gb|BE037115|BE037115 MP15C03 MP Mesembryanthemum crystallinum cD.... 153 4e-55
35
      emb|AF000939|AF000939 Hordeum vulgare aleurone ribonuclease mRNA... 89 7e-55
      gb[M83668]NELSTORAGE Nelumbo nucifera storage protein mRNA, comp... 127 2e-54
      emb|AI812905|AI812905 22D1 Pine Lambda Zap Xylem library Pinus t... 165 3e-54
      emb|AI488432|AI488432 EST246771 tomato ovary, TAMU Lycopersicon ... 211 5e-54
      emb|AW775298|AW775298 EST334363 DSIL Medicago truncatula cDNA cl... 200 7e-54
40
      emblAW279538lAW279538 sf90h05.yl Gm-c1019 Glycine max cDNA clone... 188 6e-47
      emb|AF000940|AF000940 Hordeum vulgare ribonuclease gene, complet... 116 2e-44
      gb|BE060583|BE060583 HVSMEg0012L03f Hordeum vulgare pre-anthesis... 74 5e-42
      emb|Y17445|LES17445 Lycopersicon esculentum RNALE gene, exons 1 ... 122 6e-42
      emb|AI777654|AI777654 EST258449 tomato susceptible, Cornell Lyco... 152 2e-41
45
      emb|AW596890|AW596890 sj84b03.yl Gm-c1034 Glycine max cDNA clone... 162 3e-39
      gb|BE060118|BE060118 HVSMEg0011I10f Hordeum vulgare pre-anthesis... 89 6e-37
      gb|BE060590|BE060590 HVSMEg0012L10f Hordeum vulgare pre-anthesis... 89 2e-36
      emb|AW704136|AW704136 sk16e03.yl Gm-c1028 Glycine max cDNA clone... 145 4e-34
      emb[AW289659]AW289659 NXNV003D07F Nsf Xylem Normal wood Vertical... 109 8e-32
50
      gb|U19794|MDU19794 Malus domestica S-like RNase gene, partial cds. 76 2e-25
      emb|AI967855|AI967855 Ljimpest14-054-a9 Ljimp Lambda HybriZap ... 109 4e-23
      emb|Y17446|LES17446 Lycopersicon esculentum RNALX gene, exons 1 ... 104 1e-21
      dbi|D64012|LUFRNLC2 Luffa cylindrica mRNA for ribonuclease (RNas... 95 1e-20
      emb|AW053670|AW053670 L30-1447T3 Ice plant Lambda Uni-Zap XR exp... 45 2e-20
55
      gb|BE020073|BE020073 sm38f09.yl Gm-c1028 Glycine max cDNA clone ... 45 7e-20
      emb|AW039494|AW039494 EST281775 tomato mixed elicitor, BTI Lycop... 43 6e-19
      emb|AW216541|AW216541 EST295255 tomato callus, TAMU Lycopersicon... 43 6e-19
      dbj|D64011|LUFRNLC1 Luffa cylindrica mRNA for ribonuclease (RNas... 89 8e-19
      emb|AB026836|AB026836 Prunus dulcis mRNA for Sa-RNase, complete ... 76 1e-18
60
      emb|AW980478|AW980478 EST391631 GVN Medicago truncatula cDNA clo... 44 4e-18
```

gb|BE124916|BE124916 EST393951 GVN Medicago truncatula cDNA clon... 44 4e-18

	emb AB032256 AB032256 Nicotiana glutinosa NGR2 mRNA for RNase NG 41 9e-18
	emb AW775880 AW775880 EST334945 DSIL Medicago truncatula cDNA cl 44 9e-18
	emb AW775566 AW775566 EST334631 DSIL Medicago truncatula cDNA cl 44 1e-17
_	emb AW926310 AW926310 HVSMEg0006O01 Hordeum vulgare pre-anthesis 52 4e-17
5	emb AB034248 AB034248 Volvox carteri vm1 mRNA for S-like RNase, 58 8e-17
	emb AF176533 AF176533 Solanum chacoense self-incompatibility rib 82 2e-16
•	emb AI416638 AI416638 sa17c06.y1 Gm-c1004 Glycine max cDNA clone 45 6e-16
	emb X96465 AHS2RNASE A.hispanicum mRNA for S2-Rnase. 60 2e-15
10	emb AB028153 AB028153 Prunus avium mRNA for S1-RNase, complete cds. 56 3e-15
10	emb AW223027 AW223027 EST299838 tomato fruit red ripe, TAMU Lyco 43 4e-15
	emb AW224120 AW224120 EST300931 tomato fruit red ripe, TAMU Lyco 43 5e-15
	emb AW223831 AW223831 EST300642 tomato fruit red ripe, TAMU Lyco 43 5e-15
	emb AF191732 AF191732 Solanum chacoense self-incompatibility rib 82 6e-15
15	emb AB010306 AB010306 Prunus avium mRNA for S3-RNase, complete cds. 57 2e-14 emb X76065 LPSRNASE L.peruvianum mRNA for S-RNase S3. 60 2e-14
13	emb AB010304 AB010304 Prunus avium mRNA for S2-RNase, partial cds. 60 4e-14
	emb AI729649 AI729649 BNLGHi13860 Six-day Cotton fiber Gossypium 45 9e-14
	emb AI729386 AI729386 BNLGHi13239 Six-day Cotton fiber Gossypium 45 1e-13
	emb AW671991 AW671991 LG1_353_B05.b1_A002 Light Grown 1 (LG1) So 45 1e-13
20	gb S61768 S61768 S (S5)=self-incompatibility {3' region} [Lycope 60 1e-13
	emb X56897 SCSIAP3 S.chacoense mRNA for self-incompatibility ass 63 1e-13
	emb AW563386 AW563386 LG1 214 C01.b1 A002 Light Grown 1 (LG1) So 45 1e-13
	emb AB011470 AB011470 Prunus dulcis mRNA for Sc-RNase, complete 60 3e-13
	emb AB011469 AB011469 Prunus dulcis mRNA for Sb-RNase, complete 57 4e-13
25	emb AW623083 AW623083 EST321028 tomato flower buds 3-8 mm, Corne 43 8e-13
	emb AW034883 AW034883 EST279112 tomato callus, TAMU Lycopersicon 43 8e-13
	emb AF232304 AF232304 Solanum chacoense gametophytic self-incomp 58 1e-12
	emb Z26583 LPSLGS6 L.peruvianum (Mill) self-incompatability glyc 56 1e-12
20	emb AB011471 AB011471 Prunus dulcis mRNA for Sd-RNase, partial cds. 57 1e-12
30	emb AV427528 AV427528 AV427528 Lotus japonicus young plants (two 74 2e-12
	emb AF148465 AF148465 Prunus dulcis Sa-S-RNase gene, partial cds. 73 3e-12
	emb AB026982 AB026982 Prunus salicina mRNA for Sb-RNase, partial 60 5e-12
	dbj E01266 E01266 cDNA encoding S2-protein linked to part of its 56 1e-11 gb M24600 TOBGPS N.alata stylar glycoprotein 2 mRNA, complete cds. 56 1e-11
35	dbjE01267 E01267 cDNA encoding S2-protein linked to its signal 56 1e-11
55	emb X03803 NASINCS2 Nicotiana alata mRNA for S2 self-incompatibi 56 1e-11
	gb L25930 TOBRNASESB Nicotiana alata RNase S mRNA. 56 1e-11
	emb AV410016 AV410016 AV410016 Lotus japonicus young plants (two 44 le-11
	emb AI724132 AI724132 RHIZ1_7_B07.y2_A001 Rhizomel Sorghum halep 70_2e-11
40	emb AJ271062 PHY271062 Petunia hybrida mRNA for Sv-ribonuclease 62 2e-11
	emb AB016522 AB016522 Petunia x hybrida mRNA for SB1-ribonucleas 62 2e-11
	emb AB026981 AB026981 Prunus salicina mRNA for Sa-RNase, partial 56 3e-11
	emb X96464 AHS5RNASE A.hispanicum mRNA for S5-Rnase. 57 4e-11
	gb U19791 MDU19791 Malus domestica S5-RNase (S) mRNA, partial cds. 38 4e-11
45	emb X96466 AHS4RNASE A.hispanicum mRNA for S4-Rnase. 46 7e-11
	gb M81686 PETSXPROB Petunia hybrida Sx-protein (self-incompatibi 58 1e-10
	emb Z26581 LPSLGSC L.peruvianum (Mill) mRNA for self-incompatabi 51 2e-10
	emb X56896 SCSIAP S.chacoense mRNA for self-incompatibility asso 62 3e-10
50	gb L40544 POTFSCS Solanum carolinense self-incompatibility ribon 67 3e-10
50	emb AI460477 AI460477 sa79g07.yl Gm-c1004 Glycine max cDNA clone 42 3e-10
	emb Z26582 LPSLGS7 L.peruvianum (Mill) self-incompatability glyc 61 3e-10 dbj D63887 D63887 Nicotiana alata mRNA for ribonuclease, complet 61 3e-10
	emb AF105363 AF105363 Lycium andersonii self-incompatibility rib 66 4e-10 gb U07362 PHU07362 Petunia hybrida S1 self-incompatibility ribon 62 4e-10
55	gb[L40542[POTDSCS Solanum carolinense self-incompatibility ribon 65 7e-10
	6-1

Query= af098947_s_at 17051_s_at /id_source genbank /description gb|aad09952.1| (af098947) ctf2b [arabidopsis thaliana] /blast_score 0 (1480 letters)

60

Database: plantfungal

```
661,018 sequences; 426,114,510 total letters
 5
                                          Score
                                                 E
      Sequences producing significant alignments:
                                                         (bits) Value
      emb|AI782831|AI782831 EST263710 tomato susceptible, Cornell Lyco... 270 1e-71
10
      emb|AW093706|AW093706 EST286886 tomato mixed elicitor, BTI Lycop... 256 4e-67
      emb|AW279194|AW279194 sf67g10.yl Gm-c1013 Glycine max cDNA clone... 205 2e-53
      emb|AI776928|AI776928 EST258028 tomato resistant, Cornell Lycope... 174 1e-42
      emb|AW441294|AW441294 EST310690 tomato fruit red ripe, TAMU Lyco... 88 9e-42
      emb|AW035369|AW035369 EST280931 tomato callus, TAMU Lycopersicon... 88 3e-35
15
      gb|BE037451|BE037451 MP21C02 MP Mesembryanthemum crystallinum cD... 88 2e-34
      gb|BE058288|BE058288 sn14b07.y1 Gm-c1016 Glycine max cDNA clone ... 88 2e-34
      emb|AI895992|AI895992 EST265435 tomato callus, TAMU Lycopersicon... 80 3e-34
      emb|AW441248|AW441248 EST310644 tomato fruit red ripe, TAMU Lyco... 88 2e-33
      emb|AW223990|AW223990 EST300801 tomato fruit red ripe, TAMU Lyco... 88 2e-33
20
      emb|AW761120|AW761120 sl63e05.yl Gm-c1027 Glycine max cDNA clone... 127 9e-32
      gb|BE037096|BE037096 MP14H01 MP Mesembryanthemum crystallinum cD... 86 2e-30
      emb|AW038060|AW038060 EST279717 tomato mixed elicitor, BTI Lycop... 84 1e-29
      emb|AW030010|AW030010 EST273265 tomato callus, TAMU Lycopersicon... 84 1e-29
      emb|AW035432|AW035432 EST281170 tomato callus, TAMU Lycopersicon... 83 1e-29
25
      emb|AW221846|AW221846 EST298657 tomato fruit red ripe, TAMU Lyco... 80 2e-28
      emb|AW907125|AW907125 EST343157 potato stolon, Cornell Universit... 127 3e-28
      emb[AW306189]AW306189 se47b02.y1 Gm-c1017 Glycine max cDNA clone... 112 4e-27
      emb|AW686451|AW686451 NF038B03NR1F1000 Nodulated root Medicago t... 57 1e-24
      emb|AW934306|AW934306 EST360149 tomato fruit mature green, TAMU ... 80 4e-22
30
      emb|AI896882|AI896882 EST266325 tomato callus, TAMU Lycopersicon... 84 6e-22
      emb|AW030032|AW030032 EST273287 tomato callus, TAMU Lycopersicon... 80 8e-22
      emb|AW216521|AW216521 EST295235 tomato callus, TAMU Lycopersicon... 80 8e-22
      emb|AW216877|AW216877 EST295591 tomato callus, TAMU Lycopersicon... 84 2e-21
      emb|AI895032|AI895032 EST264475 tomato callus, TAMU Lycopersicon... 98 2e-19
35
      emb|AI054656|AI054656 coau0001K05 Cotton Boll Abscission Zone cD... 95 2e-18
      emb|AW350604|AW350604 GM210008B20C3R Gm-r1021 Glycine max cDNA 3... 89 1e-16
      emb|AW985224|AW985224 NXNV_132_F08_F Nsf Xylem Normal wood Verti... 84 2e-15
      emb|AW782240|AW782240 sm03c06.yl Gm-c1027 Glycine max cDNA clone... 80 2e-15
      emb|AI894672|AI894672 EST264115 tomato callus, TAMU Lycopersicon... 80 3e-14
40
      emb|AW034079|AW034079 EST277574 tomato callus, TAMU Lycopersicon... 77 3e-13
      emb|AW991119|AW991119 SsS0174 Suaeda salsa ZAP cDNA library Suae... 58 7e-10
      emb|X95732|NPZEAXANT N.plumbaginifolia mRNA for zeaxanthin epoxi... 63 6e-09
      emb|AV418279|AV418279 AV418279 Lotus japonicus young plants (two... 48 8e-09
      emb|X91491|CAXANEPOX C.annuum mRNA for xanthophyll epoxidase.
                                                                           61 2e-08
45
      emb|Z83835|LEZEAXAN L.esculentum mRNA for zeaxanthin epoxidase.
                                                                          59 1e-07
      emb|AI966377|AI966377 sc38a10.yl Gm-c1014 Glycine max cDNA clone... 49 6e-07
      emb|AF159948|AF159948 Prunus armeniaca zeaxanthin epoxidase (ZEA... 54 3e-06
      emb|AF071888|AF071888 Prunus armeniaca zeaxanthin epoxidase (ZEA... 54 3e-06
      dbj|D38415|AED4ABH Agaricus bisporus DNA for 4-aminobenzoate hyd... 47 3e-04
50
      emb|AQ274524|AQ274524 mgxb0022E01r CUGI Rice Blast BAC Library P... 47 3e-04
      emb|AW982239|AW982239 HVSMEg0002G20f Hordeum vulgare pre-anthesi... 36 5e-04
      emb|AJ274152|AJ274152 AJ274152 Metarhizium anisopliae ARSEF 2575... 41 0.018
      emb|Z35859|SCYBL098W S.cerevisiae chromosome II reading frame OR... 39 0.12
      emb|X79489|SCDNCH2 S.cerevisiae genomic DNA, chromosome II from ... 39 0.12
      emb|AW265977|AW265977 L30-2632T3 Ice plant Lambda Uni-Zap XR exp... 39 0.12
      emb|AQ936092|AQ936092 Gm_UMb001_014_G18F UMN Soybean BAC Library...
      emb|AA786833|AA786833 m6d11a1.rl Aspergillus nidulans 24hr asexu... 38 0.23
      emb|AV425826|AV425826 AV425826 Lotus japonicus young plants (two... 37 0.42
      emb|AB017765|AB017765 Trypanosoma cruzi genes for GATase-CPSase,... 36 0.80
60
      emb|AL115728|CNS01CMW Botrytis cinerea strain T4 cDNA library un... 36 0.80
      gb|U35892|NHU35892 Nectria haematococca maackiain detoxification... 36 0.80
```

	emb AI496271 AI496271 sb01f06.yl Gm-c1004 Glycine max cDNA clone 36 0.80
	emb AJ223325 CRAJ3325 Chlamydomonas reinhardtii mRNA for ascorba 35 1.1
	emb AW185727 AW185727 se58h04.yl Gm-c1019 Glycine max cDNA clone 35 1.5
	emb AW279175 AW279175 sf67d04.yl Gm-c1013 Glycine max cDNA clone 35 1.5
5	emb AF211986 AF211986 Acleisanthes anisophylla 18S ribosomal RNA 35 1.5
•	emb AW348744 AW348744 GM210003A22C7R Gm-r1021 Glycine max cDNA 3 35 2.1
	emb AZ217020 AZ217020 Sheared DNA-75G4.TF Sheared DNA Trypanosom 35 2.1
	emb X80690 SCDNASEQ S.cerevisiae DNA sequence. 35 2.1
	emb Z73040 SCYGR255C S.cerevisiae chromosome VII reading frame O 35 2.1
10	emb AW680385 AW680385 WS1_52_D05.g1_A002 Water-stressed 1 (WS1) 35 2.1
	gb N83134 N83134 TgESTzy73d09.r1 TgRH Tachyzoite cDNA Toxoplasma 35 2.1
	emb X99228 SCCHRVII S.cerevisiae genomic sequence from chromosom 35 2.1
	emb AW311010 AW311010 sg31e02.x1 Gm-c1024 Glycine max cDNA clone 35 2.1
	emb AL114377 CNS01BLD Botrytis cinerea strain T4 cDNA library un 35 2.1
15	gb BE122310 BE122310 894019A08.yl C. reinhardtii CC-1690, normal 35 2.1
13	
	emb AF003698 AF003698 Saccharomyces cerevisiae COQ6 monooxygenas 35 2.1
	emb AW460022 AW460022 si07g06.yl Gm-c1029 Glycine max cDNA clone 27 2.5
	emb AI855502 AI855502 sc20a03.y1 Gm-c1013 Glycine max cDNA clone 34 2.9
••	emb AJ011587 KLA011587 Kluyveromyces lactis muf1 gene. 34 2.9
20	emb AI068756 AI068756 mgae0004aD11f Magnaporthe grisea Appressor 34 2.9
٠.	emb AW286092 AW286092 LG1_261_C09.b1_A002 Light Grown 1 (LG1) So 34 2.9
•	emb AW925351 AW925351 HVSMEg0001B14 Hordeum vulgare pre-anthesis 34 2.9
	emb AW760781 AW760781 sl36h06.yl Gm-c1027 Glycine max cDNA clone 34 2.9
	emb AW063028 AW063028 SBcD23 Sugar beet leaf cDNA library Beta v 34 2.9
25	emb AV429219 AV429219 AV429219 Lotus japonicus young plants (two 34 2.9
	emb AF068686 AF068686 Glycine max geranylgeranyl hydrogenase (Gg 34 2.9
	emb AQ447995 AQ447995 mgxb0015N12r CUGI Rice Blast BAC Library P 30 3.2
	embjAI398631 AI398631 NCW06C8T7 Westergaards Neurospora crassa c 29 3.3
30	
30	emb AW477291 AW477291 ga44f01.yl Moss EST library PPU Physcomitr 34 3.9
	emb AW187125 AW187125 BNLGHi10212 Six-day Cotton fiber Gossypium 34 3.9
	gb L04488 TORPHD Trichosporon cutaneum phenol hydroxylase mRNA, 34 3.9
	emb Z74962 BO13G6IG B.oleracea mRNA (unknown). 34 3.9
	emb AA519702 AA519702 TgESTzz27g11.rl TgME49 invivo Bradyzoite c 34 3.9
35	emb AF008953 AF008953 Octomeles sumatrana 18S ribosomal RNA gene 34 3.9
	emb AL096797 SPBC146 S.pombe chromosome II cosmid c146. 30 4.4
	gb M62862 TRBRTE Trypanosoma cruzi retrotransposon encoding gag 33 5.4
	emb AQ411986 AQ411986 CpG0944B CpIOWAgDNA1 Cryptosporidium parvu 33 5.4
	emb AV389573 AV389573 AV389573 Chlamydomonas reinhardtii C9 Chla 33 5.4
40	emb AC004145 AC004145 Leishmania major chromosome 3 clone L5801 33 5.4
	emb AI065213 AI065213 TENU2096 T, cruzi epimastigote normalized 33 5.4
	emb AI075591 AI075591 TENU3013 T. cruzi epimastigote normalized 33 5.4
	emb Z93115 MAZ93115 M.acuminata mRNA; clone pBAN UU131. 33 5.4
	a being a series and a series of the series
45	
+ J	emb AL160727 P417R Leishmania major Friedlin PAC P417 right end 33 5.4
	emb AW745646 AW745646 WS1_36_D09.b1_A002 Water-stressed 1 (WS1) 33 5.4
	emb AA901886 AA901886 NCM4A1T3 Mycelial Neurospora crassa cDNA c 29 6.0
50	Query= athrlpka_s_at 17068_s_at /id_source genbank /description
	gb aaa32857.1 (m84658) receptor-like protein kinase [arabidopsis
	thaliana] /blast_score 0
	(2746 letters)
55	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
	oonomis
60	. Comp. E
UU	Score E
	Sequences producing significant alignments: (bits) Value

emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 182 5e-65 emb|A67797|A67797 Sequence 2 from Patent WO9743427. gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 128 5e-51 5 emb|AW432288|AW432288 sh71g05.y1 Gm-c1015 Glycine max cDNA clone... 200 5e-50 emblAI730535lAI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 152 1e-49 emb|AF085168|AF085168 Triticum aestivum receptor-like protein ki... 77 2e-46 emb|AF085166|AF085166 Hordeum vulgare receptor-like kinase gene,... 86 2e-45 emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 85 3e-45 10 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 82 8e-45 emb|AF100771|AF100771 Hordeum vulgare receptor-like kinase (Hv3A... 100 2e-44 gb U78762 TAU78762 Triticum aestivum receptor-like kinase ARK1AS... 86 2e-44 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 129 7e-44 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 129 1e-43 15 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 82 2e-43 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 80 7e-43 dbi|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 77 3e-42 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 86 4e-42 emb|AI771630|AI771630 EST252730 tomato ovary, TAMU Lycopersicon ... 86 5e-42 20 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 123 8e-42 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 87 2e-41 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 84 2e-41 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 126 2e-41 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 75 3e-41 25 dbi|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 82 9e-41 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 76 3e-40 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 72 5e-40 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 108 2e-39 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 91 3e-39 30 emb[Y14285]BOY14285 Brassica oleracea mRNA for SFR1 protein. emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 86 5e-39 emb|AW930866|AW930866 EST356709 tomato fruit mature green, TAMU ... 126 1e-38 emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 122 1e-38 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 35 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 84 2e-38 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2.... 84 2e-38 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 68 2e-38 gb|BE057261|BE057261 sm99f12.yl Gm-c1015 Glycine max cDNA clone ... 86 3e-38 emb[Y14286]BOY14286 Brassica oleracea SFR3 gene, partial. 40 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 82 3e-38 emblZ18921BOSRKL B.oleracea gene for S-receptor kinase-like pro... 83 4e-38 emb|AQ989326|AQ989326 Gm ISb001 058 O23R ISU Soybean BAC Library... 94 5e-38 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 75 5e-38 dbj E05046 E05046 DNA encoding ZmPK1 homologue protein in tobacco. 75 5e-38 45 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 81 6e-38 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 91 1e-37 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 111 2e-37 emb|AF131222|AF131222 Lophopyrum elongatum protein serine/threon... 110 3e-37 50 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 78 5e-37 emb|AI486547|AI486547 EST244868 tomato ovary, TAMU Lycopersicon ... 100 6e-37 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 100 7e-37 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 100 9e-37 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 78 1e-36 55 emb|AW030223|AW030223 EST273478 tomato callus, TAMU Lycopersicon... 92 2e-36 emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 118 2e-36 emb|AW704997|AW704997 sk41c03.yl Gm-c1019 Glycine max cDNA clone... 89 2e-36 emb|AI967314|AI967314 Ljirnpest00-017 Ljirnp Lambda HybriZap two... 69 2e-36 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 78 2e-36 60 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 82 4e-36 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 122 8e-36

emb|AW687349|AW687349 NF008F08RT1F1074 Developing root Medicago ... 80 9e-36 emblAI487456|AI487456 EST245778 tomato ovary, TAMU Lycopersicon ... 97 1e-35 emb|AW668493|AW668493 GA_Ea0014C20 Gossypium arboreum 7-10 dpa ... 73 2e-35 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 64 2e-35 5 emb|AW565461|AW565461 LG1_344_F11.g1_A002 Light Grown 1 (LG1) So... 106 4e-35 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 76 4e-35 gb|BE059471|BE059471 sn32d11.yl Gm-c1016 Glycine max cDNA clone ... 115 5e-35 emblAA738546|AA738546 SbRLK4 Sorghum bicolor cv. TX430 leaf Sorg... 120 1e-34 emb|AW760240|AW760240 sl59g07.yl Gm-c1027 Glycine max cDNA clone... 76 1e-34 10 emb|AW597214|AW597214 si71g06.yl Gm-c1031 Glycine max cDNA clone... 126 2e-34 emb|AW092144|AW092144 EST285240 tomato mixed elicitor, BTI Lycop... 122 2e-34 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 74 2e-34 emb[Y18260]BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 74 3e-34 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 74 3e-34 emblAW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 93 3e-34 15 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 67 3e-34 emb|AI896277|AI896277 EST265720 tomato callus, TAMU Lycopersicon... 111 3e-34 emb|AW666082|AW666082 sk31h04.yl Gm-c1028 Glycine max cDNA clone... 116 3e-34 emb|AW233982|AW233982 sf32g05.y1 Gm-c1028 Glycine max cDNA clone... 130 3e-34 20 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 77 6e-34 emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 71 6e-34 emb|AW329840|AW329840 N201116e rootphos(-) Medicago truncatula c... 119 9e-34 emb|AW679172|AW679172 WS1 23 D02.b1 A002 Water-stressed I (WS1) ... 145 1e-33 emb|AA738547|AA738547 SbRLK5 Sorghum bicolor cv. TX430 leaf Sorg... 115 2e-33 25 emb|AW267961|AW267961 EST306183 DSIR Medicago truncatula cDNA cl... 76 2e-33 emb|AI736063|AI736063 sb22d04.y1 Gm-c1007 Glycine max cDNA clone... 68 8e-33 emb|AI967315|AI967315 Ljirnpest00-018 Ljirnp Lambda HybriZap two... 75 2e-32 emb|AI823209|AI823209 L30-1092T3 Ice plant Lambda Uni-Zap XR exp... 85 3e-32 30 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 72 4e-32 emblAW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 79 4e-32 emb|AW329560|AW329560 N200811e rootphos(-) Medicago truncatula c... 95 4e-32 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 78 5e-32 gb|BE058691|BE058691 sn19e05.yl Gm-c1016 Glycine max cDNA clone ... 108 5e-32 35 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 76 7e-32 emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 118 7e-32 emb|AI727531|AI727531 BNLGHi8333 Six-day Cotton fiber Gossypium ... 125 7e-32 emb|AW649958|AW649958 EST328412 tomato germinating seedlings, TA... 79 2e-31 emb|AW279355|AW279355 sf65g10.yl Gm-c1013 Glycine max cDNA clone... 118 3e-31 40 emb|AW040672|AW040672 EST283536 tomato mixed elicitor, BTI Lycop... 111 3e-31 Query= atu18770 s at 17083 s at /id source /description gb|aad25838.1|ac006951 17 (ac006951) putative 45 indole-3-glycerol phosphate synthase [arabidopsis thaliana] /blast score 0 (1362 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

Score E

55 Sequences producing significant alignments:

50

60

(bits) Value

emb|AI483399|AI483399 EST241520 tomato shoot, Cornell Lycopersic... 289 2e-89 emb|AW728148|AW728148 GA_Ea0014F23 Gossypium arboreum 7-10 dpa ... 247 1e-84 emb|AW200814|AW200814 se93h01.y1 Gm-c1027 Glycine max cDNA clone... 212 3e-78 emb|AI490817|AI490817 EST241526 tomato shoot, Cornell Lycopersic... 189 3e-71 emb|AW757393|AW757393 sl32g05.y1 Gm-c1027 Glycine max cDNA clone... 185 8e-63

emb|AI731648|AI731648 BNLGHi10360 Six-day Cotton fiber Gossypium... 182 2e-61 emb|AW458591|AW458591 shl 1b01.yl Gm-c1016 Glycine max cDNA clone... 138 1e-59 emb|AW033644|AW033644 EST277215 tomato callus, TAMU Lycopersicon... 144 1e-51 emb[AW704608]AW704608 sk54c06.yl Gm-c1019 Glycine max cDNA clone... 153 5e-51 emb|AW458875|AW458875 sh16b06.y1 Gm-c1016 Glycine max cDNA clone... 113 3e-49 5 emb|AW648549|AW648549 EST327003 tomato germinating seedlings, TA... 116 3e-48 gb|BE125163|BE125163 DG1_13_H04.b1_A002 Dark Grown 1 (DG1) Sorgh... 180 2e-44 gb|BE053284|BE053284 GA Ea0007G10f Gossypium arboreum 7-10 dpa ... 123 1e-43 emb|AW648007|AW648007 EST326461 tomato germinating seedlings, TA... 100 2e-38 10 emb|AI773256|AI773256 EST254356 tomato resistant, Cornell Lycope... 99 5e-38 gb|BE052703|BE052703 GA__Ea0031N16f Gossypium arboreum 7-10 dpa ... 86 1e-36 emb|AW676692|AW676692 DG1_13_H04.g1_A002 Dark Grown 1 (DG1) Sorg... 105 4e-31 emb|AW758260|AW758260 874006H11.y1 C. reinhardtii CC-1690, Lambd... 132 6e-30 emb|AW564868|AW564868 LG1 310 H09.b1 A002 Light Grown 1 (LG1) So... 104 3e-29 15 emb|AL096874|SPBC1539 S.pombe chromosome II cosmid c1539. emb|AW696155|AW696155 NF103A11ST1F1084 Developing stem Medicago ... 76 6e-29 emb|Y09137|SPTRP1 S.pombe trp-1 mRNA. 57 1e-28 emblAW618611|AW618611 EST320597 L. pennellii trichome, Cornell U... 82 4e-24 emb|AV420994|AV420994 AV420994 Lotus japonicus young plants (two... 106 3e-22 20 emb|AI490823|AI490823 EST241532 tomato shoot, Cornell Lycopersic... 104 2e-21 emb|AW432225|AW432225 sh70g02.y1 Gm-c1015 Glycine max cDNA clone... 95 2e-18 gb|BE059030|BE059030 sn24c03.y1 Gm-c1016 Glycine max cDNA clone ... 78 1e-13 emb|AU012336|AU012336 AU012336 Schizosaccharomyces pombe late lo... 48 1e-10 emb|X53576|ANTRPCA Aspergillus niger trpC gene for glutamine ami... 64 3e-09 25 emb[X07071]ANTRPC Aspergillus niger trpC gene. 64 3e-09 emb|X05033|PCTRPC Penicillium chrysogenum trpC gene for put. tri... 62 7e-09 emb|X02390|ANTRPC1 Aspergillus nidulans trpC gene. 62 7e-09 gb|M23177|PBLTRPX1A Phycomyces blakesleeanus (TRP1) gene, comple... 61 3e-08 dbj|E00783|E00783 DNA encoding for structural gene MOX(alcoholox... 58 1e-07 30 emb|A11156|A11156 MOX structural gene and it's 5'and 3'-flanking... 58 1e-07 emb|X02425|HPMOXG Hansenula polymorpha MOX gene for methanol oxi... 58 1e-07 emb|X70035|CHTRP1 C.heterostrophus gene for trifunctional trypto... 58 2e-07 gb[M64473]PHTTRP1 Phytophthora parasitica N-(5'-phosphoribosvl)a... 57 3e-07 gblJ01252|NEUTRP1 n.crassa trifunctional tryptophan biosynthesis... 57 3e-07 35 emb|X56047|PDTRPC P. chrysosporium trpC gene for trifunctional p... 55 1e-06 emb[X75951|SC6ORF S.cerevisiae URA1, SAC1, RSD1 and TRP3 genes a... 50 1e-06 gb|K01386|YSCTRP3 Yeast (S.cerevisiae) TRP3 gene coding for anth... 50 1e-06 emb|Z28211|SCYKL211C S.cerevisiae chromosome XI reading frame OR... 50 1e-06 emb|A86135|A86135 Sequence 794 from Patent EP0866129. 40 gb[M74901]CPCTRP1 Cryprococcus neoformans phosphoribosyl anthran... 40 0.042 emb[X75652]ALRIBT A.longa plastid genes for tRNAs, ribosomal pro... 36 0.74 emb[X14385]ALCRPEF Astasia longa chloroplast rps7 and tufA genes... 36 0.74 emb[X51672|SCRSD1 Saccharomyces cerevisiae rsd1 gene. emb|AL049180|PFMAL13P1 Plasmodium falciparum chromosome 13 strai... 34 2.6 45 gb|U33057|SCD9717 Saccharomyces cerevisiae chromosome IV cosmids... 34 2.6 emb|AV423493|AV423493 AV423493 Lotus japonicus young plants (two... 34 3.6 emb|AL353822|NC15E6 Neurospora crassa DNA linkage group V Cosmid... 34 3.6 emb|AW180222|AW180222 MgA0308f MgA Library Mycosphaerella gramin... 34 3.6 emb|AJ133598|PSA133598 Pisum sativum chloroplast gF16P gene, exo... 33 5.0 50 emb|AI054479|AI054479 coau0001B20 Cotton Boll Abscission Zone cD... 33 5.0 gb|L34806|PEAFRUBISP Pisum sativum fructose-1,6-bisphosphate mRN... 33 5.0 emb|X68826|PSF16B P.sativum mRNA for fructose 1,6 biphosphatase. emb|AV391683|AV391683 AV391683 Chlamydomonas reinhardtii C9 Chla... 33 5.0 emb|AJ231281|BSAJ1281 Brachythecium salebrosum partial mRNA for ... 33 6.8 55 emb|AQ902358|AQ902358 LMAJFV1_lm85h07.x1 Leishmania major FV1 ra... 33 6.8 emb|AQ654520|AQ654520 Sheared DNA-10A10.TF Sheared DNA Trypanoso... 32 9.3 emb|AF180022|AF180022 Adiantum capillus-veneris photosystem I P7... 32 9.3 emb|AQ649354|AQ649354 Sheared DNA-30F1.TF Sheared DNA Trypanosom... 32 9.3 gb|L44013|BLYCH Hordeum vulgare (clone WG241) STS mRNA, sequence... 32 9.3 60 emb|AA451566|AA451566 AOB168f Onion seedling leaf cDNA library A... 32 9.3 dbj|D87301|D87301 D87301 Trypanosoma cruzi Y (Tomoo Tanaka) Tryp... 28 10.0

Query= atu66345_s_at 17097 s_at /id_source genbank /description gb|aac49697.1| (u66345) calreticulin [arabidopsis thaliana] /blast score 0 5 (1424 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching......done Score E Sequences producing significant alignments: (bits) Value 15 emb|AJ002057|BVMRNAC Beta vulgaris mRNA for calreticulin. 577 e-163 emb|Z71395|NPCAL1MNR N.plumbaginifolia mRNA for calreticulin. 575 e-163 gb|U74630|RCU74630 Ricinus communis calreticulin mRNA, complete ... 575 e-163 emb|AF052040|AF052040 Berberis stolonifera calreticulin mRNA, co... 571 e-162 emb|X85382|NTRNATCAL N.tabacum mRNA for calreticulin. 20 emb|AF134733|AF134733 Prunus armeniaca calcium-binding protein c... 565 e-160 gb|L27349|BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par... 560 e-159 gb|L27348|BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par... 560 e-159 emblAF019376|AF019376 Brassica napus calreticulin mRNA, complete... 465 e-156 emb|X80756|CAPCRTC C.annuum PCRTC mRNA. 25 gb|U74631|RCU74631 Ricinus communis calreticulin gene, complete ... 149 e-123 emb|AJ000765|CRAJ765 Chlamydomonas reinhardtii mRNA for calretic... 369 e-122 emb|AI728389|AI728389 BNLGHi10665 Six-day Cotton fiber Gossypium... 438 e-122 emb|AI782264|AI782264 EST263143 tomato susceptible, Cornell Lyco... 418 e-116 emb|AB018243|AB018243 Solanum melongena EEF22 mRNA for calreticu... 402 e-111 30 emb|AW216727|AW216727 EST295441 tomato callus, TAMU Lycopersicon... 391 e-108 emb|AW509432|AW509432 si37b03.y1 Gm-r1030 Glycine max cDNA clone... 389 e-107 emb|AW039860|AW039860 EST282333 tomato mixed elicitor, BTI Lycop... 382 e-105 emb|AW624478|AW624478 EST322423 tomato flower buds 3-8 mm, Corne... 378 e-104 35 emb|AW626316|AW626316 EST320223 tomato radicle, 5 d post-imbibit... 375 e-103 emb|AW622049|AW622049 EST312847 tomato root during/after fruit s... 363 3e-99 emb|AW568477|AW568477 si59c07.yl Gm-r1030 Glycine max cDNA clone... 361 9e-99 emblAW441195|AW441195 EST310591 tomato fruit red ripe, TAMU Lyco... 359 2e-98 40 gb|BE059929|BE059929 sn38h08.yl Gm-c1016 Glycine max cDNA clone ... 350 1e-95 emb|AW944954|AW944954 EST337004 tomato flower buds 3-8 mm, Corne... 349 3e-95 emb|AW932476|AW932476 EST358319 tomato fruit mature green, TAMU ... 348 5e-95 emb|AW930392|AW930392 EST340945 tomato fruit mature green, TAMU ... 348 7e-95 emb|AW649196|AW649196 EST327650 tomato germinating seedlings, TA... 347 2e-94 45 emb|AW650460|AW650460 EST328914 tomato germinating seedlings, TA... 344 8e-94 emb|AW560421|AW560421 EST315469 DSIR Medicago truncatula cDNA cl... 330 1e-93 emb|AW650947|AW650947 EST329401 tomato germinating seedlings, TA... 343 2e-93 emb[AW685878]AW685878 NF031C11NR1F1000 Nodulated root Medicago t... 341 6e-93 emb|AW756722|AW756722 sl26d08.yl Gm-c1027 Glycine max cDNA clone... 336 2e-91 emb|AW934135|AW934135 EST359978 tomato fruit mature green, TAMU ... 333 2e-90 50 emb|AW621571|AW621571 EST312369 tomato root during/after fruit s... 333 2e-90 emb|Y09816|EGCALRPR E.gracilis mRNA for calreticulin precursor. emb|AI960982|AI960982 sc93e09.yl Gm-c1019 Glycine max cDNA clone... 328 6e-89 55 emb|AW033447|AW033447 EST277018 tomato callus, TAMU Lycopersicon... 323 2e-87 emb|AW201052|AW201052 se97c10.yl Gm-c1027 Glycine max cDNA clone... 316 2e-85 60 emb|AW773947|AW773947 EST332933 KV3 Medicago truncatula cDNA clo... 316 2e-85

emb|AI726591|AI726591 BNLGHi6198 Six-day Cotton fiber Gossypium ... 312 5e-84

	. 1.14.772.500.114.772.500.1 10.1 00. 1.007.01 '
	emb AI735991 AI735991 sb21e08.yl Gm-c1007 Glycine max cDNA clone 309 3e-83
	emb AI812952 AI812952 22G9 Pine Lambda Zap Xylem library Pinus t 247 9e-82
	emb AW219282 AW219282 EST301764 tomato root during/after fruit s 303 2e-81
-	emb AW035959 AW035959 EST282818 tomato callus, TAMU Lycopersicon 303 3e-81
5	emb Y09078 DBCALLKPR D.bioculata mRNA for calreticulin-like prot 225 7e-81
	emb AA660877 AA660877 00772 MtRHE Medicago truncatula cDNA 5' si 207 8e-80
	emb AW509028 AW509028 si39c02.y1 Gm-r1030 Glycine max cDNA clone 297 1e-79
	emb AW306403 AW306403 se50b10.yl Gm-c1017 Glycine max cDNA clone 296 3e-79
	emb AW773889 AW773889 EST332875 KV3 Medicago truncatula cDNA clo 295 7e-79
10	emb AW727696 AW727696 GA_Ea0015K01 Gossypium arboreum 7-10 dpa 258 8e-79
	emb AW705880 AW705880 sk52a09.yl Gm-c1019 Glycine max cDNA clone 293 2e-78
	emb AW299150 AW299150 EST305824 KV2 Medicago truncatula cDNA clo 293 2e-78
	emb AI898214 AI898214 EST267657 tomato ovary, TAMU Lycopersicon 292 6e-78
	emb AW738476 AW738476 EST339903 tomato flower buds, anthesis, Co 291 1e-77
15	emb AW933869 AW933869 EST359712 tomato fruit mature green, TAMU 287 1e-76
	emb AW695765 AW695765 NF098D02ST1F1016 Developing stem Medicago 286 4e-76
	emb AW220942 AW220942 EST297411 tomato fruit mature green, TAMU 285 5e-76
	emb AW649817 AW649817 EST328271 tomato germinating seedlings, TA 285 5e-76
	emb AA660477 AA660477 00363 MtRHE Medicago truncatula cDNA 5' si 281 7e-75
20	emb AW184893 AW184893 se82a03.yl Gm-c1023 Glycine max cDNA clone 281 1e-74
	emb AW309216 AW309216 sg05g07.yl Gm-c1019 Glycine max cDNA clone 281 1e-74
	emb AW979917 AW979917 EST341567 tomato root deficiency, Cornell 279 3e-74
	emb AW132963 AW132963 se12f08.y1 Gm-c1013 Glycine max cDNA clone 278 6e-74
	emb AW277466 AW277466 sf82d10.y1 Gm-c1019 Glycine max cDNA clone 276 3e-73
25	emb AW033083 AW033083 EST276642 tomato callus, TAMU Lycopersicon 275 8e-73
_	emb AI899646 AI899646 EST269089 tomato susceptible, Cornell Lyco 272 5e-72
	emb AW773817 AW773817 EST332803 KV3 Medicago truncatula cDNA clo 271 1e-71
	emb AW727636 AW727636 GA_Ea0015E17 Gossypium arboreum 7-10 dpa 270 2e-71
	emb AI973534 AI973534 sc88a04.y1 Gm-c1019 Glycine max cDNA clone 270 3e-71
30	emb AW648010 AW648010 EST326464 tomato germinating seedlings, TA 268 7e-71
	emb AI495184 AI495184 sa89b11.yl Gm-c1004 Glycine max cDNA clone 267 1e-70
	emb AI437497 AI437497 sa34a12.yl Gm-c1004 Glycine max cDNA clone 265 6e-70
	emb AI489195 AI489195 EST247534 tomato ovary, TAMU Lycopersicon 264 2e-69
	emb AI771812 AI771812 EST252912 tomato ovary, TAMU Lycopersicon 264 2e-69
35	emb AW728940 AW728940 GA_Ea0018J21 Gossypium arboreum 7-10 dpa 262 6e-69
	emb AW043340 AW043340 ST32B12 Pine TriplEx shoot tip library Pin 260 1e-68
	emb AW596414 AW596414 sj12b07.y1 Gm-c1032 Glycine max cDNA clone 256 3e-67
	emb AW731131 AW731131 GA_ Ea0008P21 Gossypium arboreum 7-10 dpa 256 3e-67
	emb AW933031 AW933031 EST358874 tomato fruit mature green, TAMU 254 9e-67
40	emb AW649360 AW649360 EST327814 tomato germinating seedlings, TA 254 1e-66
	emb AW266258 AW266258 L30-2972T3 Ice plant Lambda Uni-Zap XR exp 253 3e-66
	emb AW907386 AW907386 EST343509 potato stolon, Cornell Universit 252 4e-66
	emb AW035234 AW035234 EST280496 tomato callus, TAMU Lycopersicon 252 6e-66
	emb AI779884 AI779884 EST260763 tomato susceptible, Cornell Lyco 151 7e-66
45	emb AW587738 AW587738 ST66B09 Pine TriplEx shoot tip library Pin 248 6e-65
	gb BE055451 BE055451 GA_Ea0033B14f Gossypium arboreum 7-10 dpa 247 1e-64
	emb AI166964 AI166964 xylem.est.744 Poplar xylem Lambda ZAPII li 247 2e-64
	emb AW720057 AW720057 LjNEST13b1r Lotus japonicus nodule library 246 4e-64
	emb AV419506 AV419506 AV419506 Lotus japonicus young plants (two 242 7e-63
50	emb AW760501 AW760501 sl51b04.yl Gm-c1027 Glycine max cDNA clone 239 3e-62
	emb AF107115 AF107115 Trypanosoma cruzi calreticulin (clr) gene, 143 9e-61
	emb AF162779 AF162779 Trypanosoma cruzi Tc45-calreticulin precur 143 2e-60
	emb AW725203 AW725203 GA_Ea0015H01 Gossypium arboreum 7-10 dpa 232 4e-60
	252 40-00
55	
	Query= athrprp1a_s_at 17128_s_at /id_source
	/description gb aac69381.1 (ac005398) pathogenesis-related
	T O-lanes against (magges a) harmalements remove

Query= athrprp1a_s_at 17128_s_at /id_source /description gb|aac69381.1| (ac005398) pathogenesis-related pr-1-like protein [arabidopsis /blast_score 1.00e-94 /ec_number /family /chip nova /gb_link /ncgi (757 letters)

60

Database: plantfungal 661,018 sequences: 426,114,510 total letters Searching.....done 5 Ε Score Sequences producing significant alignments: (bits) Value gb U70666 BNU70666 Brassica napus pathogenesis-related protein P... 323 3e-89 10 gb|U21849|BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds. 323 3e-89 gb|U64806|BNU64806 Brassica napus pathogenesis-related protein P... 209 4e-86 emb|AI352851|AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl... 311 5e-84 emblAI352893|AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl... 165 3e-62 emb|AW217013|AW217013 EST295727 tomato callus, TAMU Lycopersicon... 152 4e-60 15 emblAW219671|AW219671 EST302153 tomato root during/after fruit s... 151 1e-59 emb|AW092403|AW092403 EST285583 tomato mixed elicitor, BTI Lycop... 151 1e-59 emb|AI895090|AI895090 EST264533 tomato callus, TAMU Lycopersicon... 151 1e-59 emb|AW625930|AW625930 EST319825 tomato radicle, 5 d post-imbibit... 151 1e-59 emb|AW032514|AW032514 EST276073 tomato callus, TAMU Lycopersicon... 151 1e-59 20 emb|AW034260|AW034260 EST277831 tomato callus, TAMU Lycopersicon... 151 1e-59 emblAW040983|AW040983 EST283847 tomato mixed elicitor, BTI Lycop... 151 1e-59 emb|AW034206|AW034206 EST277777 tomato callus, TAMU Lycopersicon... 151 1e-59 emb|AW219480|AW219480 EST301878 tomato root during/after fruit s... 151 1e-59 emb|AW092623|AW092623 EST285803 tomato mixed elicitor, BTI Lycop... 151 1e-59 25 emb|AW040954|AW040954 EST283818 tomato mixed elicitor, BTI Lycop... 151 1e-59 emb|AW034454|AW034454 EST278025 tomato callus, TAMU Lycopersicon... 151 1e-59 emb|AW032723|AW032723 EST276282 tomato callus, TAMU Lycopersicon... 151 1e-59 emb|AW033873|AW033873 EST277444 tomato callus, TAMU Lycopersicon... 151 1e-59 emb|AI894650|AI894650 EST264093 tomato callus, TAMU Lycopersicon... 151 1e-59 30 emb|AW033593|AW033593 EST277164 tomato callus, TAMU Lycopersicon... 151 3e-59 emb|AW034724|AW034724 EST278526 tomato callus, TAMU Lycopersicon... 148 7e-59 emb|AW041033|AW041033 EST283897 tomato mixed elicitor, BTI Lycop... 148 7e-59 emb|X66942|NTPRB1B N.tabacum prb-1b gene. 146, 9e-59 emb|AW559895|AW559895 EST314943 DSIR Medicago truncatula cDNA cl... 160 1e-58 35 emb|AW329241|AW329241 N200453e rootphos(-) Medicago truncatula c... 160 1e-58 emb|AI352771|AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl... 220 2e-58 emblAW559894|AW559894 EST314942 DSIR Medicago truncatula cDNA cl... 159 5e-58 emblAW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 145 6e-58 emb|AW032139|AW032139 EST275593 tomato callus, TAMU Lycopersicon... 145 6e-58 40 emb|AW034330|AW034330 EST277901 tomato callus, TAMU Lycopersicon... 144 2e-57 emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57 emb|AW032749|AW032749 EST276308 tomato callus, TAMU Lycopersicon... 149 3e-57 emb|AI894391|AI894391 EST263846 tomato callus, TAMU Lycopersicon... 142 4e-57 emb|AI896249|AI896249 EST265692 tomato callus, TAMU Lycopersicon... 142 6e-57 45 emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 8e-57 emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56 emb|AW981257|AW981257 EST392410 DSIL Medicago truncatula cDNA cl... 128 1e-55 emb|AW033687|AW033687 EST277258 tomato callus, TAMU Lycopersicon... 149 2e-55 emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55 50 emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 5e-55 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55 emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53 emb|X52555|NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 116 1e-52 gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 112 4e-52 emb|AW053720|AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-52 emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52 emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51 emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51 emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.

emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51

emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene.

60

	gb M69247 TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat 98 1e-50 emb A22634 LEPI4GENE L.esculentum P14 gene. 98 1e-50 emb AJ250136 STU250136 Solanum tuberosum mRNA for pathogenesis r 99 2e-50 emb AW218808 AW218808 EST301288 tomato root during/after fruit s 116 3e-50
5	emb AI896011 AI896011 EST265454 tomato callus, TAMU Lycopersicon 116 3e-50
•	emb AW094536 AW094536 EST287716 tomato mixed elicitor, BTI Lycop 116 3e-50
	emb AW038553 AW038553 EST280236 tomato mixed elicitor, BTI Lycop 116 3e-50
•	dbj D90196 TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu 104 3e-50
	emb X05959 NTPR1AG Tobacco PR-1a gene for pathogenesis-related p 104 4e-50
10	emb X12737 NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p 104 4e-50
	emb X06361 NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela 104 4e-50
	emb X12485 NTPR1A Tobacco mRNA fragment for pathogenesis-related 104 4e-50
	emb AW033469 AW033469 EST277040 tomato callus, TAMU Lycopersicon 116 5e-50
15	emb X06930 NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related 104 7e-50 emb AI352858 AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c 197 7e-50
15	emb AI782416 AI782416 EST263295 tomato susceptible, Cornell Lyco 95 7e-50
	emb AW034882 AW034882 EST279111 tomato callus, TAMU Lycopersicon 95 1e-49
	emb AW031086 AW031086 EST274393 tomato callus, TAMU Lycopersicon 116 1e-49
	emb X74939 HVPR1AR H.vulgare HvPR-1a mRNA for a basic PR-1-type 114 2e-49
20	emb AF136636 AF136636 Glycine max PR1a precursor (PR1a) mRNA, co 110 2e-49
	emb AW034167 AW034167 EST277738 tomato callus, TAMU Lycopersicon 94 2e-49
	emb X17680 NTPR1BA Tobacco gene for pathogenesis-related protein 103 4e-49
	emb X03465 NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate 103 4e-49
25	dbj D90197 TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 4e-49 emb Y08804 LEPR1B1 L.esculentum mRNA for PR protein. 92 7e-49
	gb M69248 TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat 92 7e-49
*	emb X68738 LEP1P14A L.esculentum mRNA for ethylene-induced P1(p1 92 7e-49
	emb AI781499 AI781499 EST262378 tomato susceptible, Cornell Lyco 92 7e-49
••	emb AI779424 AI779424 EST260303 tomato susceptible, Cornell Lyco 92 7e-49
30	emb AW031093 AW031093 EST274400 tomato callus, TAMU Lycopersicon 92 7e-49
	emb AI779425 AI779425 EST260304 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI782545 AI782545 EST263424 tomato susceptible, Cornell Lyco 92 7e-49 emb AI782822 AI782822 EST263701 tomato susceptible, Cornell Lyco 92 7e-49
	emb A1782822 A1782822 EST263701 tomato susceptible, Cornell Lyco 92 7e-49 emb A1778686 A1778686 EST259565 tomato susceptible, Cornell Lyco 92 7e-49
35	emb AI778680 AI778680 EST259559 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI899514 AI899514 EST268957 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI779287 AI779287 EST260166 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI773130 AI773130 EST254230 tomato resistant, Cornell Lycope 92 7e-49
40	emb A1778790 A1778790 EST259669 tomato susceptible, Cornell Lyco 92 7e-49
40	emb AI778791 AI778791 EST259670 tomato susceptible, Cornell Lyco 92 7e-49 emb AI778985 AI778985 EST259864 tomato susceptible, Cornell Lyco 92 7e-49
	emb A1778985 A1778985 EST259864 tomato susceptible, Cornell Lyco 92 7e-49 emb AW032026 AW032026 EST275480 tomato callus, TAMU Lycopersicon 92 7e-49
	emb AI782288 AI782288 EST263167 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI779013 AI779013 EST259892 tomato susceptible, Cornell Lyco 92 7e-49
45	emb AI781431 AI781431 EST262298 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI780973 AI780973 EST261852 tomato susceptible, Cornell Lyco 92 7e-49
	emb AI895236 AI895236 EST264679 tomato callus, TAMU Lycopersicon 92 7e-49
50	Query= af107726_s_at 17499_s_at /id_source genbank /description
	gb aad19610.1 (af107726) cyclic nucleotide gated channel [arabidopsis
	thaliana] /blast_score 0
	(2208 letters)
55	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
	done
60	Score E
	Sequences producing significant alignments: (bits) Value

emb|AF079872|AF079872 Nicotiana tabacum cyclic nucleotide-gated ... 380 0.0 emb|AF079871|AF079871 Nicotiana tabacum cyclic nucleotide-gated ... 373 0.0 emb|AJ002610|HVAJ2610 Hordeum vulgare mRNA for putative calmodul... 331 0.0 emb|AW625647|AW625647 EST319554 tomato radicle, 5 d post-imbibit... 255 6e-82 emb|AW038928|AW038928 EST280884 tomato mixed elicitor, BTI Lycop... 190 2e-80 emb|AI782780|AI782780 EST263659 tomato susceptible, Cornell Lyco... 259 4e-77 emb|AI486671|AI486671 EST244993 tomato ovary, TAMU Lycopersicon ... 241 4e-70 emb|AW725576|AW725576 GA Ea0018M08 Gossypium arboreum 7-10 dpa ... 196 3e-69 10 emb|AW265987|AW265987 L30-2643T3 Ice plant Lambda Uni-Zap XR exp... 150 3e-69 emb[AW033272[AW033272 EST276843 tomato callus, TAMU Lycopersicon... 260 2e-68 emb|AW126067|AW126067 N100263e rootphos(-) Medicago truncatula c... 258 1e-67 gb[U65390]NTU65390 Nicotiana tabacum CaMB-channel protein mRNA, ... 162 1e-65 emb|AI898047|AI898047 EST267490 tomato ovary, TAMU Lycopersicon ... 241 2e-62 15 emb|AI487755|AI487755 EST246077 tomato ovary, TAMU Lycopersicon ... 241 2e-62 emb|AI776725|AI776725 EST257825 tomato resistant, Cornell Lycope... 240 3e-62 emb|AI729234|AI729234 BNLGHi12947 Six-day Cotton fiber Gossypium... 176 3e-57 emb|AW705372|AW705372 sk48b11.yl Gm-c1019 Glycine max cDNA clone... 133 4e-51 emb|AW029776|AW029776 EST273031 tomato callus, TAMU Lycopersicon... 156 4e-51 20 emb|AW220952|AW220952 EST297421 tomato fruit mature green, TAMU ... 118 3e-50 emb|AW626197|AW626197 EST320104 tomato radicle, 5 d post-imbibit... 132 1e-49 gb|BE059468|BE059468 sn32d07.yl Gm-c1016 Glycine max cDNA clone ... 133 5e-46 emb|AW029909|AW029909 EST273164 tomato callus, TAMU Lycopersicon... 122 5e-45 emb|AI729590|AI729590 BNLGHi13704 Six-day Cotton fiber Gossypium... 180 4e-44 25 emb|AI490589|AI490589 EST249143 tomato ovary, TAMU Lycopersicon ... 178 1e-43 emb|AW830981|AW830981 sm31b10.yl Gm-c1028 Glycine max cDNA clone... 176 8e-43 emb|AV414437|AV414437 AV414437 Lotus japonicus young plants (two... 112 2e-41 emb|AI494870|AI494870 sb06e03.yl Gm-c1004 Glycine max cDNA clone... 125 1e-40 emb|AI055360|AI055360 coau0003M11 Cotton Boll Abscission Zone cD... 123 8e-39 30 emb|AW737921|AW737921 EST339348 tomato flower buds, anthesis, Co... 128 1e-37 emb|AI967361|AI967361 Ljirnpest02-095-a3 Ljirnp Lambda HybriZap ... 94 2e-36 emb|AI776645|AI776645 EST257745 tomato resistant, Cornell Lycope... 70 3e-35 emb|AW775519|AW775519 EST334584 DSIL Medicago truncatula cDNA cl... 147 3e-34 emb|AI778171|AI778171 EST259050 tomato susceptible, Cornell Lyco... 76 4e-34 35 emb|AW309771|AW309771 sf24f01.x1 Gm-c1028 Glycine max cDNA clone... 143 7e-33 emb|AI960258|AI960258 sc81a02.y1 Gm-c1018 Glycine max cDNA clone... 122 2e-32 emb|AW563840|AW563840 LG1 272_B06.b1_A002 Light Grown 1 (LG1) So... 113 1e-30 emb|AW774513|AW774513 EST333664 KV3 Medicago truncatula cDNA clo... 135 1e-30 emb|AI967666|AI967666 Ljimpest08-671-e8 Ljimp Lambda HybriZap ... 116 2e-30 40· emb|AW671345|AW671345 LG1_335_D05.b1_A002 Light Grown 1 (LG1) So... 100 2e-30 gb|C95565|C95565 C95565 Citrus unshiu Miyagawa-wase maturation s... 132 1e-29 emb|AW759050|AW759050 sl34a04.yl Gm-c1027 Glycine max cDNA clone... 129 9e-29 emb|AW286638|AW286638 LG1_335_D05.g1_A002 Light Grown 1 (LG1) So... 127 2e-28 emb|AW831384|AW831384 sm24g05.yl Gm-c1028 Glycine max cDNA clone... 87 9e-27 45 emb|AW037755|AW037755 EST279384 tomato mixed elicitor, BTI Lycop... 122 1e-26 emb|AW508715|AW508715 si35e10.yl Gm-r1030 Glycine max cDNA clone... 117 3e-25 emb|AW350588|AW350588 GM210009A10H2R Gm-r1021 Glycine max cDNA 3... 106 leemb|AW350847|AW350847 GM210009B20G5R Gm-r1021 Glycine max cDNA 3... 106 2e-50 emb|AI776960|AI776960 EST251986 tomato callus, TAMU Lycopersicon... 111 2e-23 emb|AW781088|AW781088 sl88h09.yl Gm-c1037 Glycine max cDNA clone... 111 3e-23 emb|AW039011|AW039011 EST280984 tomato mixed elicitor, BTI Lycop... 111 3e-23 emb|AW617273|AW617273 EST323684 L. hirsutum trichome, Cornell Un... 106 7e-22 55 gb|BE022211|BE022211 sm72b10.yl Gm-c1028 Glycine max cDNA clone ... 106 7e-22 emb|AA824914|AA824914 CT202.SK Tomato Leaf cDNA from cv. VFNT ch... 93 6e-21 emb|AT000374|AT000374 AT000374 Apple peel cDNA library Malus x d... 102 1e-20 emb|AW623583|AW623583 EST321528 tomato flower buds 3-8 mm, Corne... 69 7e-20 60 emb|AI495394|AI495394 sa97d10.y1 Gm-c1004 Glycine max cDNA clone... 98 2e-19 emb|AI725563|AI725563 BNLGHi12127 Six-day Cotton fiber Gossypium... 67 5e-18

	emb AW119379 AW119379 sd45d12.yl Gm-c1016 Glycine max cDNA clone 74 3e-17 emb AW617083 AW617083 EST323494 L. hirsutum trichome, Cornell Un 65 7e-17 emb AW832684 AW832684 00046 leafy spurge Lambda HybriZAP 2.1 two 60 4e-12
5	emb AI776961 AI776961 EST251987 tomato callus, TAMU Lycopersicon 67 5e-12 emb AI894661 AI894661 EST264104 tomato callus, TAMU Lycopersicon 68 3e-10
	emb AW217336 AW217336 EST296159 tomato flower buds 0-3 mm, Corne 67 7e-10 emb AW688833 AW688833 NF012B10ST1F1000 Developing stem Medicago 58 1e-09 emb AW164084 AW164084 Ljirnpest19-528-f6 Ljirnp Lambda HybriZap 56 1e-06
10	emb AJ249962 DCA249962 Daucus carota mRNA for potassium channel 55 3e-06 emb AW184978 AW184978 se85a09.yl Gm-c1023 Glycine max cDNA clone 54 4e-06 emb AW001651 AW001651 EST384747 towards migd alloides BZTI A control of the c
	emb AW091651 AW091651 EST284747 tomato mixed elicitor, BTI Lycop 51 3e-05 emb AW041519 AW041519 EST284383 tomato mixed elicitor, BTI Lycop 51 3e-05 emb AF145272 AF145272 Samanea saman pulvinus inward-rectifying c 49 1e-04
15	gb BE060413 BE060413 HVSMEg0012D21f Hordeum vulgare pre-anthesis 38 2e-04 emb AW928912 AW928912 EST337700 tomato flower buds 8 mm to pre-a 48 2e-04 emb AW756344 AW7756344 W775644 AW77564
	emb AW756344 AW756344 s119e03.y1 Gm-c1036 Glycine max cDNA clone 47 6e-04 emb AI494962 AI494962 sa93c01.y1 Gm-c1004 Glycine max cDNA clone 40 0.001 emb AW256509 AW256509 EST304646 KV2 Medicago truncatula cDNA clo 45 0.003
20	gb[U19908]PTU19908 Paramecium tetraurelia K+ channel (PaK2) gene 42 0.015 emb AW256736 AW256736 EST304873 KV2 Medicago truncatula cDNA clo 40 0.016
20	emb AI488021 AI488021 EST246343 tomato ovary, TAMU Lycopersicon 42 0.020 emb AI729515 AI729515 BNLGHi13574 Six-day Cotton fiber Gossypium 41 0.027
	emb AW687023 AW687023 NF005B04RT1F1032 Developing root Medicago 39 0.13 emb AL163552 LMFL5075 Leishmania major Friedlin chromosome 14 co 38 0.25
25	emb AQ847838 AQ847838 LMAJFV1_lm42a03.y1 Leishmania major FV1 ra 38 0.25 emb AI748348 AI748348 sb51d12.y1 Gm-c1016 Glycine max cDNA clone 38 0.35
	emb AL031530 SPCC970 S.pombe chromosome III cosmid c970. 38 0.35 gb U33057 SCD9717 Saccharomyces cerevisiae chromosome IV cosmids 37 0.48
30	gb M84796 YSCEUG1 Saccharomyces cerevisiae endoplasmic reticulum 37 0.48 emb AF099095 AF099095 Samanea saman pulvinus inward-rectifying c 37 0.66
	emb AI775282 AI775282 EST256382 tomato resistant, Cornell Lycope 36 0.90
	emb AF053314 AF053314 Exophiala dermatitidis chitin synthase 3 (36 1.2 emb AQ947260 AQ947260 Sheared DNA-45L23.TR Sheared DNA Trypanoso 31 1.5
35	emb AC016528 AC016528 Leishmania major chromosome 35 clone L4123 35 1.7
33	emb AI781524 AI781524 EST262403 tomato susceptible, Cornell Lyco 31 2.0 gb U28374 YSCD9740 Saccharomyces cerevisiae chromosome IV cosmid 35 2.3
	emb AW399566 AW399566 EST310066 L. pennellii trichome, Cornell U 35 2.3
	gb BE034738 BE034738 ML03G05 ML Mesembryanthemum crystallinum cD 35 2.3 emb AW929752 AW929752 EST354022 tomato flower buds 8 mm to pre-a 35 2.3
40	emb AW648153 AW648153 EST326607 tomato germinating seedlings, TA 35 2.3 gb M74798 HEVHMGR3A Hevea brasiliensis 3-hydroxy-3-methylglutary 34 4.4
	gb M74798 HEVHMGR3A Hevea brasiliensis 3-hydroxy-3-methylglutary 34 4.4 emb AW728887 AW728887 GA_Ea0018B11 Gossypium arboreum 7-10 dpa 34 4.4
	Query= athcallga_s_at 17500_s_at /id_source
45	/description emb cab42906.1 (al049862) calmodulin-like protein [arabidopsis thaliana] /blast_score 6.00e-99 (827 letters)
	Database: plantfungal
50	661,018 sequences; 426,114,510 total letters
•	Searchingdone
55	Score E Sequences producing significant alignments: (bits) Value
	emb AI489346 AI489346 EST247685 tomato ovary, TAMU Lycopersicon 79 2e-28
	emb AW350323 AW350323 GM210007B20E12R Gm-r1021 Glycine max cDNA 80 2e-27 emb AW509006 AW509006 si38h07.yl Gm-r1030 Glycine max cDNA clone 79 2e-26
	emb AW685404 AW685404 NF028H10NR1F1000 Nodulated root Medicago t 74 2e-24
60	emb AW781320 AW781320 sk68d07.yl Gm-c1016 Glycine max cDNA clone 86 2e-24 emb AI897832 AI897832 EST267275 tomato ovary, TAMU Lycopersicon 78 1e-23

	emb AW102460 AW102460 sd88d10.yl Gm-c1009 Glycine max cDNA clone 70 2e-22
	emb AI490284 AI490284 EST248610 tomato ovary, TAMU Lycopersicon 103 2e-22
	emb AI487362 AI487362 EST245684 tomato ovary, TAMU Lycopersicon 72 3e-20
	gb BE125690 BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh 96 3e-19
5	A DEPARTMENT OF THE PROPERTY O
J	
	emb AL115248 CNS01C9K Botrytis cinerea strain T4 cDNA library un 65 4e-18
•	dbj D10521 TETCALW T.pyriformis mRNA for calmodulin. 73 7e-18
	gb M76407 SLECALMODU Stylonychia lemnae calmodulin gene, complet 74 9e-18
	emb AF007889 AF007889 Symbiodinium microadriaticum calmodulin (S 74 le-17
10	emb AF078679 AF078679 Olea europaea calcium-binding protein (PCA 57 2e-17
	emb X56511 TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi 77 2e-17
	emb[X52096]TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. 77 2e-17
	emb AF030033 AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA, 75 2e-17
15	
13	gb U91642 POU91642 Pleurotus ostreatus calmodulin mRNA, complete 75 2e-17
	emb AF078680 AF078680 Olea europaea calcium-binding protein (PCA 57 2e-17
	emb X85091 MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17
	gb[M83535]PHTCALPIA P.infestans calmodulin (calA) gene, complete 75 2e-17
	emb Y08373 TGCM T.gondii mRNA for calmodulin. 74 2e-17
20	gb C96396 C96396 C96396 Marchantia polymorpha immature sex organ 73 3e-17
-	emb AL113315 CNS01ARV Botrytis cinerea strain T4 cDNA library un 72 3e-17
	emb AB044286 AB044286 Chara corallina ccam mRNA for calmodulin, 75 4e-17
	emb AB041712 AB041712 Chara corallina cccam2 mRNA for calmodulin 75 4e-17
	amble P041711 A P041711 Chara corallina cocania miniva foi caminoum 75 4e-17
25	emb AB041711 AB041711 Chara corallina cccam1 mRNA for calmodulin 75 4e-17
23	gb J05116 ACKCAL A:klebsiana calmodulin gene, complete cds. 75 4e-17
	emb X70923 NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17
	emb AI328739 AI328739 a6d02ne.fl Neurospora crassa evening cDNA 74 6e-17
	emb AF034964 AF034964 Glomerella cingulata calmodulin (cam) mRNA 74 6e-17
	gb[U12505]HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co 74 8e-17
30	gb[M34540]PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17
	gb S68025 S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic 74 8e-17
	emb AW164773 AW164773 se77e12.yl Gm-c1023 Glycine max cDNA clone 64 8e-17
	emb AW719875 AW719875 LjNEST11d4r Lotus japonicus nodule library 57 8e-17
	emb AW830090 AW830090 sm22a12.y1 Gm-c1028 Glycine max cDNA clone 64 8e-17
35	emb AW126204 AW126204 N100049e rootphos(-) Medicago truncatula c 57 8e-17
-	emb X52242 TTCALM T.thermophila mRNA for calmodulin. 73 1e-16
	gb L02963 NEUCLMDLN Neurospora crassa calmodulin mRNA, complete 74 1e-16
	emb AW625406 AW625406 EST319229 tomato radicle, 5 d post-imbibit 62 1e-16
40	gb K02944 TRBCMRSG Trypanosoma brucei gambiense calmodulin genes 73 2e-16
40	gb M88307 BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16
	gb[U10150]BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA, 73 2e-16
	emb X89890 BPCALMGEN B.pilosa mRNA for calmodulin. 73 2e-16
	emb AW099396 AW099396 sd39h01.yl Gm-c1016 Glycine max cDNA clone 76 2e-16
	emb AW101324 AW101324 sd77e09.yl Gm-c1009 Glycine max cDNA clone 59 2e-16
45	emb AL112713 CNS01AB5 Botrytis cinerea strain T4 cDNA library un 73 2e-16
	emb AL114582 CNS01BR2 Botrytis cinerea strain T4 cDNA library un 74 2e-16
	emb AL112170 CNS019W2 Botrytis cinerea strain T4 cDNA library un 74 2e-16
	emb AL114124 CNS01BEC Botrytis cinerea strain T4 cDNA library un 74 2e-16
	emb AL115056 CNS01C48 Botrytis cinerea strain T4 cDNA library un 73 2e-16
50	
50	emb AL116760 CNS01DFK Botrytis cinerea strain T4 cDNA library un 73 2e-16
	emb AW573768 AW573768 EST316359 GVN Medicago truncatula cDNA clo 72 2e-16
	emb Y13784 MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16
	emb AI727960 AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium 73 3e-16
	emb AA660367 AA660367 00239 MtRHE Medicago truncatula cDNA 5' si 71 3e-16
55	emb AW164628 AW164628 se74e01.yl Gm-c1023 Glycine max cDNA clone 60 3e-16
	emb AF150059 AF150059 Brassica napus calmodulin (CaM1) mRNA, com 72 3e-16
	emb AW738989 AW738989 gb23c06.y1 Moss EST library PPN Physcomitr 73 3e-16
	gb[U48693]TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c 73 4e-16
	gbM27303BLYCAMA Barley cam gene encoding calmodulin, complete 73 4e-16
60	gb BE033450 BE033450 ME02B08 ME Mesembryanthemum crystallinum cD 73 4e-16
	emb AF064552 AF064552 Anium graveolone calmodulin mDNA complete 72 40 16

```
gb|S81594|S81594 auxin-regulated calmodulin [Vigna radiata=mung ... 73 4e-16
      gb|L20691|VIRCALMOD Vigna radiata calmodulin mRNA, complete cds.
      gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16
 5
      emb|AF030032|AF030032 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16
      gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16
      emb|Y09853|CACAM Cicer arietinum mRNA for CaM protein.
      gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16
      gblU49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16
10
      gb[U49105]TAU49105 Triticum aestivum calmodulin TaCaM4-1 mRNA, c... 73 4e-16
      emb|AF030034|AF030034 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 73 4e-16
      emb|AW728030|AW728030 GA_Ea0029H21 Gossypium arboreum 7-10 dpa ... 73 4e-16
      gb|L20507|VIRCALMODU Vigna radiata (clone pMBCaM-1) calmodulin m... 73 4e-16
      gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16
15
      gb|M80836|PETCAM81 Petunia hybrida CAM81 mRNA...
                                                                  73 4e-16
      gb|U49103|TAU49103 Triticum aestivum calmodulin TaCaM3-2 mRNA, c... 73 4e-16
      emb|X52398|MSCAL1 Alfalfa cal1 mRNA for calmodulin.
                                                                 73 4e-16
      gb|U48688|TAU48688 Triticum aestivum calmodulin TaCaM1-2 mRNA, c... 73 4e-16
      gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
20
      emb|AW927068|AW927068 HVSMEg0009G21 Hordeum vulgare pre-anthesis... 73 4e-16
      gb|U48689|TAU48689 Triticum aestivum calmodulin TaCaM1-3 mRNA, c... 73 4e-16
      gb|M80831|PETCALPRO Petunia hybrida CAM53 mRNA, complete cds.
      emb|AW348582|AW348582 GM210002B22C3R Gm-r1021 Glycine max cDNA 3... 73 4e-16
      emb|X59751|DCCAM1G Carrot Ccam-1 gene for calmodulin.
                                                                  73 4e-16
25
      emb|AW775754|AW775754 EST334819 DSIL Medicago truncatula cDNA cl... 73 4e-16
      gb[BE052400]BE052400 GA Ea0001L24f Gossypium arboreum 7-10 dpa ... 73 4e-16
      gb|U13882|PSU13882 Pisum sativum Alaska calmodulin mRNA, complet... 73 4e-16
      gb|BE051931|BE051931 GA Ea0002G11f Gossypium arboreum 7-10 dpa ... 73 4e-16
30
      emb|AW666619|AW666619 GA Ea0005C16 Gossypium arboreum 7-10 dpa ... 73 4e-16
      emb|AW108833|AW108833 gate0001L24f Gossypium arboreum 7-10 dpa f... 73 4e-16
      emb|Z12839|LLCALMOD L.longiflorum mRNA encoding calmodulin.
                                                                       73 4e-16
      gb|L18912|LILCALMODU Lilium longiflorum calmodulin mRNA, complet... 73 4e-16
35
      Query= af067605 s at 17511 s at /id source genbank /description
      gb|aab71482.1| (ac002294) similar to s-linalool synthase
      gp|u58314|1491939 [arabidopsis thaliana] /blast score 0
          (2661 letters)
40
      Database: plantfungal
           661,018 sequences; 426,114,510 total letters
      Searching......done
45
      Sequences producing significant alignments:
                                                       (bits) Value
      gb|U58314|CBU58314 Clarkia breweri S-linalool synthase (Lis) mRN... 146 e-171
50
     emb|AF067603|AF067603 Clarkia breweri linalool synthase 2 (LIS2)... 149 e-154
     emb|AF067602|AF067602 Clarkia concinna linalool synthase gene, c... 112 1e-53
      emb|AF097310|AF097310 Stevia rebaudiana kaurene synthase (KS1-1)... 88 5e-31
      emb|AF097311|AF097311 Stevia rebaudiana kaurene synthase (KS22-1... 88 5e-31
      emb|AF067604|AF067604 Oenothera arizonica linalool synthase-like... 75 5e-24
55
     emb|AF067601|AF067601 Clarkia breweri linalool synthase 1 (LIS1)... 86 1e-17
     gb|U43904|CMU43904 Cucurbita maxima ent-kaurene synthase B mRNA,... 63 5e-17
     emb|AI485628|AI485628 EST243949 tomato ovary, TAMU Lycopersicon ... 60 3e-15
     emb|AI485623|AI485623 EST243944 tomato ovary, TAMU Lycopersicon ... 55 9e-14
     gb|U92267|AGU92267 Abies grandis gamma-humulene synthase mRNA, c... 45 2e-10
60
     gb|U50768|AGU50768 Abies grandis abietadiene synthase (ac22) mRN... 58 6e-10
     emb|AW255432|AW255432 ML454 peppermint glandular trichome Mentha... 56 1e-08
```

```
emb|AW255334|AW255334 ML343 peppermint glandular trichome Mentha... 56 1e-08
      emb|AF233894|AF233894 Perilla citriodora limonene synthase mRNA,... 62 2e-08
      gb|U87909|AGU87909 Abies grandis pinene synthase (AG3.18) mRNA, ... 61 5e-08
      dbj|D49368|D49368 Perilla frutescens mRNA for limonene cyclase, ... 61 5e-08
      emb|AF006195|AF006195 Abies grandis E-alpha-bisabolene synthase ... 55 7e-08
      emb|AF006194|AF006194 Abjes grandis E-alpha-bjsabolene synthase ... 55 7e-08
      emblAI487110|AI487110 EST245432 tomato ovary, TAMU Lycopersicon ... 60 7e-08
      emb|AW616561|AW616561 EST322972 L. hirsutum trichome, Cornell Un... 39 8e-08
      gb[U63652]PSU63652 Pisum sativum ent-kaurene synthase A (LS) mRN... 60 1e-07
10
      gb|U92266|AGU92266 Abies grandis d-selinene synthase mRNA, compl... 60 1e-07
      emb[AW738064]AW738064 EST339491 tomato flower buds, anthesis, Co... 38 le-07
      emb[AI491074]AI491074 EST241783 tomato shoot, Cornell Lycopersic... 38 1e-07
      emblAW617193|AW617193 EST323604 L. hirsutum trichome. Cornell Un...
      emb|AW616893|AW616893 EST323304 L. hirsutum trichome, Cornell Un...
      emb|AF034545|AF034545 Stevia rebaudiana copalyl pyrophosphate sy... 59 2e-07
15
      emb|AF271259|AF271259 Perilla frutescens terpene synthase mRNA, ... 59 2e-07
      emb|AW616634|AW616634 EST323045 L. hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW616591|AW616591 EST323002 L. hirsutum trichome, Cornell Un...
      emb|AW616079|AW616079 EST296838 L. hirsutum trichome, Cornell Un... 39 3e-07
20
      emb|AW616201|AW616201 EST307240 L, hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW616573|AW616573 EST322984 L. hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW616493|AW616493 EST322904 L. hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW616908|AW616908 EST323319 L. hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW617347|AW617347 EST323758 L. hirsutum trichome, Cornell Un... 39 3e-07
25
      emb|AW617467|AW617467 EST323878 L. hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW617665|AW617665 EST324076 L. hirsutum trichome, Cornell Un... 39 3e-07
      emb|AW617376|AW617376 EST323787 L. hirsutum trichome, Cornell Un...
      emb|AF049905|AF049905 Cucurbita maxima copalyl diphosphate synth... 58 3e-07
      emb|AW616328|AW616328 EST322739 L. hirsutum trichome, Cornell Un... 38 5e-07
30
      emb|AW624730|AW624730 EST322675 tomato flower buds 3-8 mm, Corne... 37 6e-07
      emb|AB042424|AB042424 Croton sublyratus cps mRNA for copalyl dip... 57 7e-07
      emb|AW254843|AW254843 ML1265 peppermint glandular trichome Menth... 57 7e-07
      emb|AW254789|AW254789 ML1071 peppermint glandular trichome Menth... 57 7e-07
      emb|AW254821|AW254821 ML1244 peppermint glandular trichome Menth... 57 7e-07
35
      emb|AW255149|AW255149 ML145 peppermint glandular trichome Mentha... 57 7e-07
      emb|AW255044|AW255044 ML1227 peppermint glandular trichome Menth... 57 7e-07
      emb|AF139207|AF139207 Abies grandis (-)-limonene/(-)-alpha-pinen... 57 9e-07
      emb|AW616366|AW616366 EST322777 L. hirsutum trichome, Cornell Un... 36 2e-06
      emb|AW255042|AW255042 ML1225 peppermint glandular trichome Menth... 55 2e-06
40
      emb|AW255052|AW255052 ML1347 peppermint glandular trichome Menth... 55 2e-06
      emb|AW254888|AW254888 ML1312 peppermint glandular trichome Menth... 55 2e-06
      emb|AW687409|AW687409 NF009C09RT1F1069 Developing root Medicago ... 54 5e-06
      emb]AB015675[AB015675 Lycopersicon esculentum CPS mRNA for copal... 54 5e-06
      emb|AF051901|AF051901 Salvia officinalis (+)-sabinene synthase m... 54 5e-06
45
      emb|AF175323|AF175323 Mentha longifolia limonene synthase mRNA, ... 54 6e-06
      gb|L13459|MHC4SLSP Mentha spicata 4S-limonene synthase mRNA, com... 54 6e-06
      emb|AW255678|AW255678 ML735 perpermint glandular trichome Mentha... 53 le-05
      emb|AF139205|AF139205 Abies grandis beta-phellandrene synthase (... 52 2e-05
      emb|AW617714|AW617714 EST324125 L. hirsutum trichome, Cornell Un... 33 2e-05
'50
      emb|AF154125|AF154125 Artemisia annua (3R)-linalool synthase (QH... 51 4e-05
      emb|AF049906|AF049906 Cucurbita maxima copalyl diphosphate synth... 51 4e-05
      emb|AW684730|AW684730 NF020C02NR1F1000 Nodulated root Medicago t... 51 4e-05
      gb[U87908|AGU87908 Abies grandis myrcene synthase (AG2.2) mRNA, ... 51 6e-05
      emb|AW255083|AW255083 ML1378 peppermint glandular trichome Menth... 51 6e-05
55
      emb|AW254876|AW254876 ML1300 perpermint glandular trichome Menth... 49 2e-04
      gb|U48796|TBU48796 Taxus brevifolia taxadiene synthase (TDC1) mR... 49 2e-04
      emb|AF051899|AF051899 Salvia officinalis 1,8-cineole synthase mR... 48 4e-04
      emb|AF006193|AF006193 Abies grandis (-)-4S-limonene synthase mRN... 47 5e-04
      emb|AF154124|AF154124 Artemisia annua (3R)-linalool synthase (QH... 46 0.001
60
      emb|AF139206|AF139206 Abies grandis terpinolene synthase (agc9) ... 45 0.004
      emb|AW687308|AW687308 NF008C02RT1F1008 Developing root Medicago ... 44 0.005
```

	emb AF051900 AF051900 Salvia officinalis (+)-bornyl diphosphate 43 0.009
	emb AF212433 AF212433 Capsicum annuum UV-induced sesquiterpene c 43 0.009
	emb AF061285 AF061285 Capsicum annuum sesquiterpene cyclase mRNA 43 0.009
	emb AW685590 AW685590 NF029D03NR1F1000 Nodulated root Medicago t 34 0.01
5	emb AW125997 AW125997 N100193e rootphos(-) Medicago truncatula c 34 0.015
	emb AW622483 AW622483 EST313271 tomato root during/after fruit s 42 0.018
	emb AW254970 AW254970 ML1141 peppermint glandular trichome Menth 41 0.034
	emb AB006530 AB006530 Citrullus lanatus Sat gene for serine acet 41 0.046
10	41
10	emb AW255471 AW255471 ML495 peppermint glandular trichome Mentha 40 0.087
	emb AB005744 AB005744 Perilla frutescens DNA for 1-limonene synt 40 0.087
	emb AW616571 AW616571 EST322982 L. hirsutum trichome, Cornell Un 30 0.17
	emb AW617415 AW617415 EST323826 L. hirsutum trichome, Cornell Un 30 0.17
	gb U20189 HMU20189 Hyoscyamus muticus clone cVS2 vetispiradiene 39 0.23
15	emb AF042382 AF042382 Solanum tuberosum vetispiradiene synthase 38 0.31
	emb AF043300 AF043300 Solanum tuberosum putative vetispiradiene 38 0.31
	emb AB022720 AB022720 Solanum tuberosum PVS3 mRNA for vetispirad 38 0.31
	gb L32134 RCCCASSYNT Ricinus communis casbene synthase mRNA. 38 0.43
	emb AW043070 AW043070 ST28H10 Pine TriplEx shoot tip library Pin 38 0.43
20	emb AI940878 AI940878 sb79b02.yl Gm-c1010 Glycine max cDNA clone 38 0.43
	emb AB022719 AB022719 Solanum tuberosum PVS2 mRNA for vetispirad 37 0.58
	emb AF043298 AF043298 Solanum tuberosum putative vetispiradiene 37 0.58
	emb AF043299 AF043299 Solanum tuberosum putative vetispiradiene 37 0.58
	emb AJ001452 FVAJ1452 Fragaria vesca partial mRNA for putative s 30 0.70
25	
2,5	
	emb AB023816 AB023816 Solanum tuberosum PVS4 mRNA for vetispirad 36 1.1
	Query= d78606_s_at 17522_s_at /id_source genbank /description
30	
50	dbj baa28538.1 (d78606) cytochrome p450 monooxygenase [arabidopsis
	thaliana] /blast_score 0
	(1580 letters)
25	Database: plantfungal
35	661,018 sequences; 426,114,510 total letters
	Searchingdone
	Scarciningdone
	Score E
40	Sequences producing significant alignments: (bits) Value
. •	todamos producing organization anguinona.
	emb AB001379 AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto 376 e-149
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy 376 e-149
45	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45 377 e-147
43	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450. 376 e-147
	emb AJ239051 CAR239051 Cicer arietinum mRNA for cytochrome P450 255 e-145
	emb AB025016 AB025016 Lotus japonicus mRNA for cytochrome P450, 340 e-142
	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro 352 3e-96
	emb AJ000478 HTCYP81L Helianthus tuberosus mRNA for cytochrome P 225 4e-84
50	emb AJ000477 HTCYP81C Helianthus tuberosus mRNA for cytochrome P 225 4e-84
	emb AW185361 AW185361 se90e02.yl Gm-c1027 Glycine max cDNA clone 302 5e-8
	emb AJ249801 CAR249801 Cicer arietinum partial mRNA for cytochro 298 6e-80
	emb AF082028 AF082028 Hemerocallis hybrid cultivar senescence-as 209 4e-76
	emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone 277 2e-75
55	emb AW307234 AW307234 sf54d12.yl Gm-c1009 Glycine max cDNA clone 275 6e-73
	emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone 273 3e-72
	emb AW775904 AW775904 EST334969 DSIL Medicago truncatula cDNA cl 242 3e-71
	emb AW171738 AW171738 N100632e rootphos(-) Medicago truncatula c 265 7e-70
60	emb AI725744 AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium 193 3e-63
60	emb AI729126 AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium 188 2e-62

emb|AW329224|AW329224 N200436e rootphos(-) Medicago truncatula c... 228 1e-58 emb|AW932147|AW932147 EST357990 tomato fruit mature green, TAMU ... 226 3e-58 emb|AW100311|AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone... 218 8e-56 emb|AF014802|AF014802 Eschscholzia californica (S)-N-methylcocla... 177 9e-56 5 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycope... 152 9e-56 emb|AW171672|AW171672 N100566e rootphos(-) Medicago truncatula c... 216 3e-55 emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 164 2e-54 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycope... 116 1e-51 emb|AV412147|AV412147 AV412147 Lotus japonicus young plants (two... 204 2e-51 10 dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 116 5e-50 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 116 5e-50 emb|AW676742|AW676742 DG1 14 A08.g1 A002 Dark Grown 1 (DG1) Sorg... 116 1e-49 emb|AI731081|AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ... 198 1e-49 emb|AW257188|AW257188 EST305325 KV2 Medicago truncatula cDNA clo... 152 2e-49 15 emb|AW309826|AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone... 196 5e-49 emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 117 5e-48 emb|AF022461|AF022461 Glycine max cytochrome P450 monooxygenase ... 108 1e-47 emb|AW736144|AW736144 EST332120 KV3 Medicago truncatula cDNA clo... 190 2e-47 dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 111 2e-47 20 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. emb|AI973839|AI973839 sd11c06.y1 Gm-c1020 Glycine max cDNA clone... 116 7e-47 emb|AB015762|AB015762 Nicotiana tabacum mRNA for cytochrome P450... 150 7e-47 emb[X71658]SMCYPEG8 S.melongena CYP76A1 mRNA. emb|AW616170|AW616170 EST307209 L. hirsutum trichome, Cornell Un... 124 9e-47 25 emb[Y10982]GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 159 9e-47 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 156 1e-46 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 156 1e-46 emb|AF124372|AF124372 Nicotiana tabacum NT7 mRNA, partial cds. emb|AW728802|AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa ... 168 2e-46 30 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 103 2e-46 emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 162 6e-46 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 157 1e-45 emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 124 2e-45 emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 124 2e-45 35 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 183 2e-45 emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 124 5e-45 gb]U72654|EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla... 160 6e-45 gb]M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 160 8e-45 emb|AW679544|AW679544 WS1_29_D01.g1_A002 Water-stressed 1 (WS1) ... 101 8e-45 40 emb|AW102198|AW102198 sd84f03.yl Gm-c1009 Glycine max cDNA clone... 181 1e-44 dbj|D14589|D14589 Eustoma russellianum mRNA for flavonoid 3',5'-... 160 2e-44 emb|AJ011862|CRO011862 Catharanthus roseus mRNA for flavonoid 3'... 161 2e-44 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 119 6e-44 emb|Y10491|GMC450CP4 G.max mRNA for putative cytochrome P450, cl... 149 7e-44 45 emb|AW309498|AW309498 sf20c05.x1 Gm-c1028 Glycine max cDNA clone... 178 1e-43 emb|AF135485|AF135485 Glycine max cytochrome P450 monooxygenaseC... 100 1e-43 gb|U29333|PSU29333 Pisum sativum novel wound-inducible cytochrom... 157 1e-43 emb|AW616143|AW616143 EST296912 L. hirsutum trichome, Cornell Un... 128 1e-43 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 122 1e-43 50 emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 162 2e-43 emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 160 3e-43 emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 104 7e-43 emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 156 9e-43 gb|L07634|PHVC4HYDRO Phaseolus aureus cinnamate 4-hydroxylase mR... 148 3e-42 55 emb|AB023636|AB023636 Glycyrrhiza echinata CYP Ge-8 mRNA for cyt... 107 4e-42 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 172 5e-42 emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 144 6e-42 emb|X92437|GMCYP73 Glycine max mRNA for cinnamic acid 4-hydroxyl... 146 8e-42 60 emb|AI731481|AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ... 171 9e-42 emb|AB024931|AB024931 Lotus japonicus mRNA for cytochrome P450, ... 105 9e-42

dbi|D87520|D87520 Glycyrrhiza echinata suspension-cultured cells... 146 1e-41 emblAB006790|AB006790 Petunia x hybrida IMT-2 mRNA for cytochrom... 144 1e-41 emb|AB001380|AB001380 Glycyrrhiza echinata CYP93B1 mRNA for cyto... 104 2e-41 emb|AF195800|AF195800 Medicago sativa isoflavone synthase 1 (ifs... 101 3e-41 5 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 104 4e-41 emb|AW560648|AW560648 EST315696 DSIR Medicago truncatula cDNA cl... 169 5e-41 emb|AF195798|AF195798 Glycine max isoflavone synthase 1 (ifs1) m... 100 6e-41 emb|AF135484|AF135484 Glycine max cytochrome P450 monooxygenase ... 100 6e-41 emb|AF195811|AF195811 Trifolium pratense isoflavone synthase 2 (... 100 6e-41 10 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 100 6e-41 emb|AF195808|AF195808 Vigna radiata isoflavone synthase 3 (ifs3)... 100 6e-41 emb|AF195807|AF195807 Vigna radiata isoflavone synthase 2 (ifs2)... 100 6e-41 emb|AF195802|AF195802 Medicago sativa isoflavone synthase 3 (ifs... 100 6e-41 emb|AF188612|AF188612 Callistephus chinensis flavone synthase II... 94 8e-41 15 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 168 9e-41 emblAF195812|AF195812 Pisum sativum isoflavone synthase 1 (ifs1)... 100 2e-40 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 100 2e-40 emb|AW560673|AW560673 EST315721 DSIR Medicago truncatula cDNA cl... 167 2e-40 emb|AW351157|AW351157 GM210010B20F8R Gm-r1021 Glycine max cDNA 3... 167 2e-40 20

Query= atu40856_s_at 17544_s_at /id_source /description gb|aac49282.1| (u40856) aig1 [arabidopsis thaliana] /blast_score 1.00e-150 (1381 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

25

30 Searching.....done

Score I

Sequences producing significant alignments:

(bits) Value

35 gb|U64925|NTU64925 Nicotiana tabacum geranylgeranylated protein ... 260 1e-68 emb|AW625701|AW625701 EST319608 tomato radicle, 5 d post-imbibit... 228 6e-59 emb|AW720227|AW720227 LjNEST17c4r Lotus japonicus nodule library... 219 4e-56 emb|AW220184|AW220184 EST302667 tomato root during/after fruit s... 208 7e-53 emb|AI774580|AI774580 EST255680 tomato resistant, Cornell Lycope... 173 2e-42 40 emb|AW685484|AW685484 NF030E02NR1F1000 Nodulated root Medicago t... 171 2e-41 emb|AI443867|AI443867 sa44d09.yl Gm-c1004 Glycine max cDNA clone... 170 3e-41 emb|AW397252|AW397252 sg76f06.yl Gm-c1007 Glycine max cDNA clone... 168 1e-40 emb|AW033368|AW033368 EST276939 tomato callus, TAMU Lycopersicon... 162 5e-39 emb|AV417858|AV417858 AV417858 Lotus japonicus young plants (two... 153 4e-36 45 emb|AI780050|AI780050 EST260929 tomato susceptible, Cornell Lyco... 138 9e-32 emb|AW039095|AW039095 EST281068 tomato mixed elicitor, BTI Lycop... 111 2e-23 emb|AI780139|AI780139 EST261018 tomato susceptible, Cornell Lyco... 86 7e-16 emb|AW164180|AW164180 Ljirnpest21-672-c8 Ljirnp Lambda HybriZap ... 84 2e-15 emblAI781596lAI781596 EST262475 tomato susceptible, Cornell Lyco... 75 1e-12 50 emb|AW774764|AW774764 EST333915 KV3 Medicago truncatula cDNA clo... 62 7e-09 emb[AW348781]AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ... 54 2e-06 emb|AI491210|AI491210 EST241919 tomato shoot, Cornell Lycopersic... 29 0.010 emb|AW651526|AW651526 EST329980 tomato germinating seedlings, TA... 29 0.011 emb|AW220594|AW220594 EST296979 tomato fruit mature green, TAMU ... 29 0.011 55 emb|AW926585|AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis... 29 0.025 emb|AW032321|AW032321 EST275775 tomato callus, TAMU Lycopersicon... 28 0.026 emb|AW736598|AW736598 EST333090 KV3 Medicago truncatula cDNA clo... 37 0.39 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 37 0.39 emb|AW713727|AW713727 h1f12ne.fl Neurospora crassa evening cDNA ... 35 1.0 60 emb|AW711542|AW711542 f3g07ne.f1 Neurospora crassa evening cDNA ... 35 1.0

emb|AB009972|AB009972 Aspergillus oryzae gene for beta-1,4-xylos... 35 1.0

	emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA 35 1.0 emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA 35 1.0 emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA 35 1.0
	emb Y09354 SPABC1 S.pombe ABC1 gene. 35 1.4
5	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9. 35 1.4
	emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc 35 1.4
	emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU 26 1.5
	emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl 31 1.5
10	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC 35 1.9
10	emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso 35 1.9
	emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom 35 1.
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC 35 1.9
	emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso 35 1.9
1.5	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano 35 1.9
15	emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom 35 1.9
	emb AW729536 AW729536 GA_Ea0025E24 Gossypium arboreum 7-10 dpa 35 1.9
	emb AW727289 AW727289 GA
	gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR 28 2.1
20	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute 28 2.1
20	emb AW776020 AW776020 EST335085 DSIL Medicago truncatula cDNA cl 28 2.2
	emb AW685649 AW685649 NF032G04NR1F1000 Nodulated root Medicago t 28 2.2
	emb AW690755 AW690755 NF037H10ST1F1000 Developing stem Medicago 28 2.2
	emb AW256896 AW256896 EST305033 KV2 Medicago truncatula cDNA clo 28 2.3
25	emb AV422565 AV422565 AV422565 Lotus japonicus young plants (two 28 2.3
23	emb AW832303 AW832303 sm07c04.y1 Gm-c1027 Glycine max cDNA clone 27 2.3 emb AL136538 SPAC30 S.pombe chromosome I cosmid c30. 34 2.6
	emb AI724721 AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale 34 2.6 emb AW256609 AW256609 EST304746 KV2 Medicago truncatula cDNA clo 34 2.6
	emb AI775696 AI775696 EST256796 tomato resistant, Cornell Lycope 28 3.1
30	emb Z71682 SCYNR067C S. cerevisiae chromosome XIV reading frame O 34 3.6
30	emb AI776315 AI776315 EST257415 tomato resistant, Cornell Lycope 34 3.6
	emb AF230371 AF230371 Lycopersicon esculentum allene oxide synth 34 3.6
	emb AA741645 AA741645 LmLv39p3/255A Leishmania major promastigot 34 3.6
	gb U08843 PPU08843 Porphyra purpurea putative polysaccharide bin 34 3.6
35	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK 29 4.7
	emb AQ399149 AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P 33 5.0
	emb AW615911 AW615911 EST325409 tomato flower buds 0-3 mm, Corne 33 5.0
	emb AW035453 AW035453 EST281191 tomato callus, TAMU Lycopersicon 33 5.0
	emb AF051695 AF051695 Trypanosoma cruzi sialidase homolog (P85.1 33 5.0
40	emb Z37538 LTGRR4 L.tarentolae mRNA encoding putative NADH subun 28 5.5
	emb X85021 SCXLTORFS S.cerevisiae DNA from left arm of chromosom 33 6.8
	gb L25088 YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi 33 6.8
	emb AQ443826 AQ443826 GSSTc01287 Trypanosoma cruzi random genomi 33 6.8
	emb AQ502942 AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc 33 6.8
45	emb Z85962 MSZ85962 Musa sp. DNA for sequence tagged microsatell 33 6.8
	emb Z49377 SCYJL102W S.cerevisiae chromosome X reading frame ORF 33 6.8
	emb AW224537 AW224537 EST302980 tomato root, plants pre-anthesis 31 7.5
	emb AW257183 AW257183 EST305320 KV2 Medicago truncatula cDNA clo 32 9.4
	emb AQ642922 AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos 32 9.4
50	emb AW738509 AW738509 EST339936 tomato flower buds, anthesis, Co 32 9.4
	emb AW217351 AW217351 EST296174 tomato flower buds 0-3 mm, Corne 32 9.4
	emb AW219255 AW219255 EST301737 tomato root during/after fruit s 32 9.4
	emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC 32 9.4
E <i>E</i>	emb AW684118 AW684118 NF012F02NR1F1000 Nodulated root Medicago t 32 9.4
55	emb AW622239 AW622239 EST313037 tomato root during/after fruit s 32 9.4
	emb AQ651543 AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom 32 9.4
	emb Y11565 NC11565 N.crassa acu-15 gene. 32 9.4
	emb AW775944 AW775944 EST335009 DSIL Medicago truncatula cDNA cl 32 9.4
60	emb AB014493 AB014493 Gibberella zeae gene for reductase, partia 32 9.4
. .	

Query= AJ002295_s_at 18012_s_at /id_source genbank /description

"emb|cab59428.1| (aj002295) inositol-1,4,5-trisphosphate 5-phosphatase [arabidopsis thaliana]" /blast_score 0 (2083 letters)

5 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 10 Score E Sequences producing significant alignments: (bits) Value emb|AI898446|AI898446 EST267889 tomato ovary, TAMU Lycopersicon ... 209 e-107 emb|AW217248|AW217248 EST295962 tomato callus, TAMU Lycopersicon... 245 1e-88 15 emb|AI485780|AI485780 EST244101 tomato ovary, TAMU Lycopersicon ... 242 1e-85 emb|AI485695|AI485695 EST244016 tomato ovary, TAMU Lycopersicon ... 261 3e-85 emb|AI485239|AI485239 EST243543 tomato ovary, TAMU Lycopersicon ... 291 1e-77 emb|AI899197|AI899197 EST268640 tomato ovary, TAMU Lycopersicon ... 161 1e-77 emb|AW034573|AW034573 EST278257 tomato callus, TAMU Lycopersicon... 272 8e-72 20 emb|AI488812|AI488812 EST247151 tomato ovary, TAMU Lycopersicon ... 251 1e-65 emb|AW687082|AW687082 NF005G09RT1F1071 Developing root Medicago ... 182 6e-65 emb|AI898248|AI898248 EST267691 tomato ovary, TAMU Lycopersicon ... 204 1e-63 emb|AI483614|AI483614 EST249464 tomato ovary, TAMU Lycopersicon ... 238 1e-61 emb|A1897089|A1897089 EST266532 tomato ovary, TAMU Lycopersicon ... 226 7e-58 25 emb|AW774994|AW774994 EST334145 KV3 Medicago truncatula cDNA clo... 182 2e-56 emb|AW559604|AW559604 EST314652 DSIR Medicago truncatula cDNA cl... 177 3e-53 emb|AI485284|AI485284 EST243588 tomato ovary, TAMU Lycopersicon ... 204 3e-51 emb|AI485664|AI485664 EST243985 tomato ovary, TAMU Lycopersicon ... 195 8e-49 emb|AW774741|AW774741 EST333892 KV3 Medicago truncatula cDNA clo... 90 2e-48 30 emb|AI487608|AI487608 EST245930 tomato ovary, TAMU Lycopersicon ... 187 3e-46 emb|AI483438|AI483438 EST249259 tomato ovary, TAMU Lycopersicon ... 169 6e-41 emb|AW775688|AW775688 EST334753 DSIL Medicago truncatula cDNA cl... 157 2e-37 emb|AI485008|AI485008 EST243271 tomato ovary, TAMU Lycopersicon ... 157 2e-37 emb|AI938737|AI938737 sb58c06.yl Gm-c1018 Glycine max cDNA clone... 151 2e-35 35 emb|AI967736|AI967736 Ljirnpestl 1-837-a7 Ljirnp Lambda HybriZap ... 147 4e-34 emb|Z50161|SCC14ORFS S.cerevisiae orfs and LEU4, MET4, POL1, RAS... 60 1e-33 emb|Z71382|SCYNL106C S.cerevisiae chromosome XIV reading frame O... 60 1e-33 emblAI973618|AI973618 sd07d04.yl Gm-c1020 Glycine max cDNA clone... 141 2e-32 emb|AI485392|AI485392 EST243713 tomato ovary, TAMU Lycopersicon ... 138 2e-31 40 emb[X94335]SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 51 1e-29 emb|Z75017|SCYOR109W S.cerevisiae chromosome XV reading frame OR... 51 1e-29 emb|AL022103|SPBC2G2 S.pombe chromosome II cosmid c2G2. 79 le-27 emb[X79743]SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes. 72 2e-27 emb|Z38062|SC9687 S.cerevisiae chromosome IX cosmid 9687. 72 2e-27 45 emb|AI488810|AI488810 EST247149 tomato ovary, TAMU Lycopersicon ... 121 3e-26 gb|BE020060|BE020060 sm38e06.yl Gm-c1028 Glycine max cDNA clone ... 119 9e-26 emb|AW685248|AW685248 NF028A10NR1F1000 Nodulated root Medicago t... 116 2e-24 emb|AW257207|AW257207 EST305344 KV2 Medicago truncatula cDNA clo... 75 2e-24 emb|AV406995|AV406995 AV406995 Lotus japonicus young plants (two... 67 2e-23 50 emb|AW034093|AW034093 EST277588 tomato callus, TAMU Lycopersicon... 111 3e-23 emb|Z98763|SPAC9G1 S.pombe chromosome I cosmid c9G1. emblAQ502761|AQ502761 V84A11 mTn-3xHA/lacZ Insertion Library Sac... 52 2e-22 emb|AI897134|AI897134 EST266577 tomato ovary, TAMU Lycopersicon ... 107 4e-22 emb|AI771644|AI771644 EST252744 tomato ovary, TAMU Lycopersicon ... 104 3e-21 55 emb|AV413397|AV413397 AV413397 Lotus japonicus young plants (two... 100 8e-20 emb|AW616540|AW616540 EST322951 L. hirsutum trichome, Cornell Un... 98 2e-19 emb|AL110506|SPBC577 S.pombe chromosome II cosmid c577. 74 le-18 emb|AW126841|AW126841 ga16f04.yl Moss EST library PPU Physcomitr... 94 4e-18 60 emb|AI780067|AI780067 EST260946 tomato susceptible, Cornell Lyco... 94 5e-18 emb|AW687035|AW687035 NF005C05RT1F1037 Developing root Medicago ... 73 2e-17

emblAW685930|AW685930 NF036F03NR1F1000 Nodulated root Medicago t... 73 2e-17 emb|AV415287|AV415287 AV415287 Lotus japonicus young plants (two... 90 4e-17 gb|BE124605|BE124605 EST393640 GVN Medicago truncatula cDNA clon... 65 5e-15 emb|AW220291|AW220291 EST302774 tomato root during/after fruit s... 68 1e-14 5 emb|AQ644913|AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso... 53 1e-13 emb|AA495505|AA495505 c430 Zhou and Ragan 1993 Gracilaria gracil... 49 4e-13 emb|AW830613|AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone... 77 4e-13 emb|AW666237|AW666237 sk34b04.y1 Gm-c1028 Glycine max cDNA clone... 77 4e-13 emb|AW285758|AW285758 LG1_223_C03.b1_A002 Light Grown 1 (LG1) So... 74 4e-12 10 emb|AQ658256|AQ658256 Sheared DNA-13C5.TR Sheared DNA Trypanosom... 73 1e-11 emb|AW704333|AW704333 sk18a03.y1 Gm-c1028 Glycine max cDNA clone... 71 4e-11 emb|AV390446|AV390446 AV390446 Chlamydomonas reinhardtii C9 Chla... 70 5e-11 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 64 7e-11 emb|AZ048449|AZ048449 PSB67 Barley PstI genomic clones Hordeum v... 69 1e-10 15 emb|AW695904|AW695904 NF099H04ST1F1043 Developing stem Medicago ... 49 2e-10 emb|AW760518|AW760518 sl51d02.yl Gm-c1027 Glycine max cDNA clone... 66 9e-10 emb|AW332143|AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car... 36 1e-09 emb|AW687790|AW687790 NF013E04RT1F1034 Developing root Medicago ... 65 2e-09 emb|AI486692|AI486692 EST245014 tomato ovary, TAMU Lycopersicon ... 54 3e-09 20 emb|AW333870|AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c... 36 4e-09 emb|AQ850639|AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra... 44 5e-09 emb|AW127178|AW127178 M110117 GVN Medicago truncatula cDNA clone... 63 8e-09 emb|AW399291|AW399291 EST309791 L. pennellii trichome, Cornell U... 62 2e-08 emb|AW616547|AW616547 EST322958 L. hirsutum trichome, Cornell Un... 62 2e-08 25 emb|AW693686|AW693686 NF068A05ST1F1036 Developing stem Medicago ... 62 2e-08 emb|AW208046|AW208046 M111077e DSIR Medicago truncatula cDNA clo... 61 4e-08 emb|AQ642482|AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos... 53 6e-08 emb|AW686583|AW686583 NF039G02NR1F1000 Nodulated root Medicago t... 45 5e-07 emb|AQ849089|AQ849089 LMAJFV1_lm41a04.y1 Leishmania major FV1 ra... 44 5e-06 30 emb|AI781410|AI781410 EST262277 tomato susceptible, Cornell Lyco... 52 2e-05 emb|AW617564|AW617564 EST323975 L. hirsutum trichome, Cornell Un... 49 2e-04 emb|AQ946427|AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom... 47 4e-04 emblAW099113|AW099113 sd34f04.y1 Gm-c1012 Glycine max cDNA clone... 46 0.001 emb|Z74807|SCYOL065C S.cerevisiae chromosome XV reading frame OR... 29 0.002 35 emb|AQ655271|AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso... 38 0.004 emb|AW685854|AW685854 NF031A06NR1F1000 Nodulated root Medicago t... 43 0.007 emblAW437996|AW437996 ST83C09 Pine TriplEx shoot tip library Pin... 42 0.014 emb|AI440709|AI440709 sa62e11.yl Gm-c1004 Glycine max cDNA clone... 31 0.021 emb|AW979881|AW979881 EST341528 tomato root deficiency, Cornell ... 37 0.45 40 gb|M28064|PFAHRKP Plasmodium brasilianum DNA homologous to the h... 37 0.45 emb|AF263282|AF263282 Filobasidiella neoformans var. neoformans ... 34 .0.54 emb|AW702543|AW702543 TgESTzz85a12.yl TgRH*-Tachyzoite cDNA Toxo... 32 0.58 emb|AQ651205|AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso... 37 0.62 emb|AQ945454|AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso... 37 0.62 45 emb|AZ214873|AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso... 37 0.62 emb|AQ939979|AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso... 37 0.62 emb|AL049180|PFMAL13P1 Plasmodium falciparum chromosome 13 strai... 36 1.2 emb|Z74892|BO15H11 B.oleracea mRNA for glycine-rich protein. 36 1.2 emb[AW774740]AW774740 EST333891 KV3 Medicago truncatula cDNA clo... 36 1.2 50 emb|Z38060|SC5610 S.cerevisiae chromosome IX sequence derived fr... 36 1.2 emb|AL031745|PFMAL1P2 Plasmodium falciparum chromosome 1 strain ... 35 2.2

Query= AJ010971_at 18022_at /id_source genbank /description
55 emb|cab52675.1| (aj010971) glucose-6-phosphate 1-dehydrogenase
[arabidopsis thaliana] /blast_score 0
(1690 letters)

Database: plantfungal
60 661,018 sequences; 426,114,510 total letters

Searching.....done Score Ε Sequences producing significant alignments: (bits) Value 5 emblX74421|STG6PDH S.tuberosum mRNA for glucose-6-phosphate dehy... 911 0.0 emb|AF012862|AF012862 Petroselinum crispum cytosolic glucose-6-p... 841 0.0 emb|AJ001770|NTTCG9 Nicotiana tabacum mRNA for cytosolic glucose... 893 0.0 gb|U18238|MSU18238 Medicago sativa glucose-6-phosphate dehydroge... 900 0.0 10 emb|AF012863|AF012863 Petroselinum crispum cytosolic glucose-6-p... 887 0.0 emb|AJ001769|NTTCG6 Nicotiana tabacum mRNA cytosolic glucose-6-p... 895 0.0 emb|AF097663|AF097663 Mesembryanthemum crystallinum cytoplasmic ... 754 0.0 emb|AB011441|AB011441 Triticum aestivum WESR5 mRNA for glucose-6... 500 e-141 emb|X70373|KLLETZWF K.lactis LET1 gene and ZWF gene for glucose-... 231 e-138 15 emb|Z69381|SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom... 244 e-136 gb|M34709|YSCG6PD S.cerevisiae glucose-6-phosphate dehydrogenase... 244 e-136 emb|X57336|SCMET19 S. cerevisiae MET19 gene for glucose-6-phosph... 244 e-136 emb|Z71517|SCYNL241C S.cerevisiae chromosome XIV reading frame O... 244 e-136 emb|AJ010712|STU010712 Solanum tuberosum mRNA for glucose-6-phos... 240 e-136 20 emb|X99405|NTG6PD N.tabacum mRNA for chloroplast glucose-6-phosp... 242 e-135 emb|AF012861|AF012861 Petroselinum crispum plastidic glucose-6-p... 248 e-135 emb|AI730607|AI730607 BNLGHi7371 Six-day Cotton fiber Gossypium ... 481 e-135 emb|X87942|ANG6PDHSE A.niger mRNA for glucose-6-phosphate dehydr... 225 e-132 emb|AW686120|AW686120 NF038D09NR1F1000 Nodulated root Medicago t... 472 e-132 25 emb|AJ132346|DBI132346 Dunaliella bioculata mRNA for plastidic g... 235 e-132 emb|AW925642|AW925642 HVSMEg0005C04 Hordeum vulgare pre-anthesis... 465 e-130 emb|AJ001772|NTTPG18 Nicotiana tabacum mRNA for plastidic glucos... 243 e-129 emb|AW930385|AW930385 EST340938 tomato fruit mature green, TAMU ... 444 e-124 emb|AW831416|AW831416 sm22g09.y1 Gm-c1028 Glycine max cDNA clone... 434 e-121 30 emb|X83923|STG6PDHPI S.tuberosum mRNA for glucose-6-phosphate de... 249 e-118 emb|AJ000182|SO000182 Spinacia oleracea mRNA for glucose-6-phosp... 242 e-117 emb|AJ001771|NTTPG16 Nicotiana tabacum mRNA for plastidic glucos... 247 e-116 emb|AI491202|AI491202 EST241911 tomato shoot, Cornell Lycopersic... 368 e-116 emb|AL121764|SPAC9 S.pombe chromosome I cosmid c9. 196 e-116 35 emb|AW233801|AW233801 sf26h03.y1 Gm-c1028 Glycine max cDNA clone... 415 e-115 emb|Z95395|SPAC3A12 S.pombe chromosome I cosmid c3A12. 196 e-108 emb|AW288048|AW288048 N100892e rootphos(-) Medicago truncatula c... 387 e-106 emb|AW685333|AW685333 NF027C04NR1F1000 Nodulated root Medicago t... 356 e-105 emb[X77830]ANWGGSDA A.nidulans (WG096) gsdA gene. 130 e-102 emb|AJ006246|CCA6246 Cyanidium caldarium mRNA for glucose-6-phos... 239 e-102 emb|AJ000184|SO000184|Spinacia oleracea mRNA for glucose-6-phosp... 242 e-100 emb|AJ000183|SO000183 Spinacia oleracea mRNA for glucose-6-phosp... 190 3e-99 emb|X84001|ANDNAG6PD A.nidulans g6pd gene. 130 2e-98 emb|AW744917|AW744917 LG1 384 F04.b1 A002 Light Grown 1 (LG1) So... 356 3e-97 45 emb|AW761534|AW761534 sl68h05.y1 Gm-c1027 Glycine max cDNA clone... 356 4e-97 emb|X74988|PFGLPH P.falciparum gene for glucose-6-phosphate dehy... 192 5e-89 emb|AW560329|AW560329 EST315377 DSIR Medicago truncatula cDNA cl... 323 2e-87 gb]M80655[PFAG6PD Plasmodium falciparum glucose-6-phosphate dehy... 192 1e-86 emb|AW497059|AW497059 ga53c08.yl Moss EST library PPU Physcomitr... 319 5e-86 50 emb|AW216550|AW216550 EST295264 tomato callus, TAMU Lycopersicon... 188 6e-84 emb|AW219903|AW219903 EST302386 tomato root during/after fruit s... 305 7e-82 emb|AW180861|AW180861 MgA1030f MgA Library Mycosphaerella gramin... 226 5e-80 emb|AW616585|AW616585 EST322996 L. hirsutum trichome, Cornell Un... 175 7e-80 emb|AW309937|AW309937 sf26h03.x1 Gm-c1028 Glycine max cDNA clone... 294 1e-78 emb|AW031447|AW031447 EST274901 tomato callus, TAMU Lycopersicon... 166 6e-78 emb|AI894720|AI894720 EST264163 tomato callus, TAMU Lycopersicon... 291 1e-77 emb|AW690515|AW690515 NF030E09ST1F1000 Developing stem Medicago ... 174 3e-77 emb|AW736245|AW736245 EST332231 KV3 Medicago truncatula cDNA clo... 278 7e-76

emb|AW455246|AW455246 EST311906 tomato root during/after fruit s... 155 6e-75

emb|AL023595|SPCC794 S.pombe chromosome III cosmid c794.

emb|AW980010|AW980010 EST310488 tomato root deficiency, Cornell ... 153 3e-74

60

emb|AW255521|AW255521 ML551 peppermint glandular trichome Mentha... 270 3e-71 emb[AW567621]AW567621 si65f02.y1 Gm-r1030 Glycine max cDNA clone... 264 1e-69 emb|AW689492|AW689492 NF019H04ST1F1000 Developing stem Medicago ... 128 3e-69 emb|AW737104|AW737104 EST338531 tomato flower buds, anthesis, Co... 141 1e-64 emb|AW255222|AW255222 ML216 peppermint glandular trichome Mentha... 142 2e-64 emb|AW737079|AW737079 EST338506 tomato flower buds, anthesis, Co... 141 3e-64 emb|AW565200|AW565200 LG1_328_D07.b1_A002 Light Grown 1 (LG1) So... 119 1e-60 emb|AW684970|AW684970 NF023F11NR1F1000 Nodulated root Medicago t... 128 1e-60 emb|AQ952407|AQ952407 Sheared DNA-32N19.TF Sheared DNA Trypanoso... 84 2e-60 10 emb|AA787466|AA787466 n3f11a1.rl Aspergillus nidulans 24hr asexu... 229 4e-59 emb|AW254983|AW254983 ML1164 peppermint glandular trichome Menth... 134 2e-58 emb|AW617385|AW617385 EST323796 L. hirsutum trichome, Cornell Un... 141 2e-57 emb|AI773327|AI773327 EST254427 tomato resistant, Cornell Lycope... 222 5e-57 emb|AW704079|AW704079 sk27e10.y1 Gm-c1028 Glycine max cDNA clone... 219 6e-56 15 emb|X77829|ANNGSDA A.niger (N400) gsdA gene. 131 4e-55 emb|AW286177|AW286177 LG1_328_D07.g1_A002 Light Grown 1 (LG1) So... 216 4e-55 emb|AW617091|AW617091 EST323502 L. hirsutum trichome, Cornell Un... 138 5e-55 emb|AI777244|AI777244 EST258209 tomato resistant, Cornell Lycope... 150 1e-54 emb|AV424412|AV424412 AV424412 Lotus japonicus young plants (two... 205 9e-52 20 emb|AQ875204|AQ875204 V123H11 mTn-3xHA/lacZ Insertion Library, s... 192 le-49 emb|AV416113|AV416113 AV416113 Lotus japonicus young plants (two... 196 4e-49 emb|Z99568|SPAC3C7 S.pombe chromosome I cosmid c3C7. emb|AQ500574|AQ500574 V36G4 mTn-3xHA/lacZ Insertion Library Sacc... 127 6e-48 emb|AI187687|AI187687 p280 Porphyra yezoensis in Lambda UniZAP P... 87 1e-47 25 emb|AJ279688|BPE279688 Betula pendula partial mRNA for Glucose-6... 93 7e-47 emb|AW700124|AW700124 gb34g09.yl Moss EST library PPN Physcomitr... 187 3e-46 emb|AW223852|AW223852 EST300663 tomato fruit red ripe, TAMU Lyco... 141 6e-46 emb|AW774199|AW774199 EST333350 KV3 Medicago truncatula cDNA clo... 143 3e-45 emb|AW621290|AW621290 EST312088 tomato root during/after fruit s... 138 3e-43 30 emb|AW980083|AW980083 EST341594 tomato root deficiency, Cornell ... 133 2e-42 emb[AZ217409]AZ217409 Sheared DNA-90C8.TR Sheared DNA Trypanosom... 90 3e-42 emb|AI941197|AI941197 sb85g11.yl Gm-c1010 Glycine max cDNA clone... 169 7e-41 emb|AW224136|AW224136 EST300947 tomato fruit red ripe, TAMU Lyco... 141 3e-40 emb|AW616535|AW616535 EST322946 L. hirsutum trichome, Cornell Un... 139 2e-38 35 emb|AU036687|AU036687 Schizosaccharomyces pombe genomic clone ha... 98 3e-38 emb|AI416414|AI416414 NCW07G12T3 Westergaards Neurospora crassa ... 103 3e-38 emb|AW286271|AW286271 LG1 329_F06.g1_A002 Light Grown 1 (LG1) So... 149 4e-35 emb|AI055328|AI055328 coau0003K24 Cotton Boll Abscission Zone cD... 78 3e-32 emb|AW698775|AW698775 r358 non-glandular-haired subtracted cDNA ... 133 5e-30 40 emb|AJ130773|LDI130773 Laminaria digitata mRNA for glucose-6-pho... 131 2e-29 emb|AI974714|AI974714 T113172e KV2 Medicago truncatula cDNA clon... 118 2e-28 emb|AF173650|AF173650 Beta vulgaris clone GPD109UNI glucose-6-ph... 77 1e-27 emb|AJ004900|GMJ004900 Glycine max mRNA for glucose-6-phosphate-... 121 1e-26 emb|AW831248|AW831248 sm13f09.yl Gm-c1027 Glycine max cDNA clone... 104 8e-26 45 Query= AJ238846 at 18054 at /id source genbank /description emb|cab54517.1| (aj238846) sgp1 monomeric g-protein [arabidopsis thaliana] /blast_score 1.00e-150 50 (887 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 55 Searching......done Ε Score Sequences producing significant alignments: (bits) Value 60 emb|AW725454|AW725454 GA__Ea0018A14 Gossypium arboreum 7-10 dpa ... 238 8e-81 emb|Z38114|SC9745 S.cerevisiae chromosome XIII cosmid 9745. 122 2e-33

	gb U34860 SCU34860 Saccharomyces cerevisiae origin recognition c 122 2e-33
	dbj D38172 YSCTEM1P Yeast gene for GTP-binding protein Tem1p, co 122 2e-33
	emb AI988573 AI988573 sd04c11.yl Gm-c1020 Glycine max cDNA clone 142 3e-33
	emb Y12314 SPSPG1GEN S.pombe spg1 gene. 67 9e-20
5	emb AJ001587 SPAJ1587 Schizosaccharomyces pombe sid3 gene. 67 9e-20
	emb AW776339 AW776339 EST335404 DSIL Medicago truncatula cDNA cl 67 5e-14
	emb AI416417 AI416417 NCW07E2T3 Westergaards Neurospora crassa c 55 1e-06
	gb U17243 YSCL8003 Saccharomyces cerevisiae chromosome XII cosmi 32 2e-06
	emb Z75093 SCYOR185C S.cerevisiae chromosome XV reading frame OR 32 2e-06
10	gb L08690 YSCGSP1X Yeast GTP-binding protein (GSP1) gene, comple 32 2e-06
	gb L08691 YSCGSP2X Yeast GTP-binding protein (GSP2) gene, comple 32 2e-06
	emb[X71946]SCCNR2A S.cerevisiae CNR2 gene. 32 2e-06
	emb X71945 SCCNR1A S.cerevisiae CNR1 gene. 32 2e-06
15	
13	dbj D21825 TETPRAN Tetrahymena pyriformis mRNA for Ran/TC4, comp 33 3e-06
	gb[U17086]TBU17086 Trypanosoma brucei rhodesiense RAN/TC4 GTPase 30 6e-05
	emb AC008031 AC008031 Trypanosoma brucei chromosome II clone RPC 35 0.001
	emb AQ661102 AQ661102 Sheared DNA-15E18.TF Sheared DNA Trypanoso 32 0.002
20	emb AW671770 AW671770 LG1_351_B08.b1_A002 Light Grown 1 (LG1) So 42 0.00
20	emb W68882 W68882 T2862 MVAT4 bloodstream form of serodeme WRATa 30 0.009
	emb AW685566 AW685566 NF031H02NR1F1000 Nodulated root Medicago t 36 0.037
	emb AB024996 AB024996 Cicer arietinum mRNA for rac-type small GT 36 0.091
	emb AW832298 AW832298 sm07b06.yl Gm-c1027 Glycine max cDNA clone 38 0.13
26	emb AW218480 AW218480 EST303663 tomato radicle, 5 d post-imbibit 36 0.13
25	emb AI437767 AI437767 sa39c11.yl Gm-c1004 Glycine max cDNA clone 37 0.17
	emb AV413867 AV413867 AV413867 Lotus japonicus young plants (two 35 0.17
	emb AW690945 AW690945 NF034H11ST1F1000 Developing stem Medicago 35 0.23
	emb AW621657 AW621657 EST312455 tomato root during/after fruit s 37 0.24
• •	emb AI775563 AI775563 EST256663 tomato resistant, Cornell Lycope 37 0.24
30	emb AW738459 AW738459 EST339886 tomato flower buds, anthesis, Co 36 0.33
	emb A1731040 A1731040 BNLGHi8453 Six-day Cotton fiber Gossypium 36 0.33
	emb AI727570 AI727570 BNLGHi8420 Six-day Cotton fiber Gossypium 36 0.33
	emb AV419645 AV419645 AV419645 Lotus japonicus young plants (two 36 0.33
	emb Z49191 BVRHO1 B.vulgaris mRNA for small G protein (clone 1S5). 36 0.33
35	emb AW930158 AW930158 EST340615 tomato fruit mature green, TAMU 36 0.33
	gb U17085 TBU17085 Trypanosoma brucei brucei RAN/TC4 GTPase homo 29 0.43
	emb AI440994 AI440994 sa63e10.y1 Gm-c1004 Glycine max cDNA clone 36 0.45
	gb U03624 PTU03624 Paramecium tetraurelia clone plg-14 guanine n 36 0.45
	gb U64924 NTU64924 Nicotiana tabacum geranylgeranylated protein 35 0.55
40	emb AW040005 AW040005 EST282496 tomato mixed elicitor, BTI Lycop 35 0.56
	emb AW039993 AW039993 EST282484 tomato mixed elicitor, BTI Lycop 35 0.56
	emb AW705028 AW705028 sk41f03.yl Gm-c1019 Glycine max cDNA clone 35 0.57
	emb AW929161 AW929161 EST337949 tomato flower buds 8 mm to pre-a 35 0.57
	emb AW705209 AW705209 sk43a11.yl Gm-c1019 Glycine max cDNA clone 35 0.57
45	emb AV414769 AV414769 AV414769 Lotus japonicus young plants (two 35 0.62
	gb U64923 NTU64923 Nicotiana tabacum geranylgeranylated protein 35 0.62
	emb Z73962 LJRAC2 L.japonicus mRNA for small GTP-binding protein 35 0.62
	gb BE021064 BE021064 sm47d01.yl Gm-c1028 Glycine max cDNA clone 35 0.62
	emb AW573660 AW573660 EST316251 GVN Medicago truncatula cDNA clo 35 0.62
50	emb AV413108 AV413108 AV413108 Lotus japonicus young plants (two 35 0.62
	emb AW202293 AW202293 sf13c10.yl Gm-c1027 Glycine max cDNA clone 35 0.62
	emb AI937960 AI937960 sc06b11.yl Gm-c1012 Glycine max cDNA clone 35 0.62
	emb Z73961 LJRAC1 L.japonicus mRNA for small GTP-binding protein 35 0.62
	emb AI162198 AI162198 A013P52U Hybrid aspen plasmid library Popu 35 0.62
55	emb AW694335 AW694335 NF075C06ST1F1049 Developing stem Medicago 35 0.62
	emb AW109094 AW109094 gate0002P07f Gossypium arboreum 7-10 dpa f 35 0.62
	gb L19093 PEARHOGTPP Pisum sativum rho (ras-related) GTP-binding 35 0.62
	emb AW565277 AW565277 LG1_332_G03.b1_A002 Light Grown 1 (LG1) So 35 0.62
	emb AV412205 AV412205 AV412205 Lotus japonicus young plants (two 35 0.62
60	gb BE054534 BE054534 GA _ Ea0033M19f Gossypium arboreum 7-10 dpa 35 0.62
	emb AW108667 AW108667 gate0001G03f Gossypium arboreum 7-10 dpa f 35 0.62

	emb AI495724 AI495724 sb15e06.yl Gm-c1004 Glycine max cDNA clone 35 0.62 gb S79309 S79309 Rac9=21.5 kda GTP-binding protein [Gossypium hi 35 0.62 gb S79308 S79308 Rac13=21.8 kda GTP-binding protein [Gossypium h 35 0.62
5	emb AJ250174 NTA250174 Nicotiana tabacum mRNA for putative rac p 35 0.62 gb BE055015 BE055015 GA Ea0001G03f Gossypium arboreum 7-10 dpa 35 0.62
	emb AW573665 AW573665 EST316256 GVN Medicago truncatula cDNA clo 35 0.62 emb AW559248 AW559248 EST306084 DSIR Medicago truncatula cDNA cl 35 0.62
10	emb AI460950 AI460950 sa78f02.y1 Gm-c1004 Glycine max cDNA clone 35 0.62 emb AW692052 AW692052 NF047B03ST1F1000 Developing stem Medicago 35 0.6
	emb AW394676 AW394676 sh34a02.y1 Gm-c1017 Glycine max cDNA clone 35 0.62 gb BE054555 BE054555 GA_Ea0002P07f Gossypium arboreum 7-10 dpa 35 0.62 emb AF146340 AF146340 Physcomitrella patens Rac-like GTP binding 35 0.85
15	emb AF233446 AF233446 Physcomitrella patens rac 1 protein (rac1) 35 0.85 emb AF115476 AF115476 Physcomitrella patens rac-like GTP binding 35 0.85
	gb U06051 PFU06051 Plasmodium falciparum Dd2 Ran/TC4 nuclear GTP 35 0.85 emb AW729788 AW729788 GA_Ea0026A18 Gossypium arboreum 7-10 dpa 35 0.8 emb AF146341 AF146341 Physcomitrella patens Rac-like GTP binding 35 0.85
20	emb AI731831 AI731831 BNLGHi11032 Six-day Cotton fiber Gossypium 35 0.85 emb AF051223 AF051223 Picea mariana Rac-like GTP binding protein 35 0.85
	gb BE055583 BE055583 GA_Ea0001102f Gossypium arboreum 7-10 dpa 35 0.85 emb AW108575 AW108575 gate0001102f Gossypium arboreum 7-10 dpa f 35 0.85 emb X73954 PFRAN1 P.falciparum gene for ras-related nuclear prot 35 0.85
25	emb AW056772 AW056772 ST55F07 Pine TriplEx shoot tip library Pin 35 1.2 emb AW559842 AW559842 EST314890 DSIR Medicago truncatula cDNA cl 34 1.6
	emb AW217581 AW217581 EST296295 tomato flower buds 3-8 mm, Corne 34 1.6 emb AW217573 AW217573 EST296287 tomato flower buds 3-8 mm, Corne 34 1.6 emb Z36133 SCYBR264C S.cerevisiae chromosome II reading frame OR 34 1.6
30	emb X70529 SCCIIORF S. cerevisiae chromosome II sequence for ORF 34 1.6
50	emb AI778114 AI778114 ES1258993 tomato susceptible, Cornell Lyco 34 1.6 emb AF042330 AF042330 Brassica rapa rac-like small GTP binding p 34 1.6 emb AW625569 AW625569 EST319476 tomato radicle, 5 d post-imbibit 34 1.6 emb AW931490 AW931490 EST357333 tomato fruit mature green, TAMU 34 1.6
25	gb BE033825 BE033825 MG04D04 MG Mesembryanthemum crystallinum cD 34 2.2
35	gb BE036577 BE036577 MP01F02 MP Mesembryanthemum crystallinum cD 34 2.2 emb AQ399302 AQ399302 mgxb0015O18f CUGI Rice Blast BAC Library P 34 2.2 emb AW697756 AW697756 Str1-D6 Sugar Beet germination cDNA librar 34 2.2
40	Query= X91916_at 18716_at /id_source genbank /description
	gb aaf26754.1 ac007396_3 (ac007396) t4o12.6 [arabidopsis thaliana] /blast_score 3.00e-36 (403 letters)
45	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
50	Score E
	Sequences producing significant alignments: (bits) Value
55	gb U18557 RSU18557 Raphanus sativus antifungal protein 1 preprot 166 7e-43 emb A26875 A26875 R.sativus AFP1 gene. 166 7e-43
<i>33</i>	emb X97318 RSAFP4 R.sativus mRNA for antifungal protein 4. 162 6e-42 gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot 160 1e-38
	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3. 133 8e-37
	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl 135 2e-36 emb AT001728 AT001728 AT001728 Flower bud cDNA Brassica rapa sub 82 2e-15
60	gb L47901 L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA 81 5e-15
	emb A26963 A26963 D.merkii AMP1 sequence. 74 5e-13

	emb A27062 A27062 C.benedictus AMP2 sequence. 73 1e-12
	emb X53375 HASF18 Sunflower anther-specific mRNA SF18. 72 3e-12
	emb A26906 A26906 C.benedictus AMP1 sequence. 72 3e-12
	emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub 69 2e-11
5	emb A27064 A27064 C.ternatea AMP1 sequence. 58 8e-10
	emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put 40 1e-05
	emb AW870017 AW870017 NXNV_122_A10_F Nsf Xylem Normal wood Verti 35 6e-05
	emb AW064751 AW064751 ST35D04 Pine TriplEx shoot tip library Pin 36 7e-05 emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo 41 0.001
10	
10	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc 41 0.003
	emb AW621708 AW621708 EST312506 tomato root during/after fruit s 36 0.007
	emb AW220215 AW220215 EST302698 tomato root during/after fruit s 36 0.007
	emb AW623112 AW623112 EST321057 tomato flower buds 3-8 mm, Corne 40 0.008
1.5	emb AW220231 AW220231 EST302714 tomato root during/after fruit s 36 0.008
15	emb AW219164 AW219164 EST301646 tomato root during/after fruit s 36 0.008
	emb AW219793 AW219793 EST302275 tomato root during/after fruit s 36 0.009
*	emb AI487824 AI487824 EST246146 tomato ovary, TAMU Lycopersicon 40 0.009
	emb AI483999 AI483999 EST249870 tomato ovary, TAMU Lycopersicon 40 0.010
	gb[U20591]SLU20591 Solanum lycopersicum flower-specific gamma-th 40 0.010
20	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Corne 40 0.010
	emb AW929929 AW929929 EST354199 tomato flower buds 8 mm to pre-a 40 0.010
	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a 40 0.010
	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Corne 40 0.012
	emb AI490062 AI490062 EST248401 tomato ovary, TAMU Lycopersicon 40 0.012
25	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne 40 0.012
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon 40 0.012
,	emb AI485550 AI485550 EST243871 tomato ovary, TAMU Lycopersicon 40 0.012
	emb AI898009 AI898009 EST267452 tomato ovary, TAMU Lycopersicon 40 0.012
30	
50	* * * * * * * * * * * * * * * * * * * *
	emb Al489818 Al489818 EST248157 tomato ovary, TAMU Lycopersicon 40 0.012
	emb AI487398 AI487398 EST245720 tomato ovary, TAMU Lycopersicon 40 0.012
	emb AI487859 AI487859 EST246181 tomato ovary, TAMU Lycopersicon 40 0.012
35	emb AI484497 AI484497 EST242507 tomato ovary, TAMU Lycopersicon 40 0.012
33	emb AI490243 AI490243 EST248569 tomato ovary, TAMU Lycopersicon 40 0.012
	emb AI897392 AI897392 EST266835 tomato ovary, TAMU Lycopersicon 40 0.012
	emb AW219347 AW219347 EST301829 tomato root during/after fruit s 33 0.014
	emb AW621529 AW621529 EST312327 tomato root during/after fruit s 35 0.025
40	emb AW622375 AW622375 EST313174 tomato root during/after fruit s 35 0.026
40	emb AW622390 AW622390 EST313189 tomato root during/after fruit s 35 0.029
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon 38 0.031
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U 38 0.043
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s 34 0.048
	emb AW622051 AW622051 EST312849 tomato root during/after fruit s 34 0.053
45	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon 37 0.059
	emb AW622079 AW622079 EST312877 tomato root during/after fruit s 33 0.061
	emb AW621330 AW621330 EST312128 tomato root during/after fruit s 33 0.061
	emb AW220086 AW220086 EST302569 tomato root during/after fruit s 33 0.065
	emb AW621962 AW621962 EST312760 tomato root during/after fruit s 33 0.070
50	emb AF153353 AF153353 Dimocarpus longan ribulose 1,5-bisphosphat 36 0.15
	emb A26964 A26964 D.merkii AMP2 sequence. 35 0.21
-	emb AW621634 AW621634 EST312432 tomato root during/after fruit s 31 0.32
	emb AW255597 AW255597 ML641 peppermint glandular trichome Mentha 35 0.40
	emb Y15150 GMY15150 Gonystylus macrophyllus rbcL gene. 34 0.54
55	emb Y15139 BOY15139 Bixa orellana chloroplast rbcL gene. 34 0.54
-	t less and and a management of the same of
	emb AF022128 AF022128 Bixa orellana ribulose 1,5-bisphosphate ca 34 0.54
	emb AF022125 AF022125 Theobroma cacao ribulose 1,5-bisphosphate 34 0.54
s۸	gb L12568 AKARBC Akania bidwillii ribulosebisphosphate carboxyla 34 0.54
50	emb A27063 A27063 L.cicera AFP sequence. 34 0.54
	ghlM95753IRCNCPRRCI Bretechneidera cinencia chloroplast ribulose 24.0.54

	gb BE124525 BE124525 EST393560 GVN Medicago truncatula cDNA clon 31 0.68 emb AW725876 AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa 34 0.75 gb L01579 PEADRR230B Pea (pi39) disease resistance response prot 34 0.75
5	emb AI757757 AI757757 EtESTea34d02.yl Eimeria S5-2 Sporozoite st 34 0.75 gb L14293 HDOCPRBCL Hydrolea ovata chloroplast ribulosebisphosph 33 1.0
	emb AL138618 LMFL2954 Leishmania major Friedlin chromosome 23 co 33 1.4 emb AJ233156 PPAJ3156 Pentace polyantha chloroplast rbcL gene, p 33 1.4
	gb L01961 TEPCPRBCL Thespesia populnea ribulose 1,5-bisphosphate 33 1.4 emb AJ233137 RTAJ3137 Reevesia thyrsoidea chloroplast rbcL gene, 33 1.4
10	emb AJ233145 ATAJ3145 Apeiba tibourbou chloroplast rbcL gene, pa 33 1.4
	emb AJ233117 MCAJ3117 Matisia cordata chloroplast rbcL gene, par 33 1.4
	emb AJ233116 CSAJ3116 Chorisia speciosa chloroplast rbcL gene, p 33 1.4 emb AJ233127 HBAJ3127 Helicteres baruensis chloroplast rbcL gene 33 1.4
	emb AJ233127 HBAJ3127 Helicteres baruensis chloroplast rbcL gene 33 1.4 gb M77700 COTRBCLA Gossypium hirsutum ribulosebiphosphate carbox 33 1.4
15	emb AJ012208 AAU012208 Abroma angusta chloroplast rbcL gene. 33 1.4
	emb AF022127 AF022127 Tilia americana ribulose 1,5-bisphosphate 33 1.4
	emb AF022126 AF022126 Sterculia tragacantha ribulose 1,5-bisphos 33 1.4
	emb AF022121 AF022121 Quararibea gomeziana ribulose 1,5-bisphosp 33 1.4
20	emb AF022120 AF022120 Camptostemon schultzii ribulose 1,5-bispho 33 1.4 emb AF022119 AF022119 Durio zibethinus ribulose 1,5-bisphosphate 33 1.4
	emb AF022118 AF022118 Bombax buonopozense ribulose 1,5-bisphosph 33 1.4
	gb L13186 COTCPRBCLA Gossypium ronbinsonii chloroplast ribuloseb 33 1.4
	emb AJ233155 MAAJ3155 Mortoniodendron anisophyllum chloroplast r 33 1.4
25	emb AJ233131 HBAJ3131 Hildegardia barteri chloroplast rbcL gene, 33 1.4
23	gb U38925 QAU38925 Quassia amara ribulose 1,5-bisphosphate carbo 33 1.4 emb AJ233134 LPAJ3134 Leptonychia pallida chloroplast rbcL gene, 33 1.4
	emb AJ233134 LPAJ3134 Leptonychia pallida chloroplast rbcL gene, 33 1.4 emb AJ233151 GMAJ3151 Goethalsia meiantha chloroplast rbcL gene, 33 1.4
	emb AJ233150 CFAJ3150 Colona floribunda chloroplast rbcL gene, p 33 1.4
••	emb AJ233149 CAAJ3149 Christiana africana chloroplast rbcL gene, 33 1.4
30	emb AJ233157 PDAJ3157 Pentaplaris doroteae chloroplast rbcL gene 33 1.4
	0
	Query= AC006577.16_i_at 12777_i_at /id_source genbank /description "gb aad25772.1 ac006577_8 (ac006577) belongs to the pf 00657
35	lipase/acylhydrolase with gdsl-motif family. ests gb t44453,
	gb t04815, gb t45993, gb r30138, gb ai099570 and gb t22281 come from
	this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
	/chip nova /gb_link
40	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac006577 /ncgi
••	http://www.ncgr.org/cgi-bin/ff?ac006577
	(1194 letters)
	Database: plantfungal
45	661,018 sequences; 426,114,510 total letters
	Searchingdone
	Score E
50	Sequences producing significant alignments: (bits) Value
55	emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c 224 e-163 emb Y10155 BNMYAP9 B.napus for myrosinase-associated protein, cl 224 e-160 gb U39289 BNU39289 Brassica napus myrosinase-associated protein 227 e-156
<i>აა</i>	gb U39319 BNU39319 Brassica napus myrosinase-associated protein 176 e-127 emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros 176 6e-99
	emb AW568594 AW568594 si78g03.y1 Gm-c1031 Glycine max cDNA clone 47 1e-13
	emb AW288014 AW288014 N100858e rootphos(-) Medicago truncatula c 67 3e-13 emb AW774945 AW774945 EST334096 KV3 Medicago truncatula cDNA clo 46 5e-13
60	emb AW685185 AW685185 NF025E06NR1F1000 Nodulated root Medicago t 62 1e-10

```
emb|AW687872|AW687872 NF014D07RT1F1061 Developing root Medicago ... 46 2e-09
      emb|AW687276|AW687276 NF007H04RT1F1043 Developing root Medicago ... 46 7e-09
      emblAW621314|AW621314 EST312112 tomato root during/after fruit s... 44 1e-08
      emb|AW922142|AW922142 LG1 323 G10.b1 A002 Light Grown 1 (LG1) So... 58 1e-07
      emb|AW164470|AW164470 se73a09.yl Gm-c1023 Glycine max cDNA clone... 58 2e-07
      emb|AW201360|AW201360 sf02b11.yl Gm-c1027 Glycine max cDNA clone... 47 2e-07
      emb|AW757161|AW757161 sl29h09.yl Gm-c1027 Glycine max cDNA clone... 46 3e-07
      emb|AW689694|AW689694 NF023C12ST1F1000 Developing stem Medicago ... 44 3e-07
      emb|AW686342|AW686342 NF040F06NR1F1000 Nodulated root Medicago t... 46 3e-07
10
      emb|AW622151|AW622151 EST312949 tomato root during/after fruit s... 47 6e-07
      emb|AW623994|AW623994 EST321939 tomato flower buds 3-8 mm, Corne... 48 6e-07
      emb|AW621737|AW621737 EST312535 tomato root during/after fruit s... 47 6e-07
      emb|AI482693|AI482693 EST242016 tomato shoot, Cornell Lycopersic... 48 7e-07
      emb|AW622612|AW622612 EST313412 tomato root during/after fruit s... 46 1e-06
15
      emb|AW596685|AW596685 sj15e02.yl Gm-c1032 Glycine max cDNA clone... 49 2e-06
      emb|AW328890|AW328890 N200082e rootphos(-) Medicago truncatula c... 41 2e-06
      emb|AW621604|AW621604 EST312402 tomato root during/after fruit s... 45 2e-06
      emb[AI725483]AI725483 BNLGHi12267 Six-day Cotton fiber Gossypium... 40 4e-06
      emb|AI726639|AI726639 BNLGHi6294 Six-day Cotton fiber Gossypium ... 51 4e-06
20
      emb|AI488194|AI488194 EST246516 tomato ovary, TAMU Lycopersicon ... 40 4e-06
      emb|AW616223|AW616223 EST307262 L. hirsutum trichome, Cornell Un... 53 5e-06
      emb|AW650481|AW650481 EST328935 tomato germinating seedlings, TA... 53 5e-06
      emb|AI731912|AI731912 BNLGHi11257 Six-day Cotton fiber Gossypium... 51 6e-06
      emb|AW981891|AW981891 PC19H06 Pine TriplEx pollen cone library P... 51 6e-06
25
      emb|AI726794|AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ... 50 7e-06
      gb|BE057806|BE057806 sn07e03.yl Gm-c1016 Glycine max cDNA clone ... 48 1e-05
      emb|AI731726|AI731726 BNLGHi10587 Six-day Cotton fiber Gossypium... 37 1e-05
      emb|AI959774|AI959774 sc94a03.yl Gm-c1019 Glycine max cDNA clone... 36 2e-05
      emb|AW509227|AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone... 42 2e-05
30
      emb|AI054484|AI054484 coau0001C01 Cotton Boll Abscission Zone cD... 42 3e-05
      emb|AW127684|AW127684 M110431 DSLC Medicago truncatula cDNA clon... 38 3e-05
      emb|AW564505|AW564505 LG1 295 D11.b1 A002 Light Grown 1 (LG1) So... 49 9e-05
      emb|AI487871|AI487871 EST246193 tomato ovary, TAMU Lycopersicon ... 39 1e-04
      emb|AJ276421|CAR276421 Cicer arietinum partial mRNA for putative... 48 1e-04
35
      emb|AW277884|AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone... 42 2e-04
      emb[AW459066]AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone... 40 2e-04
      emb|AW926586|AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis... 47 2e-04
      emb|AI731989|AI731989 BNLGHill1154 Six-day Cotton fiber Gossypium... 45 3e-04
      emb|AW011080|AW011080 ST16D12 Pine TriplEx shoot tip library Pin... 43 3e-04
40
      gb|BE124032|BE124032 EST394157 DSIL Medicago truncatula cDNA clo... 47 3e-04
      emb|AI730716|AI730716 BNLGHi7722 Six-day Cotton fiber Gossypium ... 47 3e-04
      emb|AW929104|AW929104 EST337808 tomato flower buds 8 mm to pre-a... 33 5e-04
      emb|AW624906|AW624906 EST313735 tomato radicle, 5 d post-imbibit... 35 Se-04
      emb|AW706408|AW706408 sj56h10.yl Gm-c1033 Glycine max cDNA clone... 46 6e-04
45
      emb|AW109570|AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f... 45 7e-04
      emb|AW279386|AW279386 sf66f11.yl Gm-c1013 Glycine max cDNA clone... 37 7e-04
      emb|AW720472|AW720472 LjNEST19f4r Lotus japonicus nodule library... 35 7e-04
      emb|AW458524|AW458524 sh10c06.yl Gm-c1016 Glycine max cDNA clone... 37 8e-04
50
      emb|AI731645|AI731645 BNLGHi10354 Six-day Cotton fiber Gossypium... 46 8e-04
      emb|AI729137|AI729137 BNLGHi12747 Six-day Cotton fiber Gossypium... 46 8e-04
      emb|AW574285|AW574285 EST316876 GVN Medicago truncatula cDNA clo... 33 0.001
      emb|AI728284|AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium... 45 0.001
      emb|AW160215|AW160215 EST290073 L. pennellii trichome, Cornell U... 45 0.002
55
      emb|AI729089|AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium... 45 0.002
      gb[H74345]H74345 249 Deletion-treated Brassica napus cDNA clone ... 37 0.002
      emb|AW733443|AW733443 sk73f03.y1 Gm-c1016 Glycine max cDNA clone... 37 0.002
      emb|AW509209|AW509209 sh92f05.yl Gm-c1016 Glycine max cDNA clone... 38 0.002
      emb|AW459862|AW459862 sh96c02.yl Gm-c1016 Glycine max cDNA clone... 37 0.002
60
      emb|AW459861|AW459861 sh96c01.y1 Gm-c1016 Glycine max cDNA clone... 37 0.002
      emb|AJ011567|DLA011567 Digitalis lanata mRNA for lanatoside 15'-... 38 0.002
```

	emb AW616728 AW616728 EST323139 L. hirsutum trichome, Cornell Un 33 0.003 emb AW733540 AW733540 sk74h07.y1 Gm-c1016 Glycine max cDNA clone 37 0.003 emb AW733459 AW733459 sk73h02.y1 Gm-c1016 Glycine max cDNA clone 37 0.003
5	emb AW396681 AW396681 sh29d09.yl Gm-c1017 Glycine max cDNA clone 44 0.003 gb BE023812 BE023812 sm92g03.yl Gm-c1015 Glycine max cDNA clone 44 0.003 gb BE023398 BE023398 sm81c12.yl Gm-c1015 Glycine max cDNA clone 44 0.003
	emb AW984927 AW984927 NXNV_131_B12_F Nsf Xylem Normal wood Verti 38 0.003 emb AW127455 AW127455 M110643 DSIL Medicago truncatula cDNA clon 36 0.003 gb L37975 L37975 BNAF0021E Mustard flower buds Brassica rapa cDN 35 0.004
10	emb AW099099 AW099099 sd34d08.yl Gm-c1012 Glycine max cDNA clone 43 0.004 gb BE057305 BE057305 sn01c10.yl Gm-c1015 Glycine max cDNA clone 43 0.004
1.5	emb AW923224 AW923224 DG1_50_A07.b1_A002 Dark Grown 1 (DG1) Sorg 43 0.004 emb AW648494 AW648494 EST326948 tomato germinating seedlings, TA 43 0.005
15	emb AI965889 AI965889 sc79c08.y1 Gm-c1018 Glycine max cDNA clone 43 0.005 emb AI487258 AI487258 EST245580 tomato ovary, TAMU Lycopersicon 43 0.005 emb AW218200 AW218200 EST303381 tomato radicle, 5 d post-imbibit 43 0.005 emb AI486112 AI486112 EST244433 tomato ovary, TAMU Lycopersicon 43 0.005
20	gb BE033445 BE033445 ME02B01 ME Mesembryanthemum crystallinum cD 38 0.006 emb AW348454 AW348454 GM210002A22E12R Gm-r1021 Glycine max cDNA 39 0.006 emb AI900221 AI900221 sc02f01.y1 Gm-c1012 Glycine max cDNA clone 32 0.006 emb AW666820 AW666820 GA_Ea0006B14 Gossypium arboreum 7-10 dpa 35 0.006 emb AW624162 AW624162 EST322107 tomato flower buds 3-8 mm, Corne 34 0.006
25	emb AW667892 AW667892 GA Ea0011E24 Gossypium arboreum 7-10 dpa 42 0.007 emb AW667522 AW667522 GA Ea0009J12 Gossypium arboreum 7-10 dpa 42 0.007 emb AW730008 AW730008 GA Ea0027E20 Gossypium arboreum 7-10 dpa 36 0.008 emb AT000294 AT000294 AT000294 Apple young fruit cDNA library Ma 42 0.010
30	emb AW394864 AW394864 sh36e01.yl Gm-c1017 Glycine max cDNA clone 41 0.014
	Query= AC006577.16_r_at 12778_r_at /id_source genbank /description "gb aad25772.1 ac006577_8 (ac006577) belongs to the pf 00657 lipase/acylhydrolase with gdsl-motif family. ests gb t44453, gb t04815, gb t45993, gb r30138, gb ai099570 and gb t22281 come from
35	this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
40	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac006577 /ncgi http://www.ncgr.org/cgi-bin/ff?ac006577 (1194 letters)
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
45	Searchingdone
	Score E Sequences producing significant alignments: (bits) Value
50	emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c 224 e-163 emb Y10155 BNMYAP9 B.napus for myrosinase-associated protein, cl 224 e-160 gb U39289 BNU39289 Brassica napus myrosinase-associated protein 227 e-156 gb U39319 BNU39319 Brassica napus myrosinase-associated protein 176 e-127
55	emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros 176 6e-99 emb AW568594 AW568594 si78g03.yl Gm-c1031 Glycine max cDNA clone 47 1e-13 emb AW288014 AW288014 N100858e rootphos(-) Medicago truncatula c 67 3e-13 emb AW774945 AW774945 EST334096 KV3 Medicago truncatula cDNA clo 46 5e-13 emb AW685185 AW685185 NF025E06NR1F1000 Nodulated root Medicago t 62 1e-10
60	emb AW922141 AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So 65 5e-10 emb AW687872 AW687872 NF014D07RT1F1061 Developing root Medicago 46 2e-09 emb AW687276 AW687276 NF007H04RT1F1043 Developing root Medicago 46 7e-09

```
emblAW621314|AW621314 EST312112 tomato root during/after fruit s... 44 1e-08
       emb|AW922142|AW922142 LG1_323_G10.b1_A002 Light Grown 1 (LG1) So... 58_1e-07
       emb|AW164470|AW164470 se73a09.yl Gm-c1023 Glycine max cDNA clone... 58 2e-07
      emb|AW201360|AW201360 sf02b11.yl Gm-c1027 Glycine max cDNA clone... 47 2e-07
      emb|AW757161|AW757161 sl29h09.yl Gm-c1027 Glycine max cDNA clone... 46 3e-07
       emb|AW689694|AW689694 NF023C12ST1F1000 Developing stem Medicago ... 44 3e-07
       emb|AW686342|AW686342 NF040F06NR1F1000 Nodulated root Medicago t... 46 3e-07
       emblAW622151lAW622151 EST312949 tomato root during/after fruit s... 47 6e-07
      emb|AW623994|AW623994 EST321939 tomato flower buds 3-8 mm, Corne... 48 6e-07
10
      emb|AW621737|AW621737 EST312535 tomato root during/after fruit s... 47 6e-07
      emb|AI482693|AI482693 EST242016 tomato shoot, Cornell Lycopersic... 48 7e-07
      emb|AW622612|AW622612 EST313412 tomato root during/after fruit s... 46 1e-06
      emb|AW596685|AW596685 si15e02.yl Gm-c1032 Glycine max cDNA clone... 49 2e-06
      emb|AW328890|AW328890 N200082e rootphos(-) Medicago truncatula c... 41 2e-06
15
      emb|AW621604|AW621604 EST312402 tomato root during/after fruit s... 45 2e-06
      emb|AI725483|AI725483 BNLGHi12267 Six-day Cotton fiber Gossypium... 40 4e-06
      emb|AI726639|AI726639 BNLGHi6294 Six-day Cotton fiber Gossypium ... 51 4e-06
      emb|AI488194|AI488194 EST246516 tomato ovary, TAMU Lycopersicon ... 40 4e-06
      emb|AW616223|AW616223 EST307262 L. hirsutum trichome, Cornell Un... 53 5e-06
20
      emb|AW650481|AW650481 EST328935 tomato germinating seedlings, TA... 53 5e-06
      emblAI731912lAI731912 BNLGHi11257 Six-day Cotton fiber Gossypium... 51 6e-06
      emb|AW981891|AW981891 PC19H06 Pine TriplEx pollen cone library P... 51 6e-06
      emb|AI726794|AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ... 50 7e-06
      gb|BE057806|BE057806 sn07e03.y1 Gm-c1016 Glycine max cDNA clone ... 48 1e-05
25
      emb|AI731726|AI731726 BNLGHi10587 Six-day Cotton fiber Gossypium... 37 1e-05
      emb|AI959774|AI959774 sc94a03.y1 Gm-c1019 Glycine max cDNA clone... 36 2e-05
      emb|AW509227|AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone... 42 2e-05
      emb|AI054484|AI054484 coau0001C01 Cotton Boll Abscission Zone cD... 42 3e-05
      emb|AW127684|AW127684 M110431 DSLC Medicago truncatula cDNA clon... 38 3e-05
30
      emb|AW564505|AW564505 LG1_295_D11.b1_A002 Light Grown 1 (LG1) So... 49 9e-05
      emb|AI487871|AI487871 EST246193 tomato ovary, TAMU Lycopersicon ... 39 1e-04
      emb|AJ276421|CAR276421 Cicer arietinum partial mRNA for putative... 48 1e-04
      emb|AW277884|AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone... 42 2e-04
      emb|AW459066|AW459066 sh18h02.yl Gm-c1016 Glycine max cDNA clone... 40 2e-04
35
      emb|AW926586|AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis... 47 2e-04
      emb|AI731989|AI731989 BNLGHi11154 Six-day Cotton fiber Gossypium... 45 3e-04
      emb|AW011080|AW011080 ST16D12 Pine TriplEx shoot tip library Pin... 43 3e-04
      gb|BE124032|BE124032 EST394157 DSIL Medicago truncatula cDNA clo... 47 3e-04
      emb|AI730716|AI730716 BNLGHi7722 Six-day Cotton fiber Gossypium ... 47 3e-04
40
      emb|AW929104|AW929104 EST337808 tomato flower buds 8 mm to pre-a... 33 5e-04
      emb|AW624906|AW624906 EST313735 tomato radicle, 5 d post-imbibit... 35 5e-04
      emb|AW706408|AW706408 sj56h10.yl Gm-c1033 Glycine max cDNA clone... 46 6e-04
      gb|BE054438|BE054438 GA Ea0004H20f Gossypium arboreum 7-10 dpa ... 45 7e-04
      emb|AW109570|AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f... 45 7e-04
45
      emb|AW279386|AW279386 sf66f11.yl Gm-c1013 Glycine max cDNA clone... 37 7e-04
      emb|AW720472|AW720472 LiNEST19f4r Lotus japonicus nodule library... 35 7e-04
      emb|AW458524|AW458524 sh10c06.yl Gm-c1016 Glycine max cDNA clone... 37 8e-04
      emb|AI731645|AI731645 BNLGHi10354 Six-day Cotton fiber Gossypium... 46 8e-04
      emb|Al729137|Al729137 BNLGHi12747 Six-day Cotton fiber Gossypium... 46 8e-04
50
      emb|AW574285|AW574285 EST316876 GVN Medicago truncatula cDNA clo... 33 0.001
      emb|AI728284|AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium... 45 0.001
      emb|AW160215|AW160215 EST290073 L. pennellii trichome, Cornell U... 45 0.002
      emb|AI729089|AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium... 45 0.002
      gb|H74345|H74345 249 Deletion-treated Brassica napus cDNA clone ... 37 0.002
      emb|AW733443|AW733443 sk73f03.yl Gm-c1016 Glycine max cDNA clone... 37 0.002
55
      emb|AW509209|AW509209 sh92f05.yl Gm-c1016 Glycine max cDNA clone... 38 0.002
      emb|AW459862|AW459862 sh96c02.yl Gm-c1016 Glycine max cDNA clone... 37 0.002
      emb|AW459861|AW459861 sh96c01.yl Gm-c1016 Glycine max cDNA clone... 37 0.002
      emb|AJ011567|DLA011567 Digitalis lanata mRNA for lanatoside 15'-... 38 0.002
60
      emblAW616728|AW616728 EST323139 L. hirsutum trichome, Cornell Un... 33 0.003
      emb|AW733540|AW733540 sk74h07.y1 Gm-c1016 Glycine max-cDNA clone... 37 0.003
```

	emb AW733459 AW733459 sk73h02.yl Gm-c1016 Glycine max cDNA clone 37 0.003 emb AW396681 AW396681 sh29d09.yl Gm-c1017 Glycine max cDNA clone 44 0.003 gb BE023812 BE023812 sm92g03.yl Gm-c1015 Glycine max cDNA clone 44 0.003
5	gb BE023398 BE023398 sm81c12.y1 Gm-c1015 Glycine max cDNA clone 44 0.003 emb AW984927 AW984927 NXNV_131_B12_F Nsf Xylem Normal wood Verti 38 0.003 emb AW127455 AW127455 M110643 DSIL Medicago truncatula cDNA clon 36 0.003
	gb L37975 L37975 BNAF0021E Mustard flower buds Brassica rapa cDN 35 0.004 emb AW099099 AW099099 sd34d08.y1 Gm-c1012 Glycine max cDNA clone 43 0.004 gb BE057305 BE057305 sn01c10.y1 Gm-c1015 Glycine max cDNA clone 43 0.004
10	emb AW458657 AW458657 sh12a06.yl Gm-c1016 Glycine max cDNA clone 43 0.004 emb AW923224 AW923224 DG1_50_A07.bl_A002 Dark Grown 1 (DG1) Sorg 43 0.004 emb AW648494 AW648494 EST326948 tomato germinating seedlings, TA 43 0.005
15	emb AI965889 AI965889 sc79c08.y1 Gm-c1018 Glycine max cDNA clone 43 0.005 emb AI487258 AI487258 EST245580 tomato ovary, TAMU Lycopersicon 43 0.005 emb AW218200 AW218200 EST303381 tomato radicle, 5 d post-imbibit 43 0.005
	emb AI486112 AI486112 EST244433 tomato ovary, TAMU Lycopersicon 43 0.005 gb BE033445 BE033445 ME02B01 ME Mesembryanthemum crystallinum cD 38 0.006 emb AW348454 AW348454 GM210002A2E12R Gm-r1021 Glycine max cDNA 39 0.006
20	emb AI900221 AI900221 sc02f01.y1 Gm-c1012 Glycine max cDNA clone 32 0.006 emb AW666820 AW666820 GA_Ea0006B14 Gossypium arboreum 7-10 dpa 35 0.006 emb AW624162 AW624162 EST322107 tomato flower buds 3-8 mm, Corne 34 0.006 emb AW667892 AW667892 GA_Ea0011E24 Gossypium arboreum 7-10 dpa 42 0.007
25	emb AW667522 AW667522 GA_Ea0009J12 Gossypium arboreum 7-10 dpa 42 0.007 emb AW730008 AW730008 GA_Ea0027E20 Gossypium arboreum 7-10 dpa 36 0.008 emb AT000294 AT000294 AT000294 Apple young fruit cDNA library Ma 42 0.010 emb AW100112 AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone 30 0.012
	emb AW394864 AW394864 sh36e01.yl Gm-c1017 Glycine max cDNA clone 41 0.014
30	Query= AC006577.16_f_at 12779_f_at /id_source genbank /description "gb aad25772.1 ac006577_8 (ac006577) belongs to the pf 00657 lipase/acylhydrolase with gdsl-motif amily. ests gb t4453,
35	gb t04815, gb t45993, gb r30138, gb ai099570 and gb t22281 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1194 letters)
40	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
45	Score E Sequences producing significant alignments: (bits) Value
	emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c 224 e-163 emb Y10155 BNMYAP9 B.napus for myrosinase-associated protein, cl 224 e-160 gb U39289 BNU39289 Brassica napus myrosinase-associated protein 227 e-156
50	gb U39319 BNU39319 Brassica napus myrosinase-associated protein 176 e-127 emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros 176 6e-99 emb AW568594 AW568594 si78g03.yl Gm-c1031 Glycine max cDNA clone 47 1e-13 emb AW288014 AW288014 N100858e rootphos(-) Medicago truncatula c 67 3e-13
55	emb AW774945 AW774945 EST334096 KV3 Medicago truncatula cDNA clo 46 5e-13 emb AW685185 AW685185 NF025E06NR1F1000 Nodulated root Medicago t 62 1e-10 emb AW922141 AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So 65 5e-10
	emb AW687872 AW687872 NF014D07RT1F1061 Developing root Medicago 46 2e-09 emb AW687276 AW687276 NF007H04RT1F1043 Developing root Medicago 46 7e-09 emb AW621314 AW621314 EST312112 tomato root during/after fruit s 44 1e-08
60	emb AW922142 AW922142 LG1_323_G10.b1_A002 Light Grown 1 (LG1) So 58 1e-07 emb AW164470 AW164470 se73a09.y1 Gm-c1023 Glycine max cDNA clone 58 2e-07 emb AW201360 AW201360 sf02b11.y1 Gm-c1027 Glycine max cDNA clone 47 2e-07

```
emb|AW757161|AW757161 sl29h09.yl Gm-c1027 Glycine max cDNA clone... 46 3e-07
      emb|AW689694|AW689694 NF023C12ST1F1000 Developing stem Medicago ... 44 3e-07
      emb|AW686342|AW686342 NF040F06NR1F1000 Nodulated root Medicago t... 46 3e-07
      emb|AW622151|AW622151 EST312949 tomato root during/after fruit s... 47 6e-07
      emb|AW623994|AW623994 EST321939 tomato flower buds 3-8 mm, Corne... 48 6e-07
      emb|AW621737|AW621737 EST312535 tomato root during/after fruit s... 47 6e-07
      emb|AI482693|AI482693 EST242016 tomato shoot, Cornell Lycopersic... 48 7e-07
      emb|AW622612|AW622612 EST313412 tomato root during/after fruit s... 46 1e-06
      emb|AW596685|AW596685 sj15e02.yl Gm-c1032 Glycine max cDNA clone... 49 2e-06
10
      emb|AW328890|AW328890 N200082e rootphos(-) Medicago truncatula c... 41 2e-06
      emb|AW621604|AW621604 EST312402 tomato root during/after fruit s... 45 2e-06
      emb|AI725483|AI725483 BNLGHi12267 Six-day Cotton fiber Gossypium... 40 4e-06
      emb|AI726639|AI726639 BNLGHi6294 Six-day Cotton fiber Gossypium ... 51 4e-06
      emb|AI488194|AI488194 EST246516 tomato ovary, TAMU Lycopersicon ... 40 4e-06
15
      emb|AW616223|AW616223 EST307262 L. hirsutum trichome, Cornell Un... 53 5e-06
      emb|AW650481|AW650481 EST328935 tomato germinating seedlings, TA... 53 5e-06
      emb|AI731912|AI731912 BNLGHil1257 Six-day Cotton fiber Gossypium... 51 6e-06
      emb|AW981891|AW981891 PC19H06 Pine TriplEx pollen cone library P... 51 6e-06
      emb|AI726794|AI726794 BNLGHi6582 Six-day Cotton fiber Gossypium ... 50 7e-06
20
      gb|BE057806|BE057806 sn07e03.yl Gm-c1016 Glycine max cDNA clone ... 48 1e-05
      emblAI731726|AI731726 BNLGHi10587 Six-day Cotton fiber Gossypium... 37 1e-05
      emb|AI959774|AI959774 sc94a03.yl Gm-c1019 Glycine max cDNA clone... 36 2e-05
      emb|AW509227|AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone... 42 2e-05
      emb|AI054484|AI054484 coau0001C01 Cotton Boll Abscission Zone cD... 42 3e-05
25
      emblAW127684|AW127684 M110431 DSLC Medicago truncatula cDNA clon... 38 3e-05
      emb|AW564505|AW564505 LG1 295 D11.b1 A002 Light Grown 1 (LG1) So... 49 9e-05
      emb|AI487871|AI487871 EST246193 tomato ovary, TAMU Lycopersicon ... 39 1e-04
      emb|AJ276421|CAR276421 Cicer arietinum partial mRNA for putative... 48 1e-04
      emb|AW277884|AW277884 sf88f10.yl Gm-c1019 Glycine max cDNA clone... 42 2e-04
30
      emb|AW459066|AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone... 40 2e-04
      emb|AW926586|AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis... 47 2e-04
      emb|AI731989|AI731989 BNLGHi11154 Six-day Cotton fiber Gossypium... 45 3e-04
      emb|AW011080|AW011080 ST16D12 Pine TriplEx shoot tip library Pin... 43 3e-04
      gb[BE124032]BE124032 EST394157 DSIL Medicago truncatula cDNA clo... 47 3e-04
35
      emb|AI730716|AI730716 BNLGHi7722 Six-day Cotton fiber Gossypium ... 47 3e-04
      emb|AW929104|AW929104 EST337808 tomato flower buds 8 mm to pre-a... 33 5e-04
      emb|AW624906|AW624906 EST313735 tomato radicle, 5 d post-imbibit... 35 5e-04
      emb|AW706408|AW706408 sj56h10.yl Gm-c1033 Glycine max cDNA clone... 46 6e-04
      gb|BE054438|BE054438 GA_Ea0004H20f Gossypium arboreum 7-10 dpa ... 45 7e-04
40
      emb|AW109570|AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f... 45 7e-04
      emb|AW279386|AW279386 sf66f11.y1 Gm-c1013 Glycine max cDNA clone... 37 7e-04
      emb|AW720472|AW720472 LjNEST19f4r Lotus japonicus nodule library... 35 7e-04
      emb|AW458524|AW458524 sh10c06.y1 Gm-c1016 Glycine max cDNA clone... 37 8e-04
      emb|AI731645|AI731645 BNLGHi10354 Six-day Cotton fiber Gossypium... 46 8e-04
45
      emb|AI729137|AI729137 BNLGHi12747 Six-day Cotton fiber Gossypium... 46 8e-04
      emb|AW574285|AW574285 EST316876 GVN Medicago truncatula cDNA clo... 33 0.001
      emb|AI728284|AI728284 BNLGHi10336 Six-day Cotton fiber Gossypium... 45 0.001
      emb|AW160215|AW160215 EST290073 L. pennellii trichome, Cornell U... 45 0.002
      emb|AI729089|AI729089 BNLGHi12599 Six-day Cotton fiber Gossypium... 45 0.002
50
      gb[H74345]H74345 249 Deletion-treated Brassica napus cDNA clone ... 37 0.002
      emb|AW733443|AW733443 sk73f03.yl Gm-c1016 Glycine max cDNA clone... 37 0.002
      emb|AW509209|AW509209 sh92f05.yl Gm-c1016 Glycine max cDNA clone... 38 0.002
      emb|AW459862|AW459862 sh96c02.y1 Gm-c1016 Glycine max cDNA clone... 37 0.002
      emb|AW459861|AW459861 sh96c01.yl Gm-c1016 Glycine max cDNA clone... 37 0.002
55
      emb|AJ011567|DLA011567 Digitalis lanata mRNA for lanatoside 15'-... 38 0.002
      emb|AW616728|AW616728 EST323139 L. hirsutum trichome, Cornell Un... 33 0.003
      emb|AW733540|AW733540 sk74h07.yl Gm-c1016 Glycine max cDNA clone... 37 0.003
      emb|AW733459|AW733459 sk73h02.y1 Gm-c1016 Glycine max cDNA clone... 37 0.003
      emb|AW396681|AW396681 sh29d09.y1 Gm-c1017 Glycine max cDNA clone... 44 0.003
60
      gb|BE023812|BE023812 sm92g03.yl Gm-c1015 Glycine max cDNA clone ... 44 0.003
      gb|BE023398|BE023398 sm81c12.yl Gm-c1015 Glycine max cDNA clone ... 44 0.003
```

```
emb|AW984927|AW984927 NXNV_131_B12 F Nsf Xylem Normal wood Verti... 38 0.003
      emb|AW127455|AW127455 M110643 DSIL Medicago truncatula cDNA clon... 36 0.003
      gb|L37975|L37975 BNAF0021E Mustard flower buds Brassica rapa cDN... 35 0.004
      emblAW099099lAW099099 sd34d08.yl Gm-c1012 Glycine max cDNA clone... 43 0.004
 5
      gb|BE057305|BE057305 sn01c10.y1 Gm-c1015 Glycine max cDNA clone ... 43 0.004
      emb|AW458657|AW458657 sh12a06.y1 Gm-c1016 Glycine max cDNA clone... 43 0.004
      emb[AW923224]AW923224 DG1 50 A07.b1 A002 Dark Grown 1 (DG1) Sorg... 43 0.004
      emblAW648494|AW648494 EST326948 tomato germinating seedlings, TA... 43 0.005
      emb|AI965889|AI965889 sc79c08.yl Gm-c1018 Glycine max cDNA clone... 43 0.005
      emb|AI487258|AI487258 EST245580 tomato ovary, TAMU Lycopersicon ... 43 0.005
10
      emb|AW218200|AW218200 EST303381 tomato radicle, 5 d post-imbibit... 43 0.005
      emb|AI486112|AI486112 EST244433 tomato ovary, TAMU Lycopersicon ... 43 0.005
      gb|BE033445|BE033445 ME02B01 ME Mesembryanthemum crystallinum cD... 38 0.006
      emb|AW348454|AW348454 GM210002A22E12R Gm-r1021 Glycine max cDNA ... 39 0.006
15
      emb|AI900221|AI900221 sc02f01.yl Gm-c1012 Glycine max cDNA clone... 32 0.006
      emblAW666820lAW666820 GA Ea0006B14 Gossypium arboreum 7-10 dpa ... 35 0.006
      emblAW624162|AW624162 EST322107 tomato flower buds 3-8 mm, Corne... 34 0.006
      emb|AW667892|AW667892 GA_Ea0011E24 Gossypium arboreum 7-10 dpa ... 42 0.007
      emb|AW667522|AW667522 GA_Ea0009J12 Gossypium arboreum 7-10 dpa ... 42 0.007
20
      emb|AT000294|AT000294 AT000294 Apple young fruit cDNA library Ma... 42 0.010
      emb|AW100112|AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone... 30 0.012
      emb|AW394864|AW394864 sh36e01.yl Gm-c1017 Glycine max cDNA clone... 41 0.014
25
      Query= AC003114.16 s at 13067 s at /id source genbank /description
      "gb|aac24083.1| (ac003114) match to calreticulin (atcrtl) mrna
      gb|u27698 and dna gb|u66344. ests gb|t45719, gb|t22451, gb|h36323 and
      gb|aa042519 come from this gene. [arabidopsis thaliana]" /blast_score
30
      0 /ec number /family /chip nova /gb link /ncgi
           (1335 letters)
      Database: plantfungal
           661,018 sequences; 426,114,510 total letters
35
      Searching.....done
      Sequences producing significant alignments:
                                                       (bits) Value
40
      emblAF019376|AF019376 Brassica napus calreticulin mRNA, complete... 619 0.0
      gb[U74630]RCU74630 Ricinus communis calreticulin mRNA, complete ... 747 0.0
      emb|Z71395|NPCAL1MNR N.plumbaginifolia mRNA for calreticulin.
                                                                     742 0.0
      emb|AF134733|AF134733 Prunus armeniaca calcium-binding protein c... 741 0.0
45
      emb|AJ002057|BVMRNAC Beta vulgaris mRNA for calreticulin.
      emb[X85382]NTRNATCAL N.tabacum mRNA for calreticulin.
                                                                   726 0.0
      emb|AF052040|AF052040 Berberis stolonifera calreticulin mRNA, co... 722 0.0
      emb|X80756|CAPCRTC C.annuum PCRTC mRNA.
      gb|L27348|BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par... 670 0.0
50
      gb|L27349|BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par... 669 0.0
      gb|U74631|RCU74631 Ricinus communis calreticulin gene, complete ... 201 e-172
     emb|AW039860|AW039860 EST282333 tomato mixed elicitor, BTI Lycop... 517 e-145
     emb|AB018243|AB018243 Solanum melongena EEF22 mRNA for calreticu... 510 e-143
     emb|AI782264|AI782264 EST263143 tomato susceptible, Cornell Lyco... 497 e-140
55
     emb|AW441195|AW441195 EST310591 tomato fruit red ripe, TAMU Lyco... 487 e-136
     emb|AJ000765|CRAJ765 Chlamydomonas reinhardtii mRNA for calretic... 393 e-135
     emb|AW930392|AW930392 EST340945 tomato fruit mature green, TAMU ... 478 e-134
     emb|AW944954|AW944954 EST337004 tomato flower buds 3-8 mm, Corne... 469 e-131
60
     emb|AW773947|AW773947 EST332933 KV3 Medicago truncatula cDNA clo... 469 e-131
     emblAW650947|AW650947 EST329401 tomato germinating seedlings, TA... 468 e-131
```

emb|AW622049|AW622049 EST312847 tomato root during/after fruit s... 467 e-131 emb|AW216727|AW216727 EST295441 tomato callus, TAMU Lycopersicon... 460 e-128 emb|AW731454|AW731454 GA_Ea0030H17 Gossypium arboreum 7-10 dpa ... 456 e-127 emb|AI735991|AI735991 sb21e08.y1 Gm-c1007 Glycine max cDNA clone... 450 e-125 5 emb|Y09078|DBCALLKPR D.bioculata mRNA for calreticulin-like prot... 228 e-124 emb|AA660877|AA660877 00772 MtRHE Medicago truncatula cDNA 5' si... 310 e-123 emb|AW509432|AW509432 si37b03.y1 Gm-r1030 Glycine max cDNA clone... 321 e-122 emb|AW773889|AW773889 EST332875 KV3 Medicago truncatula cDNA clo... 437 e-122 10 gb|BE059929|BE059929 sn38h08.yl Gm-c1016 Glycine max cDNA clone ... 431 e-120 emb|AW219282|AW219282 EST301764 tomato root during/after fruit s... 426 e-118 emb|AW695765|AW695765 NF098D02ST1F1016 Developing stem Medicago ... 421 e-118 emb|AW626316|AW626316 EST320223 tomato radicle, 5 d post-imbibit... 422 e-117 emb|AA660477|AA660477 00363 MtRHE Medicago truncatula cDNA 5' si... 421 e-117 15 emb|AW727433|AW727433 GA_Ea0012B12 Gossypium arboreum 7-10 dpa ... 421 e-117 emb|AW650460|AW650460 EST328914 tomato germinating seedlings, TA... 419 e-116 emb|AW621571|AW621571 EST312369 tomato root during/after fruit s... 419 e-116 emb|AW309216|AW309216 sg05g07.y1 Gm-c1019 Glycine max cDNA clone... 414 e-115 emb|AW184893|AW184893 se82a03.y1 Gm-c1023 Glycine max cDNA clone... 413 e-114 20 emb|AW738476|AW738476 EST339903 tomato flower buds, anthesis, Co... 412 e-114 emb|AW685878|AW685878 NF031C11NR1F1000 Nodulated root Medicago t... 411 e-114 emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 407 e-113 emb|AW220942|AW220942 EST297411 tomato fruit mature green, TAMU ... 406 e-112 emb|AW277466|AW277466 sf82d10.yl Gm-c1019 Glycine max cDNA clone... 406 e-112 25 emb|AW568477|AW568477 si59c07.yl Gm-r1030 Glycine max cDNA clone... 403 e-111 emb|AW649817|AW649817 EST328271 tomato germinating seedlings, TA... 402 e-111 emb|AW773817|AW773817 EST332803 KV3 Medicago truncatula cDNA clo... 399 e-110 emb|AI495184|AI495184 sa89b11.yl Gm-c1004 Glycine max cDNA clone... 398 e-110 emb|AI973534|AI973534 sc88a04.yl Gm-c1019 Glycine max cDNA clone... 397 e-110 30 emb|AW035959|AW035959 EST282818 tomato callus, TAMU Lycopersicon... 396 e-109 emb|AW932476|AW932476 EST358319 tomato fruit mature green, TAMU ... 395 e-109 emb|AW979917|AW979917 EST341567 tomato root deficiency, Cornell ... 395 e-109 emb|AW649196|AW649196 EST327650 tomato germinating seedlings, TA... 391 e-108 emb|AI960982|AI960982 sc93e09.yl Gm-c1019 Glycine max cDNA clone... 386 e-106 35 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 385 e-106 emb|AW596414|AW596414 sj12b07.yl Gm-c1032 Glycine max cDNA clone... 384 e-106 emb|AW648010|AW648010 EST326464 tomato germinating seedlings, TA... 382 e-105 emb|AW725587|AW725587 GA_Ea0018N14 Gossypium arboreum 7-10 dpa ... 379 e-104 40 emb|AW705880|AW705880 sk52a09.yl Gm-c1019 Glycine max cDNA clone... 372 e-102 emb|AW306403|AW306403 se50b10.yl Gm-c1017 Glycine max cDNA clone... 369 e-101 emb|AW720057|AW720057 LjNEST13b1r Lotus japonicus nodule library... 367 e-101 emb|AW033447|AW033447 EST277018 tomato callus, TAMU Lycopersicon... 367 e-101 45 emb|AW933031|AW933031 EST358874 tomato fruit mature green, TAMU ... 366 e-100 emb|AW649360|AW649360 EST327814 tomato germinating seedlings, TA... 366 e-100 emb|AW035234|AW035234 EST280496 tomato callus, TAMU Lycopersicon... 364 1e-99 emb|AW907386|AW907386 EST343509 potato stolon, Cornell Universit... 361 9e-99 emb|AW756722|AW756722 sl26d08.yl Gm-c1027 Glycine max cDNA clone... 359 3e-98 50 emb|AW760501|AW760501 sl51b04.yl Gm-c1027 Glycine max cDNA clone... 358 6e-98 emb|AI726591|AI726591 BNLGHi6198 Six-day Cotton fiber Gossypium ... 354 8e-97 emb|AW201052|AW201052 se97c10.yl Gm-c1027 Glycine max cDNA clone... 347 1e-94 emb|Y09816|EGCALRPR E.gracilis mRNA for calreticulin precursor. 255 1e-93 emb|AI728389|AI728389 BNLGHi10665 Six-day Cotton fiber Gossypium... 329 4e-89 55 emb|AI437497|AI437497 sa34a12.yl Gm-c1004 Glycine max cDNA clone... 329 4e-89 emb|AW509028|AW509028 si39c02.yl Gm-r1030 Glycine max cDNA clone... 325 4e-88 emb|AI896365|AI896365 EST265808 tomato callus, TAMU Lycopersicon... 325 6e-88 emb|AW043340|AW043340 ST32B12 Pine TriplEx shoot tip library Pin... 324 1e-87 emb|AI812952|AI812952 22G9 Pine Lambda Zap Xylem library Pinus t... 255 1e-86 60 emb|AW648456|AW648456 EST326910 tomato germinating seedlings, TA... 316 3e-85 emb|AI899646|AI899646 EST269089 tomato susceptible, Cornell Lyco... 316 3e-85

emb|AW624478|AW624478 EST322423 tomato flower buds 3-8 mm, Corne... 312 3e-84 emb|AV407468|AV407468 AV407468 Lotus japonicus young plants (two... 310 1e-83 emblAI895452|AI895452 EST264895 tomato callus, TAMU Lycopersicon... 310 2e-83 emb|AW649764|AW649764 EST328218 tomato germinating seedlings, TA... 308 5e-83 5 emb|AW132963|AW132963 se12f08.yl Gm-c1013 Glycine max cDNA clone... 307 le-82 emb|AI726703|AI726703 BNLGHi6370 Six-day Cotton fiber Gossypium ... 301 8e-81 emb|AW727636|AW727636 GA Ea0015E17 Gossypium arboreum 7-10 dpa ... 300 1e-80 emb|AW216358|AW216358 EST295102 tomato callus, TAMU Lycopersicon... 295 7e-79 10 emb|AI771812|AI771812 EST252912 tomato ovary, TAMU Lycopersicon ... 290 2e-77 emb|AI489195|AI489195 EST247534 tomato ovary, TAMU Lycopersicon ... 290 2e-77 emb|AW266258|AW266258 L30-2972T3 Ice plant Lambda Uni-Zap XR exp... 283 2e-75 emb|AV413324|AV413324 AV413324 Lotus japonicus young plants (two... 283 2e-75 15 emb|AW560421|AW560421 EST315469 DSIR Medicago truncatula cDNA cl... 270 1e-74 emb|AW754529|AW754529 PC03C03 Pine TriplEx pollen cone library P... 280 2e-74 emb|AW042889|AW042889 ST26F06 Pine TriplEx shoot tip library Pin... 279 3e-74 emb|AW043146|AW043146 ST29H08 Pine TriplEx shoot tip library Pin... 273 2e-73 20 Query= AC003680.50 at 13100 at /id source genbank /description gb|aac06158.1| (ac003680) putative cytochrome p450 [arabidopsis thaliana] /blast_score 0 /ec_number /family monooxygenase /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbin-25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003680| /ncgi http://www.ncgr.org/cgi-bin/ff?ac003680 (1647 letters) Database: plantfungal 30 661,018 sequences; 426,114,510 total letters Searching......done Score Ε 35 Sequences producing significant alignments: (bits) Value emb|AJ249799|CAR249799 Cicer arietinum partial mRNA for cytochro... 308 e-114 emb|AB032833|AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... 289 5e-87 emb|AJ011862|CRO011862 Catharanthus roseus mRNA for flavonoid 3'... 191 5e-86 40 gb|U72654|EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla... 179 8e-85 emb|AI897763|AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... 305 7e-82 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 278 3e-81 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 269 6e-81 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 300 2e-80 45 emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 300 2e-80 dbi|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 121 9e-79 emb|X70824|SMPEG1 S.melongena pEG1 mRNA for hydroxylase P450. 171 le-77 dbj|E05111|E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... 171 1e-77 gb[M32885]AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 283 3e-75 50 emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 223 6e-75 emb|AF191772|AF191772 Papaver somniferum (S)-N-methylcoclaurine ... 221 1e-74 emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 280 3e-74 emb|AI484957|AI484957 EST243220 tomato ovary, TAMU Lycopersicon ... 280 3e-74 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 186 2e-70 55 emb|AF014800|AF014800 Eschscholzia californica (S)-N-methylcocla... 212 9e-70 gb U09610 U09610 Berberis stolonifera cytochrome P-450 CYP80 mRN... 264 1e-69 emb|AF014801|AF014801 Eschscholzia californica (S)-N-methylcocla... 211 3e-69 emb|AI488646|AI488646 EST246985 tomato ovary, TAMU Lycopersicon ... 260 2e-68 emb|Y09424|NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... 260 2e-68

emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 259 3e-68 emb|AI938505|AI938505 sb46e03.y1 Gm-c1015 Glycine max cDNA clone... 259 4e-68

60

emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 259 4e-68 emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 258 8e-68 emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 256 3e-67 emb|AW726065|AW726065 GA_ Ea0020I21 Gossypium arboreum 7-10 dpa ... 186 4e-67 emb|AI897760|AI897760 EST267203 tomato ovary, TAMU Lycopersicon ... 138 2e-66 emb|Y10489|GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 248 1e-64 emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. gb|U48435|SCU48435 Solanum chacoense putative cytochrome P450 ge... 247 2e-64 emb|AW730128|AW730128 GA Ea0027P19 Gossypium arboreum 7-10 dpa ... 184 6e-63 10 emb|AI777331|AI777331 EST263739 tomato seed, TAMU Lycopersicon e... 240 3e-62 emb|AF029858|AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... 208 3e-62 emb|AW728802|AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa ... 166 5e-62 emb|AW668189|AW668189 GA_Ea0013B20 Gossypium arboreum 7-10 dpa ... 184 5e-62 emb|AW666599|AW666599 GA_Ea0005B16 Gossypium arboreum 7-10 dpa ... 175 5e-62 15 emb|Y10493|GMC450CP7 G.max mRNA for putative cytochrome P450, cl... 160 2e-61 emb|AW394470|AW394470 sh05e04.y1 Gm-c1016 Glycine max cDNA clone... 237 3e-61 emb|AW234222|AW234222 sf22f08.yl Gm-c1028 Glycine max cDNA clone... 237 3e-61 emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 162 3e-61 gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 236 3e-61 20 dbj|D14589|D14589 Eustoma russellianum mRNA for flavonoid 3',5'-... 179 5e-61 gb|BE023051|BE023051 sm78h02.yl Gm-c1015 Glycine max cDNA clone ... 235 7e-61 gb|L24438|THLCYP450A Thlaspi arvense germline cytochrome P450 mR... 235 7e-61 emb|AJ249802|CAR249802 Cicer arietinum partial mRNA for cytochro... 235 9e-61 emb|AF166332|AF166332 Nicotiana tabacum cytochrome P450 gene, co... 235 9e-61 25 gb|BE054146|BE054146 GA_Ea0034H12f Gossypium arboreum 7-10 dpa ... 234 2e-60 emb|AW569699|AW569699 si79c08.yl Gm-c1031 Glycine max cDNA clone... 233 2e-60 emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. dbj|D14588|PETHF1 Petunia hybrida Hf1 mRNA for flavonoid-3',5'-h... 182 3e-60 emb|AI730111|AI730111 BNLGHi6162 Six-day Cotton fiber Gossypium ... 226 5e-60 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 231 8e-60 emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 230 2e-59 emb|Z22544|PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. dbi|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 178 5e-59 emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 228 8e-59 35 emb|AI726383|AI726383 BNLGHi5702 Six-day Cotton fiber Gossypium ... 227 2e-58 emb|AI779370|AI779370 EST260249 tomato susceptible, Cornell Lyco... 225 7e-58 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 225 1e-57 emb|AB006790|AB006790 Petunia x hybrida IMT-2 mRNA for cytochrom... 150 1e-57 emb|AI728431|AI728431 BNLGHi10763 Six-day Cotton fiber Gossypium... 154 2e-57 40 emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 146 2e-57 emb|AF081575|AF081575 Petunia x hybrida flavonoid 3',5'-hydroxyl... 172 4e-57 emb|X70981|SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 140 4e-57 emb|X95342|NTHSR515 N.tabacum mRNA for HSR515 protein. 100 5e-57 emb|AB028151|AB028151 Antirrhinum majus AFNS2 mRNA for cytochrom... 115 9e-57 45 emb|AW459662|AW459662 sh90c05.yl Gm-c1016 Glycine max cDNA clone... 221 9e-57 emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 124 4e-56 emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 168 5e-56 emb|AW255799|AW255799 ML868 peppermint glandular trichome Mentha... 217 2e-55 emb|AF124817|AF124817 Mentha x piperita cytochrome p450 isoform ... 141 2e-55 50 emb|AW832652|AW832652 sm15g02.y1 Gm-c1027 Glycine max cDNA clone... 121 3e-55 emb|X71654|SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. dbi|D14990|POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... 144 4e-55 emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 182 2e-54 emb|AW930824|AW930824 EST356667 tomato fruit mature green, TAMU ... 214 2e-54 55 emblAW395730|AW395730 sg74f08.yl Gm-c1007 Glycine max cDNA clone... 213 3e-54 emb|AW726043|AW726043 GA Ea0020H22 Gossypium arboreum 7-10 dpa ... 143 4e-54 emb|AI895030|AI895030 EST264473 tomato callus, TAMU Lycopersicon... 211 1e-53 emb|AB028152|AB028152 Torenia hybrida TFNS5 mRNA for cytochrome ... 114 1e-53 emb|AW832405|AW832405 sm09e01.yl Gm-c1027 Glycine max cDNA clone... 210 2e-53 60 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 109 3e-53 emb|AW308831|AW308831 sf72g04.y1 Gm-c1013 Glycine max cDNA clone... 203 5e-53

emblAF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 158 7e-53 emb|AW774664|AW774664 EST333815 KV3 Medicago truncatula cDNA clo... 208 9e-53 emb|AF029857|AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C... 98 1e-52 emb|AB001380|AB001380 Glycyrrhiza echinata CYP93B1 mRNA for cyto... 109 1e-52 5 emb|AW616345|AW616345 EST322756 L. hirsutum trichome, Cornell Un... 208 1e-52 emb|AW690420|AW690420 NF033B04ST1F1000 Developing stem Medicago ... 129 1e-52 emb|AF000403|AF000403 Lotus japonicus putative cytochorome P450 ... 145 2e-52 emb|AW922446|AW922446 DG1_19_F10.g1_A002 Dark Grown 1 (DG1) Sorg... 204 2e-51 emb|AI729430|AI729430 BNLGHi13332 Six-day Cotton fiber Gossypium... 171 2e-51 10 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 93 4e-51 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 110 4e-51 emb|AB025016|AB025016 Lotus japonicus mRNA for cytochrome P450, ... 152 6e-51 emb|AI779369|AI779369 EST260248 tomato susceptible, Cornell Lyco... 202 8e-51 emb|AI727414|AI727414 BNLGHi7936 Six-day Cotton fiber Gossypium ... 181 1e-50 15 Query= AC000375.44_at 13115_at /id_source genbank /description gb|aab60774.1| (ac000375) ests gb|u75592,gb|t13956,gb|t43869 come" from from this gene. [arabidopsis thaliana]" /blast score 0 /ec number 20 /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000375| /ncgi http://www.ncgr.org/cgi-bin/ff?ac000375 (1533 letters) 25 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 30 Ε Score Sequences producing significant alignments: (bits) Value gb|BE020282|BE020282 sm42g12.y1 Gm-c1028 Glycine max cDNA clone ... 91 2e-39 35 emb|AW831934|AW831934 sm18a01.yl Gm-c1027 Glycine max cDNA clone... 91 3e-38 emb|AI895084|AI895084 EST264527 tomato callus, TAMU Lycopersicon... 88 2e-37 emblAW731252lAW731252 GA Ea0030E03 Gossypium arboreum 7-10 dpa ... 93 2e-31 emb|AW650703|AW650703 EST329157 tomato germinating seedlings, TA... 88 2e-28 emb|AW648696|AW648696 EST327066 tomato germinating seedlings, TA... 85 7e-25 40 emb|AT000481|AT000481 AT000481 Brassica rapa guard cell Brassica... 62 3e-23 emb|AI895460|AI895460 EST264903 tomato callus, TAMU Lycopersicon... 77 2e-22 emb|AW776692|AW776692 EST335757 DSIL Medicago truncatula cDNA cl... 68 7e-21 emb|AI774644|AI774644 EST255744 tomato resistant, Cornell Lycope... 65 4e-19 emblAW560992|AW560992 EST316040 DSIR Medicago truncatula cDNA cl... 68 2e-18 45 emb|AW034968|AW034968 EST279197 tomato callus, TAMU Lycopersicon... 61 2e-15 emb|AW034372|AW034372 EST277943 tomato callus, TAMU Lycopersicon... 62 1e-13 gb|BE021411|BE021411 sm48g02.y1 Gm-c1028 Glycine max cDNA clone ... 60 6e-13 emb|AW032312|AW032312 EST275766 tomato callus, TAMU Lycopersicon... 69 9e-12 emb|AW399297|AW399297 EST309797 L. pennellii trichome, Cornell U... 46 2e-11 50 emb|AW032231|AW032231 EST275685 tomato callus, TAMU Lycopersicon... 62 6e-11 emb|AW032133|AW032133 EST275587 tomato callus, TAMU Lycopersicon... 62 6e-11 emb|AW030333|AW030333 EST273588 tomato callus, TAMU Lycopersicon... 55 8e-11 gb|BE020267|BE020267 sm42f07.yl Gm-c1028 Glycine max cDNA clone ... 69 1e-10 emb|AW773655|AW773655 EST332641 KV3 Medicago truncatula cDNA clo... 55 1e-10 55 emb|AI896893|AI896893 EST266336 tomato callus, TAMU Lycopersicon... 62 1e-10 emb|AW278353|AW278353 sf43a06.y1 Gm-c1009 Glycine max cDNA clone... 49 2e-09 emb|AW687210|AW687210 NF007B09RT1F1076 Developing root Medicago ... 55 1e-08 emb|AT000955|AT000955 AT000955 Brassica rapa guard cell Brassica... 60 3e-08 emb|AW029692|AW029692 EST272947 tomato callus, TAMU Lycopersicon... 48 4e-08 60 emb|AT000818|AT000818 AT000818 Brassica rapa guard cell Brassica... 59 7e-08

emb|AW774597|AW774597 EST333748 KV3 Medicago truncatula cDNA clo... 47 2e-07

```
emb|AW127319|AW127319 M110490 DSIL Medicago truncatula cDNA clon... 48 2e-05
      emb|AW279607|AW279607 sf67d05.y1 Gm-c1013 Glycine max cDNA clone... 49 1e-04
      emb|AI966004|AI966004 sc25c10.yl Gm-c1013 Glycine max cDNA clone... 49 1e-04
      emb|Z48431|AFABF2 A.fatua mRNA for DNA-binding protein (clone AB... 48 2e-04
 5
      emb|AB024510|AB024510 Nicotiana tabacum mRNA for TMV response-re... 48 2e-04
      emb|AI485065|AI485065 EST243369 tomato ovary, TAMU Lycopersicon ... 47 3e-04
      gb|BE058097|BE058097 sn11c07.yl Gm-c1016 Glycine max cDNA clone ...
      emb|AF211645|AF211645 AF211645 34.1B Nicotiana tabacum cDNA clon... 45 0.001
      emb|AV419361|AV419361 AV419361 Lotus japonicus young plants (two... 45 0.001
10
      emb|AI488776|AI488776 EST247115 tomato ovary, TAMU Lycopersicon ... 45 0.001
      emb|AB028022|AB028022 Nicotiana tabacum wizz mRNA, complete cds.
      emb|AI930972|AI930972 sb45e05.yl Gm-c1015 Glycine max cDNA clone... 45 0.002
      emb|AW693799|AW693799 NF069C11ST1F1085 Developing stem Medicago ... 44 0.003
      emb|AW696711|AW696711 NF110A11ST1F1084 Developing stem Medicago ... 44 0.003
15
      emb|AW222373|AW222373 EST299184 tomato fruit red ripe, TAMU Lyco... 44 0.004
      emb|AW164824|AW164824 se78d01.yl Gm-c1023 Glycine max cDNA clone... 43 0.005
      emb|AI900530|AI900530 sc07d02.y1 Gm-c1012 Glycine max cDNA clone... 43 0.005
      gb|BE022598|BE022598 sm75a10.y1 Gm-c1015 Glycine max cDNA clone ... 43 0.007
      emb|AW459004|AW459004 sh18a06.yl Gm-c1016 Glycine max cDNA clone... 43 0.007
20
      emb|AW186261|AW186261 se65e10.yl Gm-c1019 Glycine max cDNA clone... 43 0.007
      emblAI966537|AI966537 sc51e10.yl Gm-c1015 Glycine max cDNA clone... 43 0.007
      emb|AW569748|AW569748 si79h08.y1 Gm-c1031 Glycine max cDNA clone... 43 0.007
      emb|AW568563|AW568563 si78d04.y1 Gm-c1031 Glycine max cDNA clone... 43 0.007
      emb|AW219364|AW219364 EST301846 tomato root during/after fruit s... 43 0.007
25
      gb|BE059498|BE059498 sn32h03.yl Gm-c1016 Glycine max cDNA clone ... 42 0.013
      emb|AW432526|AW432526 sh75d09.yl Gm-c1015 Glycine max cDNA clone... 42 0.013
      emb|AW930573|AW930573 EST341030 tomato fruit mature green, TAMU ... 42 0.013
      emb|AW310205|AW310205 sf32g08.x1 Gm-c1028 Glycine max cDNA clone... 42 0.013
      gb|L35779|L35779 BNAESTG Mustard flower buds Brassica rapa cDNA ... 42 0.013
30
      emb|AW233985|AW233985 sf32g08.y1 Gm-c1028 Glycine max cDNA clone... 42 0.013
      emb|AI899266|AI899266 EST268709 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI486062|AI486062 EST244383 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI487230|AI487230 EST245552 tomato ovary, TAMU Lycopersicon ... 41 0.017
      gb|BE021550|BE021550 sm59h03.yl Gm-c1028 Glycine max cDNA clone ... 41 0.017
35
      emb|AI483704|AI483704 EST249575 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AW032373|AW032373 EST275827 tomato callus, TAMU Lycopersicon... 41 0.017
      emb|AI490542|AI490542 EST249096 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI490377|AI490377 EST248703 tomato ovary, TAMU Lycopersicon ...
      emb|AI488666|AI488666 EST247005 tomato ovary, TAMU Lycopersicon ... 41 0.017
40
      emb|AI771634|AI771634 EST252734 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI771930|AI771930 EST253030 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AW030227|AW030227 EST273482 tomato callus, TAMU Lycopersicon... 41 0.017
      emb|AI488453|AI488453 EST246792 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI489221|AI489221 EST247560 tomato ovary, TAMU Lycopersicon ... 41 0.017
45
      emb|AI485880|AI485880 EST244201 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI484959|AI484959 EST243222 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI485716|AI485716 EST244037 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI489915|AI489915 EST248254 tomato ovary, TAMU Lycopersicon ...
      emb|AI486696|AI486696 EST245018 tomato ovary, TAMU Lycopersicon ... 41 0.017
50
      emb|AW035780|AW035780 EST281934 tomato callus, TAMU Lycopersicon... 41 0.017
      emb|AI895108|AI895108 EST264551 tomato callus, TAMU Lycopersicon... 41 0.017
      emb|AI486874|AI486874 EST245196 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI489796|AI489796 EST248135 tomato ovary, TAMU Lycopersicon ...
                                                                         41 0.017
      emb|AI771686|AI771686 EST252786 tomato ovary, TAMU Lycopersicon ... 41 0.017
55
      emb|AW254736|AW254736 ML1023 peppermint glandular trichome Menth... 41 0.017
      emb|AW031802|AW031802 EST275256 tomato callus, TAMU Lycopersicon... 41 0.017
      emb|AI489016|AI489016 EST247355 tomato ovary, TAMU Lycopersicon ... 41 0.017
      emb|AI054839|AI054839 coau0002E21 Cotton Boll Abscission Zone cD... 32 0.018
      emb|AW568786|AW568786 si61a10.yl Gm-r1030 Glycine max cDNA clone... 41 0.024
60
      emb|AI938647|AI938647 sb56f08.yl Gm-c1018 Glycine max cDNA clone... 41 0.024
      emb|AI938638|AI938638 sb56e08.yl Gm-c1018 Glycine max cDNA clone... 41 0.024
```

emb|AW775215|AW775215 EST331937 GVN Medicago truncatula cDNA clo... 40 0.044 emb|AW685095|AW685095 NF025C08NR1F1000 Nodulated root Medicago t... 40 0.044 emb|AW686657|AW686657 NF043G05NR1F1000 Nodulated root Medicago t... 40 0.044 gb|BE020052|BE020052 sm38d10.y1 Gm-c1028 Glycine max cDNA clone ... 40 0.060 5 emb|AW733406|AW733406 sk73b02.yl Gm-c1016 Glycine max cDNA clone... 40 0.060 emb|AW597599|AW597599 sj96c04.yl Gm-c1023 Glycine max cDNA clone... 40 0.060 emb|AI774675|AI774675 EST255775 tomato resistant, Cornell Lycope... 39 0.083 emb|AW685473|AW685473 NF030C03NR1F1000 Nodulated root Medicago t... 39 0.083 emb|AI774760|AI774760 EST255860 tomato resistant, Cornell Lycope... 39 0.083 10 emb|AW559645|AW559645 EST314757 DSIR Medicago truncatula cDNA cl... 39 0.083 emb|AW458207|AW458207 sh79g06.yl Gm-c1016 Glycine max cDNA clone... 39 0.083 Query= AC002333.210_s_at 13154_s_at /id_source genbank /description 15 gb|aab64047.1| (ac002333) putative endochitinase [arabidopsis thaliana] /blast_score 1.00e-148 /ec number /family /chip nova /gb link /ncgi (1062 letters) 20 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 25 Score E Sequences producing significant alignments: (bits) Value emb|X61488|BNCHITIN B.napus mRNA for chitinase. 453 e-166 gb[U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 212 1e-95 30 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 211 4e-95 emb[X57187]PVCHITIN P.vulgaris mRNA for chitinase. 135 8e-86 dbilD45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 136 5e-82 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 185 5e-81 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 182 8e-80 35 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 156 4e-79 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 156 4e-79 dbi|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 119 4e-78 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 119 7e-78 dbj D45184 D45184 Chenopodium amaranticolor mRNA for chitinase, ... 119 1e-77 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 103 6e-77 gb|LA2467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 105 1e-75 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 84 7e-73 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 140 1e-72 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 139 3e-72 45 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 133 2e-70 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 131 1e-69 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 239 1e-66 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 177 5e-66 50 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 167 9e-65 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 172 2e-64 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 165 4e-64 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 111 7e-64 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 162 2e-63 55 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 93 4e-63 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 161 1e-62 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 144 2e-62 gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 141 1e-59 emb|AW680953|AW680953 WS1 9 A06.b1_A002 Water-stressed 1 (WS1) S... 139 4e-58 60 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 147 3e-57 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 177 4e-57

```
emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycope... 177 5e-56
       emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 141 2e-55
       gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 86 3e-55
       emblAW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 140 6e-55
       emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 138 3e-54
       emblAW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 137 4e-54
       emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 98 1e-53
       emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 134 2e-53
       emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 139 4e-53
 10
       emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 130 7e-53
       gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 86 8e-53
       emb[Y10373[MTCHITIN1 M.truncatula mRNA for chitinase.
                                                                      116 2e-52
       gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
       gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
15
       gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 117 9e-51
       emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 124 2e-50
       gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 141 6e-50
       emblAF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 149 1e-49
       emblAI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 165 4e-49
20
       emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 120 4e-49
       emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14).
                                                                    115 9e-49
       emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2).
       gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 112 1e-48
       emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 115 1e-48
25
       emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed I (WS1) ... 140 2e-48
       gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 83 3e-48
       gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 112 5e-48
       emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 112 5e-48
      emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 139 9e-48
30
      emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 139_9e-48
       emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 118 3e-47
       emb|AF061806|AF061806 Elaeagnus umbellata basic chitinase mRNA, ... 118 4e-47
      gb[M94105]ALCCHITIN Allium sativum chitinase mRNA, 3' end.
      emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 120 2e-46
35
      gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds.
      emb|AW922596|AW922596 DG1 46_C01.b1 A002 Dark Grown 1 (DG1) Sorg... 79 3e-46
      emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 116 3e-46
      gb|BE034267|BE034267 MH02D06 MH Mesembryanthemum crystallinum cD... 74 3e-46
      gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 122 4e-46
40
      emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 116 4e-46
      emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 112 7e-46
      emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 121 9e-46
      emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 109 1e-45
      emb|Z15140|LECHI9 L.esculentum mRNA for chitinase.
                                                                   112 2e-45
45
      emb|X74919|PVGEC9 P.vulgaris gene for endochitinase.
                                                                  135 2e-45
      gblS43926lS43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 116 2e-45
      gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 109 2e-45
      gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end.
      gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 109 6e-45
50
      gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 108 8e-45
      emb|AW922776|AW922776 DG1 46 C01.g1 A002 Dark Grown 1 (DG1) Sorg... 147 2e-44
      gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 141 4e-44
      emb|AA739579|AA739579 344 PtIFG2 Pinus taeda cDNA clone 8562M 3'... 107 1e-43
      emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 116 1e-43
      emb|A23396|A23396 B.vulgaris gene for chitinase 76.
                                                               105 3e-43
      emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 115 4e-43
      emb|Z78202|PACHI1 Persea americana mRNA for endochitinase.
      emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 125 1e-42
      emb|AI352718|AI352718 MB46-29 PZ204.BNlib Brassica napus cDNA cl... 144 4e-42
60
      gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 80 5e-42
      emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 111 2e-41
```

emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 116 3e-41 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 117 4e-41 emb|Z15138|LECHI14 L.esculentum mRNA for chitinase (partial). gb|U30465|LEU30465 Lycopersicon esculentum class II chitinase (C... 114 2e-40 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 100 le-39 Query= AL031394.56 at 13176 at /id source genbank /description emblcaa20567.1 (al031394) putative protein [arabidopsis thaliana] 10 /blast_score 0 /ec number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|al031394| /ncgi http://www.ncgr.org/cgi-bin/ff?al031394 (1116 letters) 15 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 20 Score Sequences producing significant alignments: (bits) Value emb|AW671006|AW671006 LG1_278_H12.b1_A002 Light Grown 1 (LG1) So... 81 6e-28 25 emb|AA520813|AA520813 TgESTzz64d07.r1 TgME49 invivo Bradyzoite c... 38 0.16 gb|U43491|SCU43491 Saccharomyces cerevisiae cosmid clone pEOA156... 37 0.31 emb|Z74916|SCYOR008C S.cerevisiae chromosome XV reading frame OR... 37 0.31 gb|U39481|SCU39481 Saccharomyces cerevisiae Slglp (SLG1) gene, c... 37 0.31 emb|AA680906|AA680906 LmFrAm0494 Leishmania major Amastigote ful... 33 1.0 30 emb|AF193903|AF193903 Cafeteria roenbergensis mitochondrial DNA,... 35 1.1 emb|AF229795|AF229795 Vigna radiata beta galactosidase mRNA, com... 35 1.5 emb|AW683786|AW683786 NF001A06NR1F1038 Nodulated root Medicago t... 35 1.5 emb|AC005802|AC005802 Leishmania major chromosome 3 clone L6202 ... 34 2.1 emb|AC005893|AC005893 Leishmania major chromosome 3 clone L822 s... 34 2.1 emb|AA520166|AA520166 TgESTzz39b08.s1 TgME49 invivo Bradyzoite c... 34 2.9 35 emb|AW618793|AW618793 EST320779 L. pennellii trichome, Cornell U... 34 2.9 emb|AW306460|AW306460 se51a02.y1 Gm-c1017 Glycine max cDNA clone... 34 2.9 emb|AQ502036|AQ502036 V10E12 mTn-3xHA/lacZ Insertion Library Sac... 33 3.9 gb[U87148]HVU87148 Hordeum vulgare nucellin mRNA, complete cds. 40 emb|AF017430|AF017430 Hordeum vulgare EEA1 mRNA, complete cds. emb|AQ500344|AQ500344 V41B12 mTn-3xHA/lacZ Insertion Library Sac... 33 3.9 emb|Z71686|SCYNR071C S.cerevisiae chromosome XIV reading frame O... 33 3.9 emb|AQ501720|AQ501720 V15F6 mTn-3xHA/lacZ Insertion Library Sacc... 33 3.9 emb|AQ872965|AQ872965 V56D9 mTn-3xHA/lacZ Insertion Library, str... 33 3.9 45 emb|AW126050|AW126050 N100246e rootphos(-) Medicago truncatula c... 33 5.4 emb|AW127669|AW127669 M110413 DSLC Medicago truncatula cDNA clon... 33 5.4 emb|AW126177|AW126177 N100022e rootphos(-) Medicago truncatula c... 33 5.4 emb|AW126137|AW126137 N100334e rootphos(-) Medicago truncatula c... 33 5.4 emb|AW509583|AW509583 ga61f07.yl Moss EST library PPU Physcomitr... 33 5.4 50 emb|AQ503147|AQ503147 V44D10 mTn-3xHA/lacZ Insertion Library Sac... 33 5.4 emb|AQ501343|AQ501343 V23B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 5.4 emb|Z98559|SPAC23C11 S.pombe chromosome I cosmid c23C11. emb|AW672219|AW672219 LG1_358_B09.b1_A002 Light Grown 1 (LG1) So... 33 5.4 emb|AW925272|AW925272 HVSMEg0001G19 Hordeum vulgare pre-anthesis... 33 5.4 55 emb|AA783066|AA783066 a1h02c9.rl Aspergillus nidulans 24hr asexu... 26 5.7 emb|AC013353|AC013353 Trypanosoma brucei chromosome VI clone RPC... 32 7.4 emb|AV409938|AV409938 AV409938 Lotus japonicus young plants (two... 32 7.4 emb|AW780906|AW780906 sl86c03.yl Gm-c1037 Glycine max cDNA clone... 32 7.4 emb|AI443278|AI443278 sa46f11.yl Gm-c1004 Glycine max cDNA clone... 32 7.4 60 emb|AW156670|AW156670 se29c01.yl Gm-c1015 Glycine max cDNA clone... 32 7.4 emb|AW277786|AW277786 sf86e12.yl Gm-c1019 Glycine max cDNA clone... 32 7.4

	emb AE001432 AE001432 Plasmodium falciparum chromosome 2, sectio 32 7.4 emb AW734710 AW734710 sk98e12.yl Gm-c1035 Glycine max cDNA clone 32 7.4 emb AW099005 AW099005 sd33a02.yl Gm-c1012 Glycine max cDNA clone 32 7.4
5	emb AW704821 AW704821 sk40a01.y1 Gm-c1019 Glycine max cDNA clone 32 7.4 emb AW277436 AW277436 sf82a10.y1 Gm-c1019 Glycine max cDNA clone 32 7.4 emb AW459299 AW459299 sh23c01.y1 Gm-c1016 Glycine max cDNA clone 32 7.4 emb AW407743 AV407743 AV407743 Lotus japonicus young plants (two 32 7.4 emb AW757240 AW757240 sl30h11.y1 Gm-c1027 Glycine max cDNA clone 32 7.4
10	
	Query= AL021961.24_at 13588_at /id_source genbank /description emb caa17552.1 (al021961) phosphoglycerate dehydrogenase - like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family
15	dehydrogenase /chip nova /gb_link
13	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb al021961 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al021961 (1812 letters)
20	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
25	Score E
	Sequences producing significant alignments: (bits) Value
	emb AW930291 AW930291 EST340748 tomato fruit mature green, TAMU 415 e-115
30	emb AW625643 AW625643 EST319550 tomato radicle, 5 d post-imbibit 398 e-110 emb AW666282 AW666282 sk34f11.yl Gm-c1028 Glycine max cDNA clone 393 e-108
	emb AW650696 AW650696 EST329150 tomato germinating seedlings, TA 226 e-103
	emb AW691093 AW691093 NF041B09ST1F1000 Developing stem Medicago 355 e-102
	emb AW926942 AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis 339 e-102 gb BE055044 BE055044 GA_Ea0031H08f Gossypium arboreum 7-10 dpa 341 2e-99
35	emb AW696933 AW696933 NF112E03ST1F1021 Developing stem Medicago 357 4e-98
	emb AW731385 AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa 344 2e-95
	emb AW688234 AW688234 NF005A05ST1F1000 Developing stem Medicago 348 6e-95
	gb BE036418 BE036418 MO24D12 MO Mesembryanthemum crystallinum cD 279 1e-94 gb BE052354 BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa 346 3e-94
40	emb AW423801 AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone 339 4e-92
	emb AI813214 AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta 336 4e-92
	emb AW692700 AW692700 NF054C07ST1F1000 Developing stem Medicago 304 7e-87
	emb AW737130 AW737130 EST338557 tomato flower buds, anthesis, Co 318 1e-85 emb AW727978 AW727978 GA_Ea0029C18 Gossypium arboreum 7-10 dpa 285 3e-80
45	gb BE020170 BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone 291 1e-77
	emb AW944677 AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two 291 1e-77
	emb AW926887 AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis 280 3e-74
	emb AW689358 AW689358 NF018C09ST1F1000 Developing stem Medicago 253 3e-73
50	emb AW755716 AW755716 sl08b12.y1 Gm-c1036 Glycine max cDNA clone 267 2e-70 emb AW625020 AW625020 EST313849 tomato radicle, 5 d post-imbibit 253 4e-66
	gb BE060782 BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis 234 1e-60
	emb AW687344 AW687344 NF008F03RT1F1029 Developing root Medicago 215 1e-54
	emb AV395160 AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla 208 1e-52
55	emb AW907004 AW907004 EST343231 potato stolon, Cornell Universit 205 7e-52 emb AW398821 AW398821 EST309321 L. pennellii trichome, Cornell U 201 2e-50
<i></i>	emb AW203801 AW203801 sf38d05.yl Gm-c1028 Glycine max cDNA clone 196 5e-49
•	emb AW923236 AW923236 DG1_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg 191 1e-47
	emb AW428657 AW428657 Ljirnpest22-731-a5 Ljirnp Lambda HybriZap 185 8e-46
60	emb AW650818 AW650818 EST329272 tomato germinating seedlings, TA 155 2e-44 emb AW736943 AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti 180 3e-44
55	emb AW697347 AW697347 NF115F08ST1F1074 Developing stem Medicago 175 9e-43
	· · · · · · · · · · · · · · · · · · ·

```
emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 172 6e-42
      gb|BE055879|BE055879 GA_Ea0026P04f Gossypium arboreum 7-10 dpa ... 172 8e-42
      gb|L47851|L47851 BNAF1389 Mustard flower buds Brassica rapa cDNA... 166 8e-41
      emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 112 2e-39
 5
      gb|BE123645|BE123645 NXNV 150 D07 F Nsf Xylem Normal wood Vertic... 164 2e-39
      emb|AA660997|AA660997 00894 MtRHE Medicago truncatula cDNA 5' si... 73 3e-39
      emb|AV428639|AV428639 AV428639 Lotus japonicus young plants (two... 160 3e-38
      emb|AV408249|AV408249 AV408249 Lotus japonicus young plants (two... 160 3e-38
      emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11.
10
      dbi|D89185|D89185 Schizosaccharomyces pombe mRNA, partial cds, c... 103 1e-36
      emb|AW317181|AW317181 sf38d05.x1 Gm-c1028 Glycine max cDNA clone... 148 1e-34
      dbj|E12500|E12500 Nucleotide sequence of eta gene of cephalospor... 89 2e-34
      emb|Z97052|SPCC4G3 S.pombe chromosome III cosmid c4G3.
                                                                     83 2e-33
      emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 101 5e-33
15
      emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186.
                                                                     98 1e-32
      emb|AJ273311|AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575... 91 1e-32
      gb|BE058285|BE058285 sn14b01.y1 Gm-c1016 Glycine max cDNA clone ... 138 1e-31
      gb|BE060772|BE060772 HVSMEg0013F04f Hordeum vulgare pre-anthesis... 95 2e-31
      gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 84 6e-31
20
      emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 7e-31
      emb|AW693956|AW693956 NF071B03ST1F1027 Developing stem Medicago ... 89 Se-30
      emb|AI165568|AI165568 A086P59U Hybrid aspen plasmid library Popu... 132 5e-30
      emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877.
                                                                    84 5e-30
      emb|AW599036|AW599036 gb01c10.yl Moss EST library PPN Physcomitr... 116 5e-25
25
      emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 56 1e-24
      emb|AL033389|SPBC1773 S.pombe chromosome II cosmid c1773.
      emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 89 8e-22
      emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 105 1e-21
      30
      emb|AT000607|AT000607 AT000607 Brassica rapa guard cell Brassica... 100 9e-21
      gb|U43503|SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi... 89 1e-16
      emb|AW283359|AW283359 LG1_223_C04.g1_A002 Light Grown 1 (LG1) So... 89 1e-16
      emb|AW736063|AW736063 EST332049 KV3 Medicago truncatula cDNA clo... 88 2e-16
      emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 86 7e-16
35
      emb|AQ874261|AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st... 84 2e-15
      gb[H74366]H74366 270 Deletion-treated Brassica napus cDNA clone ... 82 2e-14
      emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 78 3e-13
      emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase.
                                                                         78 3e-13
      gb|BE055276|BE055276 GA Ea0034L16f Gossypium arboreum 7-10 dpa ...
      emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco...
40
      emb|AW625680|AW625680 EST319587 tomato radicle, 5 d post-imbibit... 77 4e-13
      emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 77 4e-13
      emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 77 4e-13
      emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 77 4e-13
45
      emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 77 4e-13
      emb|AW647711|AW647711 EST307192 tomato germinating seedlings, TA... 77 4e-13
      emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 77 4e-13
      emb|AI490350|AI490350 EST248676 tomato ovary, TAMU Lycopersicon ... 77 5e-13
      emb|AW981354|AW981354 EST392507 DSIL Medicago truncatula cDNA cl... 75 1e-12
50
      dbj|D88272|D88272 Hordeum vulgare mRNA for formate dehydrogenase... 75 2e-12
      emb|AI488120|AI488120 EST246442 tomato ovary, TAMU Lycopersicon ... 74 3e-12
      emb|AW780701|AW780701 s175g02.y1 Gm-c1027 Glycine max cDNA clone... 55 3e-12
      emb|AW266848|AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr... 74 4e-12
      emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 66 4e-12
55
      dbj|D49433|D49433 Pumpkin colne HPR2 hydroxypyruvate reductases ... 72 1e-11
      dbj|D49432|D49432 Pumpkin clone HPR1 hydroxypyruvate reductases ... 72 1e-11
      emb|AW278707|AW278707 sf96b06.yl Gm-c1019 Glycine max cDNA clone... 72 1e-11
      gb|U01067|PUMHPR Cucurbita pepo Halloween NADH-dependent hydroxy... 72 2e-11
      emb|AI490396|AI490396 EST248734 tomato ovary, TAMU Lycopersicon ... 71 3e-11
60
      emb|X14609|CSNDHR Cucumis sativus mRNA for NAPH-dependent hydrox... 70 5e-11
      emb|AJ001429|RGDMANDER Rhodotorula graminis mRNA for D-mandelate... 70 6e-11
```

emb|AW040337|AW040337 EST283201 tomato mixed elicitor, BTI Lycop... 70 6e-11 emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 70 6e-11 emb|AL033497|CAC49C10 C.albicans cosmid Ca49C10. emb|AI897727|AI897727 EST267170 tomato ovary, TAMU Lycopersicon ... 69 9e-11 5 emb|AI898454|AI898454 EST267897 tomato ovary, TAMU Lycopersicon ... 69 9e-11 Query= AL035394.196 at 13627 at /id source genbank /description emb|caa23036.1| (al035394) putative na+/h+-exchanging protein 10 [arabidopsis thaliana] /blast score 0 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|a1035394| /ncgi http://www.ncgr.org/cgi-bin/ff?al035394 (2463 letters) 15 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 20 E Score Sequences producing significant alignments: (bits) Value emb|AW736388|AW736388 EST332307 KV3 Medicago truncatula cDNA clo... 243 5e-63 25 emb|AW622441|AW622441 EST313229 tomato root during/after fruit s... 204 2e-51 emb|AL157994|SPAC105 S.pombe chromosome I cosmid c105. emb|AQ841817|AQ841817 T134068 Soybean RFLP probe Glycine max gen... 186 8e-46 emb|X77087|SJ100567 S.cerevisiae (S288C) J0909, J0911, J0914 and... 150 5e-35 emb|Z49369|SCYJL094C S.cerevisiae chromosome X reading frame ORF... 150 5e-35 30 emb|AW774205|AW774205 EST333356 KV3 Medicago truncatula cDNA clo... 120 8e-28 emb|AW559356|AW559356 EST314404 DSIR Medicago truncatula cDNA cl... 104 2e-23 emb|AQ361449|AQ361449 mgxb0004G06r CUGI Rice Blast BAC Library P... 59 4e-16 emb|AT000678|AT000678 AT000678 Brassica rapa guard cell Brassica... 79 2e-13 emb|AV409975|AV409975 AV409975 Lotus japonicus young plants (two... 59 5e-11 35 emb|AT000552|AT000552 AT000552 Brassica rapa guard cell Brassica... 57 6e-07 emb|AW980088|AW980088 EST341613 tomato root deficiency, Cornell ... 45 8e-07 emb|AW307241|AW307241 sf54e09.y1 Gm-c1009 Glycine max cDNA clone... 48 1e-06 emblAW334422|AW334422 S34F3 AGS-1 Pneumocystis carinii f. sp. ca... 52 2e-05 emblAO842018/AO842018 T134304 Soybean RFLP probe Glycine max gen... 47 1e-04 emb|AV410314|AV410314 AV410314 Lotus japonicus young plants (two... 40 0.010 emb|AW163886|AW163886 Ljirnpest17-312-a12 Ljirnp Lambda HybriZap... 34 0.019 emb|AQ849208|AQ849208 LMAJFV1 lm43f12.yl Leishmania major FV1 ra... 41 0.042 emb|AW690188|AW690188 NF029E07ST1F1000 Developing stem Medicago ... 35 0.044 emb[Y15086]CFHEPABC Cylindrotheca fusiformis hepA, hepB, hepC ge... 39 0.21 45 emb|AL112906|CNS01AGI Botrytis cinerea strain T4 cDNA library un... 38 0.28 emb|AW725682|AW725682 GA_Ea0019E05 Gossypium arboreum 7-10 dpa ... 37 0.54 emb|AW727060|AW727060 GA_Ea0011B07 Gossypium arboreum 7-10 dpa ... 36 1.0 emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 36 1.4 emb|AF127331|AF127331 Euplotes crassus histone H1-1 (H1-1) gene,... 36 1.4 50 emb|AW729298|AW729298 GA_Ea0024K04 Gossypium arboreum 7-10 dpa ... 28 1.6 emb|AL139794|LMFP1105 Leishmania major Friedlin chromosome 4 PAC... 35 1.9 emb|AB028188|AB028188 Penicillium digitatum DNA fragment contain... 35 2.6 emb|Z48093|GVEITS133 G.verna DNA for internal transcribed spacer... 28 3.2 emb|AL353012|SPBC1711 S.pombe chromosome II cosmid c1711. gb|BE036059|BE036059 MO19C02 MO Mesembryanthemum crystallinum cD... 35 3.6 55 gb|BE036176|BE036176 MO20A07 MO Mesembryanthemum crystallinum cD... 35 3.6 emb|AW693672|AW693672 NF067B05ST1F1044 Developing stem Medicago ... 35 3.6 emb|AJ274013|AJ274013 AJ274013 Metarhizium anisopliae ARSEF 2575... 35 3.6 gb|U80041|AFU80041 Avena fatua Af10-protein mRNA, complete cds. 60 emb|AI612607|AI612607 TENG0370 T. Cruzi epimastigote normalised ... emb|X04693|SOPCG Spinach gene for plastocyanin.

	emb AW010989 AW010989 ST15D02 Pine TriplEx shoot tip library Pin 34 5.0 emb AB013876 AB013876 Chlorella vulgaris gene, a unique region o 34 5.0 emb AZ215593 AZ215593 Sheared DNA-74E9 TR Sheared DNA Trypanosom 34 6.8
5	emb AQ845769 AQ845769 LMAJFV1 lm25g04.x1 Leishmania major FV1 ra 34 6.8 gb M33825 TRBMVAT5A T.brucei MVAT5-like variant surface glycopro 34 6.8 emb AC005802 AC005802 Leishmania major chromosome 3 clone L6202 34 6.8
10	emb AQ640120 AQ640120 927P1-18A3.TP 927P1 Trypanosoma brucei gen 34 6.8 emb AW299087 AW299087 EST305761 KV2 Medicago truncatula cDNA clo 34 6.8 emb AQ163144 AQ163144 mgxb0023A11r CUGI Rice Blast BAC Library P 34 6.8
10	emb AF183445 CLITSYDK1 Codonopsis lanceolata internal transcribe 34 6.8 emb AC005893 AC005893 Leishmania major chromosome 3 clone L822 s 34 6.8 gb L06030 TRBVSGH Trypanosoma brucei MVAT5-RX2 variant surface g 34 6.8 gb L04971 TRBVSGM Trypanosoma brucei variant surface glycoprotei 34 6.8 emb AW564995 AW564995 LG1_313_B04.b1_A002 Light Grown 1 (LG1) So 34 6.8
15	emb AI050199 AI050199 TENU1447 T. cruzi epimastigote normalized 34 6.8 emb AW597619 AW597619 sj96f04.yl Gm-c1023 Glycine max cDNA clone 34 6.8 emb AF224499 AF224499 Triticum aestivum KNOTTED-1-like homeobox 34 6.8 gb N60227 N60227 TgESTzy10g08.rl TgRH Tachyzoite cDNA Toxoplasma 33 9.4
20	emb X68032 MTENOD12 M.truncatula ENOD12 gene. 33 9.4 emb AW126974 AW126974 ga16h04.y1 Moss EST library PPU Physcomitr 33 9.4 emb AA274329 AA274329 TgESTzz24g03.s1 TgME49 invivo Bradyzoite c 33 9.4 gb BE054344 BE054344 GA_Ea0035E03f Gossypium arboreum 7-10 dpa 33 9.4 emb AA009393 AA009393 TgESTzz08e11.r1 TgME49 Tachyzoite cDNA Tox 33 9.4
25	emb Y16262 DCY16262 Daucus carota mRNA for neutral invertase. 33 9.4 gb BE035627 BE035627 MO12F02 MO Mesembryanthemum crystallinum cD 33 9.4 emb AA274264 AA274264 TgESTzz25f05.s1 TgME49 invivo Bradyzoite c 33 9.4
30	Query= AC002387.185_at 13631_at /id_source genbank /description gb aab82634.1 (ac002387) putative transketolase precursor [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac002387 /ncgi http://www.ncgr.org/cgi-bin/ff?ac002387
35	(2371 letters)
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
40	Searchingdone
	Score E Sequences producing significant alignments: (bits) Value
45	emb Z50099 STTKETMR S.tuberosum mRNA for transketolase. 1372 0.0 gb L76554 SPITRAN Spinacia oleracea transketolase mRNA, chloropl 1350 0.0 emb Y15781 CAY15781 Capsicum annuum mRNA for plastid transketola 1344 0.0 emb A52295 A52295 Sequence 1 from Patent EP0723017. 1283 0.0 cmb Z46648 CDTXIII C. lateralization platform for translation of the control of the co
50	emb Z46648 CPTKT7 C.plantagineum tkt7 gene for transketolase. 1063 0.0 emb Z46647 CPTKT10 C.plantagineum tkt10 gene for transketolase. 1038 0.0 emb Z46646 CPTKT3 C.plantagineum tkt3 gene for transketolase. 1014 0.0 emb AJ249787 CPA249787 Cyanophora paradoxa mRNA for putative tra 557 0.0 emb AL033501 CAC41C10 C.albicans cosmid Ca41C10. 253 e-175
55 · ·	emb AC007872 AC007872 The sequence of an Aspergillus parasiticus 167 e-158 gb H55032 H55032 HHU58a Sorghum bicolor cv. TX430 Sorghum bicolo 233 e-151 emb AC005299 AC005299 emericella nidulans chromosome viii cosmid 166 e-147 emb AC004395 AC004395 Emericella nidulans Chromosome VIII Cosmid 166 e-147 emb AW443928 AW443928 EST308858 tomato mixed elicitor, BTI Lycop 468 e-131
60	emb AW667519 AW667519 GA_Ea0009J09 Gossypium arboreum 7-10 dpa 463 e-129 emb AI778813 AI778813 EST259692 tomato susceptible, Cornell Lyco 453 e-126 emb AW776720 AW776720 EST335785 DSIL Medicago truncatula cDNA cl 450 e-125

emb|AW695194|AW695194 NF092E10ST1F1082 Developing stem Medicago ... 370 e-124 emb|AI774685|AI774685 EST255785 tomato resistant, Cornell Lycope... 444 e-123 emb|AW618386|AW618386 EST320372 L. pennellii trichome, Cornell U... 434 e-120 gb|BE052708|BE052708 GA Ea0031N21f Gossypium arboreum 7-10 dpa ... 431 e-119 5 emb|AW737315|AW737315 EST338838 tomato flower buds, anthesis, Co... 409 e-113 emb|AW694020|AW694020 NF071G12ST1F1099 Developing stem Medicago ... 406 e-112 gb|BE060293|BE060293 HVSMEg0011O04f Hordeum vulgare pre-anthesis... 405 e-112 emb|AW649769|AW649769 EST328223 tomato germinating seedlings, TA... 377 e-111 emb|AW234850|AW234850 sf19h07.y1 Gm-c1028 Glycine max cDNA clone... 399 e-110 10 emb|AW760220|AW760220 sl59e08.yl Gm-c1027 Glycine max cDNA clone... 388 e-106 emb|AW929526|AW929526 EST338314 tomato flower buds 8 mm to pre-a... 386 e-106 emb|AW596420|AW596420 sj12c01.y1 Gm-c1032 Glycine max cDNA clone... 380 e-104 emb|AI730390|AI730390 BNLGHi6849 Six-day Cotton fiber Gossypium ... 302 e-102 emb|AI778812|AI778812 EST259691 tomato susceptible, Cornell Lyco... 372 e-102 15 emb|AW720123|AW720123 LjNEST14e4r Lotus japonicus nodule library... 369 e-101 emb|AW697121|AW697121 NF115C09ST1F1069 Developing stem Medicago ... 334 e-101 emb|AW726320|AW726320 GA __Ea0021F03 Gossypium arboreum 7-10 dpa ... 354 1e-99 emb|AQ841855|AQ841855 T134114 Soybean RFLP probe Glycine max gen... 358 4e-98 emb|AW564025|AW564025 LG1 281 F10.b1 A002 Light Grown 1 (LG1) So... 359 4e-98 20 emblAW979915|AW979915 EST341564 tomato root deficiency, Cornell ... 349 6e-95 emb|AI781665|AI781665 EST262544 tomato susceptible, Cornell Lyco... 348 1e-94 emb|Z26486|PSTKTG P.stipitis TKT gene for transketolase. 261 8e-93 emb|AW039152|AW039152 EST281387 tomato mixed elicitor, BTI Lycop... 339 7e-92 gb|BE053034|BE053034 GA_Ea0031O21f Gossypium arboreum 7-10 dpa ... 338 9e-92 25 emb|AW691000|AW691000 NF040C09ST1F1000 Developing stem Medicago ... 338 9e-92 emb|AW290149|AW290149 NXNV012F12F Nsf Xylem Normal wood Vertical... 337 2e-91 emb|AW203636|AW203636 sf36e03.y1 Gm-c1028 Glycine max cDNA clone... 332 6e-90 emb|AI966148|AI966148 sc34c04.y1 Gm-c1014 Glycine max cDNA clone... 330 4e-89 emb|Z71255|SCCHRXVI S.cerevisiae chromosome XVI 165536 bp sequen... 225 2e-88 30 gb[U51033]YSCP9513 Saccharomyces cerevisiae chromosome XVI cosmi... 225 2e-88 emb|Z49219|SC9499X S.cerevisiae chromosome XVI cosmid 9499. 225 2e-88 emb|X73224|SCTKL1 S.cerevisiae TKL1 gene for transketolase. 225 2e-88 emb|AL033385|SPBC2G5 S.pombe chromosome II cosmid c2G5. 198 2e-87 emb|AV388967|AV388967 AV388967 Chlamydomonas reinhardtii C9 Chla... 322 8e-87 35 emb|AV391940|AV391940 AV391940 Chlamydomonas reinhardtii C9 Chla... 321 1e-86 emb|AW587453|AW587453 IPPGHZ0039 Cotton fiber and embryo Lambda ... 276 3e-86 gb|U65983|KLU65983 Kluyveromyces lactis transketolase (TKL1) gen... 211 1e-85 emb|AW035937|AW035937 EST282796 tomato callus, TAMU Lycopersicon... 316 5e-85 emb|AW156809|AW156809 se31b02.yl Gm-c1015 Glycine max cDNA clone... 315 1e-84 emb|AA660853|AA660853 00748 MtRHE Medicago truncatula cDNA 5' si... 282 1e-83 40 emb|AV393839|AV393839 AV393839 Chlamydomonas reinhardtii C9 Chla... 230 1e-83 emb|AA556878|AA556878 720 Loblolly pine C Pinus taeda cDNA clone... 289 2e-83 emb|AW689533|AW689533 NF021G12ST1F1000 Developing stem Medicago ... 308 8e-83 emblAW776795|AW776795 EST335860 DSIL Medicago truncatula cDNA cl... 307 2e-82 45 emb|AW694632|AW694632 NF078D05ST1F1045 Developing stem Medicago ... 285 4e-82 emb|AV391577|AV391577 AV391577 Chlamydomonas reinhardtii C9 Chla... 304 1e-81 emb|AV388182|AV388182 AV388182 Chlamydomonas reinhardtii C9 Chla... 304 2e-81 emb|AW688641|AW688641 NF009H10ST1F1000 Developing stem Medicago ... 282 8e-80 emb|AW508848|AW508848 si41b02.yl Gm-r1030 Glycine max cDNA clone... 298 9e-80 50 emb|AW695046|AW695046 NF082H06ST1F1059 Developing stem Medicago ... 297 3e-79 emb|X78993|SCRACII S.cerevisiae genomic DNA 70kb region of the r... 200 3e-79 emb[X73532]SCTKL2 S.cerevisiae gene for transketolase. 200 3e-79 emb|Z35985|SCYBR116C S.cerevisiae chromosome II reading frame OR... 200 3e-79 emb|AW564318|AW564318 LG1_290_F06.b1_A002 Light Grown 1 (LG1) So... 293 4e-78 emb|AW201472|AW201472 sf03e09.yl Gm-c1027 Glycine max cDNA clone... 292 6e-78 55 emb|AB025004|AB025004 Cicer arietinum mRNA for transketolase, pa... 292 8e-78 emb|AW746874|AW746874 WS1 56 C06.b1 A002 Water-stressed 1 (WS1) ... 291 2e-77 emb|AW776336|AW776336 EST335401 DSIL Medicago truncatula cDNA cl... 290 4e-77 emb|AW696241|AW696241 NF104D02ST1F1016 Developing stem Medicago ... 288 1e-76 60 emb|AV395290|AV395290 AV395290 Chlamydomonas reinhardtii C9 Chla... 288 1e-76 emb|AW287516|AW287516 LG1 242 A07.b1 A002 Light Grown 1 (LG1) So... 283 4e-75

emb|AW907301|AW907301 EST343424 potato stolon, Cornell Universit... 281 1e-74 dbi|D89172|D89172 Schizosaccharomyces pombe mRNA, partial cds, c... 171 3e-73 emb|AV394221|AV394221 AV394221 Chlamydomonas reinhardtii C9 Chla... 275 4e-73 emb|AV387871|AV387871 AV387871 Chlamydomonas reinhardtii C9 Chla... 275 1e-72 emb|AI162975|AI162975 A028P14U Hybrid aspen plasmid library Popu... 273 1e-72 emb|AJ234429|HVU234429 Hordeum vulgare partial mRNA; clone cMWG0... 271 1e-71 emb|AW398784|AW398784 EST309284 L. pennellii trichome, Cornell U... 271 2e-71 gb|BE056580|BE056580 894010C09.yl C. reinhardtii CC-1690, normal... 267 2e-70 emb|AW694944|AW694944 NF081G03ST1F1023 Developing stem Medicago ... 258 4e-70 10 emb|AW041543|AW041543 EST284407 tomato mixed elicitor, BTI Lycop... 265 8e-70 emb|AW980590|AW980590 EST391743 GVN Medicago truncatula cDNA clo... 265 1e-69 emb|AF173677|AF173677 Beta vulgaris clone TK109UNI transketolase... 132 2e-69 emb|AQ842082|AQ842082 T134371 Soybean RFLP probe Glycine max gen... 263 4e-69 emb|AQ842006|AQ842006 T134292 Soybean RFLP probe Glycine max gen... 263 4e-69 15 emb|AI726103|AI726103 BNLGHi5028 Six-day Cotton fiber Gossypium ... 260 3e-68 emb|AW695133|AW695133 NF091E12ST1F1098 Developing stem Medicago ... 258 6e-68 emb|AA819992|AA819992 LO-171M13R Ice plant Lambda Uni-Zap XR exp... 258 1e-67 emb|AW180358|AW180358 MgA0465f MgA Library Mycosphaerella gramin... 144 1e-66 emb|AI563214|AI563214 EST00338 watermelon lambda zap library Cit... 249 1e-65 20 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 163 7e-65 emb|AW696579|AW696579 NF106E10ST1F1082 Developing stem Medicago ... 249 7e-65 gb[M63302]YSCTRANSK S.cerevisiae transketolase gene, complete cds. 168 5e-64

Query= AL022347.46_at 13659_at /id_source genbank /description emb|caa18462.1| (al022347) serine/threonine kinase-like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi http://www.ncgr.org/cgi-bin/ff?al022347 (2037 letters)

Database: plantfungal

40

55

661,018 sequences; 426,114,510 total letters

Searching......done

Score E

Sequences producing significant alignments:

(bits) Value

emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 385 e-125 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 343 e-111 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 348 e-109 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 346 e-109 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 347 e-109 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 333 e-108 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 342 e-107 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 328 e-106 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 334 e-105 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 329 e-104 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 205 e-104 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 326 e-103

emb|AB012106|AB012106 Brassica oleracea SFR3 gene, partial. 205 e-104
emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 326 e-103
gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 330 e-103
gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 336 e-102
emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 325 e-101
dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 290 e-100
emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 131 1e-95
emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 282 3e-94

dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 281 3e-93 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 276 4e-93 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 129 1e-91

emb|AW620957|AW620957 sj98a07.yl Gm-c1023 Glycine max cDNA clone... 275 9e-91 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 254 1e-90 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 115 8e-90 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 292 1e-89 5 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 127 2e-88 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 219 9e-88 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 284 8e-86 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 118 3e-85 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 313 4e-84 10 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 6e-84 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 112 8e-84 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 113 7e-83 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 113 1e-82 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 15 gb[BE057261]BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ... 296 4e-79 emb|AW831390|AW831390 sm22a06.yl Gm-c1028 Glycine max cDNA clone... 216 1e-75 emb[Y12531]BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 126 2e-75 emb|AW760240|AW760240 sl59g07.yl Gm-c1027 Glycine max cDNA clone... 283 4e-75 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 122 5e-75 20 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 221 3e-72 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 269 7e-71 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 125 8e-71 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 268 1e-70 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 188 7e-68 25 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 242 2e-66 emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 172 3e-65 emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 205 5e-64 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 197 5e-64 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 237 1e-62 30 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 166 1e-61 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 236 6e-61 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 166 1e-60 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 132 2e-58 emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 177 4e-58 35 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 126 3e-57 emb|AI967314|AI967314 Ljirnpest00-017 Ljirnp Lambda HybriZap two... 138 4e-57 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 223 4e-57 emb|AI822355|AI822355 LO-804T3 Ice plant Lambda Uni-Zap XR expre... 126 7e-57 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 131 2e-56 40 emblAW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 219 8e-56 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 172 6e-55 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 171 3e-54 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 169 7e-54 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 169 7e-54 45 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 109 1e-53 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 172 3e-53 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 126 5e-53 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 172 1e-52 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 137 2e-52 50 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 1e-51 emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 118 5e-51 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 172 7e-51 emb|AW667985|AW667985 GA_ Ea0012C15 Gossypium arboreum 7-10 dpa ... 106 1e-50 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 72 2e-50 55 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 135 2e-50 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 108 3e-49 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 179 3e-49 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 121 1e-48 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 134 7e-48 60 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 192 1e-47 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 96 1e-47

emb|AW394449|AW394449 sh05d09.y1 Gm-c1016 Glycine max cDNA clone... 121 1e-47 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 190 3e-47 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 111 3e-47 gb|U59317|LPU59317 Lycopersicon pimpinellifolium serine/threonin... 107 3e-47 5 gb U13923 LEU13923 Lycopersicon pimpinellifolium serine/threonin... 107 3e-47 emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 178 4e-47 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 131 8e-47 emb|AW053331|AW053331 L30-1528T3 Ice plant Lambda Uni-Zap XR exp... 126 1e-46 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 188 1e-46 10 emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 118 2e-46 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 128 3e-46 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 108 7e-46 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 109 1e-45 emb|AI775997|AI775997 EST257097 tomato resistant, Cornell Lycope... 185 1e-45 15 gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 105 1e-45 emb|AW775756|AW775756 EST334821 DSIL Medicago truncatula cDNA cl... 135 2e-45 emb|Z73295|CRPK1 C.roseus mRNA for receptor-like protein kinase. gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 103 1e-44 20 Query= AC005662.56_at 14083_at /id_source genbank /description gb|aac78535.1| (ac005662) putative embryo-abundant protein [arabidopsis thaliana] /blast score 1.00e-155 /ec number /family /chip nova /gb link 25 http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005662| /ncgi http://www.ncgr.org/cgi-bin/ff?ac005662 (966 letters) 30 Database: plantfungal 661,018 sequences; 426,114,510 total letters 35 Score Ε Sequences producing significant alignments: (bits) Value emb|AW685935|AW685935 NF031H09NR1F1000 Nodulated root Medicago t... 299 1e-83 emb|AW032722|AW032722 EST276281 tomato callus, TAMU Lycopersicon... 310 1e-83 40 emb|AI489127|AI489127 EST247466 tomato ovary, TAMU Lycopersicon ... 310 1e-83 emblAI489097|AI489097 EST247436 tomato ovary, TAMU Lycopersicon ... 310 1e-83 emb|AI781847|AI781847 EST262726 tomato susceptible, Cornell Lyco... 309 2e-83 emb|AW442260|AW442260 EST311656 tomato fruit red ripe, TAMU Lyco... 308 4e-83 emb|AI781496|AI781496 EST262375 tomato susceptible, Cornell Lyco... 308 4e-83 45 emb|AI898923|AI898923 EST268366 tomato ovary, TAMU Lycopersicon ... 307 8e-83 emb|AI894834|AI894834 EST264277 tomato callus, TAMU Lycopersicon... 306 2e-82 emb|AW033760|AW033760 EST277331 tomato callus, TAMU Lycopersicon... 306 2e-82 emb|AI490417|AI490417 EST248743 tomato ovary, TAMU Lycopersicon ... 304 7e-82 emb|AW686492|AW686492 NF042A07NR1F1000 Nodulated root Medicago t... 299 8e-82 50 emb|AI898538|AI898538 EST267981 tomato ovary, TAMU Lycopersicon ... 303 1e-81 emb|AI488586|AI488586 EST246925 tomato ovary, TAMU Lycopersicon ... 303 2e-81 emb|AI775239|AI775239 EST256339 tomato resistant, Cornell Lycope... 302 4e-81 emb|AI771731|AI771731 EST252831 tomato ovary, TAMU Lycopersicon ... 301 5e-81 emb|AI780639|AI780639 EST261614 tomato susceptible, Cornell Lyco... 299 2e-80 55 emb|AW029697|AW029697 EST272952 tomato callus, TAMU Lycopersicon... 299 2e-80 emb|AI485286|AI485286 EST243590 tomato ovary, TAMU Lycopersicon ... 298 5e-80 emb|AI897802|AI897802 EST267245 tomato ovary, TAMU Lycopersicon ... 297 6e-80 emb|AW223714|AW223714 EST300525 tomato fruit red ripe, TAMU Lyco... 297 9e-80 emb|AW220845|AW220845 EST297314 tomato fruit mature green, TAMU ... 292 3e-78 60 emb|AW684608|AW684608 NF018H07NR1F1000 Nodulated root Medicago t... 292 3e-78

emb|AI489777|AI489777 EST248116 tomato ovary, TAMU Lycopersicon ... 292 4e-78

```
emb|AW132650|AW132650 se08b10.y1 Gm-c1013 Glycine max cDNA clone... 291 7e-78
      emb|AI483572|AI483572 EST249422 tomato ovary, TAMU Lycopersicon ... 288 4e-77
      emb|AI778435|AI778435 EST259314 tomato susceptible, Cornell Lyco... 286 1e-76
      emb|AI897140|AI897140 EST266583 tomato ovary, TAMU Lycopersicon ... 286 1e-76
 5
      emb|AI488011|AI488011 EST246333 tomato ovary, TAMU Lycopersicon ... 286 2e-76
      emb|AI771230|AI771230 EST252246 tomato ovary, TAMU Lycopersicon ... 281 4e-75
      emb|AW218445|AW218445 EST303628 tomato radicle, 5 d post-imbibit... 281 6e-75
      emb|AI897359|AI897359 EST266802 tomato ovary, TAMU Lycopersicon ... 279 2e-74
      emb|AW931636|AW931636 EST357479 tomato fruit mature green, TAMU ... 277 7e-74
10
      emb|AI898026|AI898026 EST267469 tomato ovary, TAMU Lycopersicon ... 276 2e-73
      emb|Al897018|Al897018 EST266461 tomato ovary, TAMU Lycopersicon ... 270 9e-72
      emb|AI487404|AI487404 EST245726 tomato ovary, TAMU Lycopersicon ... 270 2e-71
      emb|AI485049|AI485049 EST243353 tomato ovary, TAMU Lycopersicon ... 269 3e-71
      emb|AI484072|AI484072 EST249943 tomato ovary, TAMU Lycopersicon ... 267 8e-71
15
      emb|AI485145|AI485145 EST243449 tomato ovary, TAMU Lycopersicon ... 266 2e-70
      emb|AW708004|AW708004 EST0051 Grape berries Lambda Zap II Librar... 266 2e-70
      emb|AW038382|AW038382 EST280065 tomato mixed elicitor, BTI Lycop... 264 5e-70
      emb|AI898224|AI898224 EST267667 tomato ovary, TAMU Lycopersicon ... 245 1e-69
      emb|AI483780|AI483780 EST249651 tomato ovary, TAMU Lycopersicon ... 259 2e-68
20
      gb|L47672|PIAEMB34R Picea glauca embryo-abundant protein (EMB34)... 199 3e-66
      emb|AW684859|AW684859 NF022D03NR1F1000 Nodulated root Medicago t... 189 1e-64
      emb|AW222134|AW222134 EST298945 tomato fruit red ripe, TAMU Lyco... 243 2e-63
      emb|AW625379|AW625379 EST319202 tomato radicle, 5 d post-imbibit... 242 4e-63
      emb|AI485781|AI485781 EST244102 tomato ovary, TAMU Lycopersicon ... 240 1e-62
25
      emb|AW728861|AW728861 GA_Ea0028O02 Gossypium arboreum 7-10 dpa ... 189 2e-59
      emb|AI489435|AI489435 EST247774 tomato ovary, TAMU Lycopersicon ... 224 7e-58
      emb|AI485480|AI485480 EST243801 tomato ovary, TAMU Lycopersicon ... 221 5e-57
      emb|AW030923|AW030923 EST274230 tomato callus, TAMU Lycopersicon... 219 3e-56
      emb|AI771831|AI771831 EST252931 tomato ovary, TAMU Lycopersicon ... 219 3e-56
30
      emb|AI488694|AI488694 EST247033 tomato ovary, TAMU Lycopersicon ... 216 2e-55
      emb|AI897044|AI897044 EST266487 tomato ovary, TAMU Lycopersicon ... 216 2e-55
      emb|AW127616|AW127616 M110351 DSLC Medicago truncatula cDNA clon... 207 1e-52
      emb|AW221131|AW221131 EST297600 tomato fruit mature green, TAMU ... 203 2e-51
      gb|BE036025|BE036025 MO18F06 MO Mesembryanthemum crystallinum cD... 197 1e-49
35
      emb|AW310620|AW310620 sg22b10.x1 Gm-c1024 Glycine max cDNA clone... 138 4e-49
      emb|AA660966|AA660966 00863 MtRHE Medicago truncatula cDNA 5' si... 193 2e-48
      emb|AI488052|AI488052 EST246374 tomato ovary, TAMU Lycopersicon ... 191 6e-48
      emb|AI483934|AI483934 EST249805 tomato ovary, TAMU Lycopersicon ... 190 2e-47
      emb|AW687553|AW687553 NF010H04RT1F1043 Developing root Medicago ... 189 2e-47
40
      emb|AI488394|AI488394 EST246716 tomato ovary, TAMU Lycopersicon ... 189 3e-47
      emb|AW687876|AW687876 NF014D11RT1F1093 Developing root Medicago ... 179 2e-44
      emb|AW031053|AW031053 EST274360 tomato callus, TAMU Lycopersicon... 175 6e-43
      emb|AI771906|AI771906 EST253006 tomato ovary, TAMU Lycopersicon ... 174 1e-42
      emb[AI771730]AI771730 EST252830 tomato ovary, TAMU Lycopersicon ... 171 5e-42
45
      emblAI895638|AI895638 EST265081 tomato callus, TAMU Lycopersicon... 164 9e-40
      emb|AW441823|AW441823 EST311219 tomato fruit red ripe, TAMU Lyco... 164 9e-40
      emb|AW981333|AW981333 EST392486 DSIL Medicago truncatula cDNA c1... 156 3e-37
      emb|AI486213|AI486213 EST244534 tomato ovary, TAMU Lycopersicon ... 153 2e-36
      emb|AV425590|AV425590 AV425590 Lotus japonicus young plants (two... 148 6e-35
50
      emb|AW563884|AW563884 LG1 272 D05.b1 A002 Light Grown 1 (LG1) So... 136 3e-31
      emb|AI489302|AI489302 EST247641 tomato ovary, TAMU Lycopersicon ... 129 4e-29
      emb|AI967559|AI967559 Ljirnpest05-409-e8 Ljirnp Lambda HybriZap ... 120 2e-26
      emb|AI898395|AI898395 EST267838 tomato ovary, TAMU Lycopersicon ... 115 7e-25
      emb|AI782642|AI782642 EST263521 tomato susceptible, Cornell Lyco... 105 7e-22
     emb|AI725304|AI725304 1170 PtIFG2 Pinus taeda cDNA clone 9256r, ... 78 2e-18
      emb|AW096566|AW096566 EST289746 tomato mixed elicitor, BTI Lycop...
      emb|AI899609|AI899609 EST269052 tomato susceptible, Cornell Lyco... 90 3e-17
      emb|AI899596|AI899596 EST269039 tomato susceptible, Cornell Lyco... 90 3e-17
      emb|AW443878|AW443878 EST308808 tomato mixed elicitor, BTI Lycop... 90 3e-17
60
      emb|AI486045|AI486045 EST244366 tomato ovary, TAMU Lycopersicon ... 90 3e-17
      emb|AW222135|AW222135 EST298946 tomato fruit red ripe, TAMU Lyco... 89 4e-17
```

```
emb|AW032431|AW032431 EST275970 tomato callus, TAMU Lycopersicon... 87 2e-16
      emb|AI778055|AI778055 EST258934 tomato susceptible, Cornell Lyco... 87 2e-16
      emb|AW185076|AW185076 se86d10.y1 Gm-c1023 Glycine max cDNA clone... 69 4e-14
      emb|AA740029|AA740029 794 PtIFG2 Pinus taeda cDNA clone 9256M 3'... 77 3e-13
      emb|Z92685|Z92685 223/4 Norway spruce mRNA Picea abies cDNA clon... 76 5e-13
      emb|AW564832|AW564832 LG1 305 G04.b1 A002 Light Grown 1 (LG1) So... 51 2e-05
      gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 35 2e-05
      emb|AW670960|AW670960 LG1_278 A08.b1_A002 Light Grown 1 (LG1) So... 50 3e-05
      emb|AW713879|AW713879 h3g02ne.fl Neurospora.crassa evening cDNA ... 40 1e-04
10
      emb|AW443870|AW443870 EST308800 tomato mixed elicitor, BTI Lycop... 41 0.011
      emb|AW678240|AW678240 WS1 14_G12.b1_A002 Water-stressed 1 (WS1) ... 37 0.26
      emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 36 0.50
      gb[U10549|ANU10549 Aspergillus niger protein kinase C (pkcA) gen... 35 0.94
      gb|U74447|ZAU74447 Zinnia angustifolia internal transcribed spac... 33 0.95
15
      emb|AZ217616|AZ217616 Sheared DNA-90G1.TF Sheared DNA Trypanosom... 31 2.1
      Query= AC002291.12 at 14096 at /id source genbank /description no hits
20
      found. /blast_score /ec_number /family /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002291|/ncgi
      http://www.ncgr.org/cgi-bin/ff?ac002291
           (159 letters)
25
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
      Searching.....done
30
                                         Score
      Sequences producing significant alignments:
                                                        (bits) Value
      emb|AQ161515|AQ161515 mgxb0008C06r CUGI Rice Blast BAC Library P... 32 0.026
35
      emblAQ324421|AQ324421 mgxb0018F21r CUGI Rice Blast BAC Library P... 32 0.026
      emb|AL116063|CNS01CW7 Botrytis cinerea strain T4 cDNA library un... 29 0.24
      emb|AQ940444|AQ940444 Sheared DNA-35C4.TF Sheared DNA Trypanosom... 24 0.40
      emb|AQ362000|AQ362000 mgxb0004E15r CUGI Rice Blast BAC Library P... 28 0.62
      emblAQ945662|AQ945662 Sheared DNA-49E8.TR Sheared DNA Trypanosom... 25 1.5
40
      emb|AW266254|AW266254 L30-2966T3 Ice plant Lambda Uni-Zap XR exp... 27 1.6
      emb|AL355929|NCB21J21 Neurospora crassa DNA linkage group II BAC... 27 1.6
      emb|AW661015|AW661015 832009D11.yl C. reinhardtii CC-125 nutrien... 23 2.7
      emb|AV391625|AV391625 AV391625 Chlamydomonas reinhardtii C9 Chla... 23 2.7
45
      emb|AI055219|AI055219 coau0003G03 Cotton Boll Abscission Zone cD... 23 2.7
      emb|AL354533|LMFL6294 Leishmania major Friedlin chromosome 21 co... 26 4.1
      gb|N98018|N98018 2045C3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 26 4.1
      emb|AA519693|AA519693 TgESTzz27f07.rl TgME49 invivo Bradyzoite c... 26 4.1
      emb|AA519224|AA519224 TgESTzz39g08.s1 TgME49 invivo Bradyzoite c... 26 4.1
50
      emb|AW650822|AW650822 EST329276 tomato germinating seedlings, TA... 26 4.1
      emb|AA531994|AA531994 TgESTzz46c10.rl TgME49 invivo Bradyzoite c... 26 4.1
      emb|AA520816|AA520816 TgESTzz64d11.rl TgME49 invivo Bradyzoite c... 26 4.1
      gb[U15615]TCU15615 Trypanosoma cruzi reverse transcriptase-like ... 26 4.1
      emb|AQ848398|AQ848398 LMAJFV1_lm61f01.x1 Leishmania major FV1 ra... 26 4.1
55
      emb|AL136536|SPBC1703 S.pombe chromosome II cosmid c1703.
      emb|AA520593|AA520593 TgESTzz62e12.rl TgME49 invivo Bradyzoite c... 26 4.1
      emb|Z81402|CAZ81402 C.aeruginosa 28S rRNA gene.
      emb|AW979496|AW979496 EST310517 tomato root deficiency, Cornell ... 26 4.1
      emb|AW671199|AW671199 LG1_330_F04.b1_A002 Light Grown 1 (LG1) So... 25 5.7
60
      emb|Z74775|SCYOL033W S.cerevisiae chromosome XV reading frame OR... 25 5.7
```

emb|AA897901|AA897901 NCP4C5T3 Perithecial Neurospora crassa cDN... 25 5.7

	emb AW694603 AW694603 NF078B02ST1F1015 Developing stem Medicago 25 5.7 emb Z74776 SCYOL034W S.cerevisiae chromosome XV reading frame OR 25 5.7 emb AQ904542 AQ904542 GSSTc04164 Trypanosome cruzi random genomi 25 5.7
5	gb L39015 YSCMSE1G Saccharomyces cerevisiae nuclear-encoded mito 25 5.7 gb BE054352 BE054352 GA_Ea0035E11f Gossypium arboreum 7-10 dpa 25 5.7 emb AI707320 AI707320 T7446 MVAT4 bloodstream form of serodeme W 25 5.7 emb AW730403 AW730403 GA_Ea0023O04 Gossypium arboreum 7-10 dpa 25 5.7 emb X87148 VPPPCGEN V.planifolia mRNA for phosphoenolpyruvate ca 25 5.7
10	emb AW031408 AW031408 EST274862 tomato callus, TAMU Lycopersicon 25 5.7 emb AI730886 AI730886 BNLGHi8147 Six-day Cotton fiber Gossypium 25 5.7 emb AW695893 AW695893 NF100D11ST1F1093 Developing stem Medicago 25 5.7 emb AW310777 AW310777 sg25a11.x1 Gm-c1024 Glycine max cDNA clone 22 6.0 emb AV410755 AV410755 AV410755 Lotus japonicus young plants (two 25 7.8
15	emb AQ445006 AQ445006 GSSTc0636 Trypanosoma cruzi random genomic 25 7.8 emb Z49821 SCPDR10 S.cerevisiae PDR10, MYO2, PDR10, SCD5, MIP1, 25 7.8 emb AC008152 AC008152 Leishmania major chromosome 35 clone L7936 25 7.8 emb AQ399859 AQ399859 mgxb0012H02f CUGI Rice Blast BAC Library P 25 7.8 emb AF175710 AF175710 Pleurotus eryngii peroxidase PS1 precursor 25 7.8
20	emb AW186653 AW186653 BNLGHi12240 Six-day Cotton fiber Gossypium 25 7.8 emb AJ131048 CAR131048 Cicer arietinum mRNA for protein kinase, 25 7.8 emb AW775371 AW775371 EST334436 DSIL Medicago truncatula cDNA cl 25 7.8 emb AC021894 AC021894 Leishmania major chromosome 35 clone L8650 25 7.8 emb Z75236 SCYOR328W S.cerevisiae chromosome XV reading frame OR 25 7.8
25	emb AI069165 AI069165 mgae0005dC01f Magnaporthe grisea Appressor 25 7.8 emb AI068528 AI068528 mgae0002dE03f Magnaporthe grisea Appressor 25 7.8 emb AI068407 AI068407 mgae0002aH09f Magnaporthe grisea Appressor 25 7.8 emb AL109846 SPBC17G9 S.pombe chromosome II cosmid c17G9. 23 9.1 emb Z72244 CNIGRITS1 C.nigricans DNA for internal transcribed sp 21 9.5
30	Query= AL035528.279_i_at 14110_i_at /id_source genbank /description emb cab36854.1 (al035528) putative disease resistance protein [arabidopsis thaliana] /blast_score 0 /ec_number /family disease /chip nova /gb_link
35	http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb al035528 /ncgi http://www.ncgr.org/cgi-bin/ff?al035528 (2508 letters)
40	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
45	Score E Sequences producing significant alignments: (bits) Value
50	emb AF119041 AF119041 Lycopersicon esculentum haplotype Southern 105 4e-61 emb AF119040 AF119040 Lycopersicon esculentum haplotype Northern 112 1e-59 emb AJ002235 LHJ002235 Lycopersicon hirsutum Cf-4 resistance gen 103 1e-59 emb AJ002236 LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist 103 2e-57 gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe 122 4e-57 emb A57130 A57130 Sequence 1 from Patent WO9531564. 122 4e-57
55	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe 122 4e-57 emb A57133 A57133 Sequence 4 from Patent WO9531564. 122 4e-57 emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) 121 2e-56 emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) 109 1e-52 emb A67432 A67432 Sequence 5 from Patent WO9743429. 109 1e-52
50	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr 101 5e-49 emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) 127 7e-49 emb AF053993 AF053993 Lycopersicon esculentum disease resistance 127 7e-49 emb AF053993 AF053993 Lycopersicon esculentum disease resistance 127 7e-49

	emb A67429 A67429 Sequence 2 from Patent WQ9743429. 127 7e-49
	emb A67428 A67428 Sequence 1 from Patent WO9743429. 127 7e-49
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci 102 3e-48
	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) 103 2e-42
5	emb Y12640 LECF4A L.esculentum Cf-4A gene. 100 1e-40
	emb AJ002237 LEJ002237 Lycopersicon esculentum haplotype of the 100 8e-39
	A DECEMBER OF THE PROPERTY OF
	gb U15936 LPU15936 Lycopersicon pimpinellifolium Cf-9 precursor 93 3e-36
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (inr 99 4e-29
10	emb AI778581 AI778581 EST259460 tomato susceptible, Cornell Lyco 99 3e-26
- •	emb AI486572 AI486572 EST244893 tomato ovary, TAMU Lycopersicon 88 5e-26
	emb AI898269 AI898269 EST267712 tomato ovary, TAMU Lycopersicon 88 5e-26
	emb AW267955 AW267955 EST306297 DSIR Medicago truncatula cDNA cl 81 3e-25
	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like 84 1e-24
15	4 1 1 4 5 4 5 4 5 4 5 4 5 4 5 4 5 5 5 5
13	
	emb AW306675 AW306675 se53h08.yl Gm-c1017 Glycine max cDNA clone 90 6e-23
	emb AW299082 AW299082 EST305756 KV2 Medicago truncatula cDNA clo 83 1e-22
	emb AW980804 AW980804 EST391957 GVN Medicago truncatula cDNA clo 86 3e-22
	emb AW616452 AW616452 EST322863 L. hirsutum trichome, Cornell Un 86 8e-22
20	amble 70/4/6001470/4/600 Cm. IB 4/601 11/6 Col. B. IB 310.01 11/6 Col. B. IB 4/601 11/6
20	emb AZ044600 AZ044600 Gm_UMb001_116_G01.R UMN Soybean BAC Librar 106 8e-22
	emb AF197946 AF197946 Glycine max receptor protein kinase-like p 85 1e-21
	emb AF197947 AF197947 Glycine max receptor protein kinase-like p 82 1e-21
	emb AW775087 AW775087 EST334238 KV3 Medicago truncatula cDNA clo 85 2e-21
	emb AW033129 AW033129 EST276688 tomato callus, TAMU Lycopersicon 86 5e-21
25	ombly 127 ITA A WIT 172 To otherwood contact can us 172 172 A WIT
23	emb X81367 TAAWJL172 T.aestivumn (subclone pAWJL172) AWJL172 gene. 71 9e-21
	emb AW398661 AW398661 EST309161 L. pennellii trichome, Cornell U 85 2e-20
	emb AW398651 AW398651 EST309151 L. pennellii trichome, Cornell U 85 2e-20
	emb AW217935 AW217935 EST296649 tomato flower buds, anthesis, Co 79 4e-20
	emb AI726155 AI726155 BNLGHi5095 Six-day Cotton fiber Gossypium 78 5e-20
30	emb AF159296 AF159296 Lycopersicon esculentum pollen extensin-li 70 1e-19
50	and AT 132290 AT 132290 Lycopersicon esculentum ponen extensin-n /0 16-19
	emb AW267958 AW267958 EST306300 DSIR Medicago truncatula cDNA cl 97 6e-19
	emb Y10816 LIY10816 L.infantum psa gene. 70 7e-19
	gb U77041 MDU77041 Malus domestica polygalacturonase-inhibiting 76 7e-19
•	emb AI898226 AI898226 EST267669 tomato ovary, TAMU Lycopersicon 95 2e-18
35	emb AW030004 AW030004 EST273259 tomato callus, TAMU Lycopersicon 95 2e-18
	amble F1501711AF150171 Fucely management and the latest and the first an
	emb AF159171 AF159171 Eucalyptus nitens polygalacturonase-inhibi 74 3e-18
	emb AF159170 AF159170 Eucalyptus saligna polygalacturonase-inhib 74 3e-18
	emb AF159167 AF159167 Eucalyptus grandis polygalacturonase-inhib 74 3e-18
	emb AI352869 AI352869 MB70-4A PZ204.BNlib Brassica napus cDNA cl 89 3e-18
40	emb[X81370]TAAWJL236 T.aestivumn (subclone pAWJL236) AWJL236 gene. 78 4e-18
	emb Z49063 ADPGIP A.deliciosa pgip mRNA for polygalacturonase in 74 5e-18
	cinication of Aldenciosa pgip inicitation polygaracturonase in 74 5e-18
	emb AF159169 AF159169 Eucalyptus urophylla polygalacturonase-inh 74 7e-18
	gb U62279 SBU62279 Sorghum bicolor leucine-rich repeat-containin 93 8e-18
	emb AW738046 AW738046 EST339473 tomato flower buds, anthesis, Co 93 le-17
45	emb AW307311 AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone 80 1e-17
_	
	gb L09264 PYPPGI Pyrus communis polygalacturonase inhibitor mRNA 71 2e-17
	emb AF159168 AF159168 Eucalyptus camaldulensis polygalacturonase 74 2e-17
	emb AW689207 AW689207 NF016F04ST1F1000 Developing stem Medicago 78 2e-17
	emb AA738549 AA738549 SbRLK7 Sorghum bicolor cv. TX430 leaf Sorg 90 5e-17
50	emb AI897228 AI897228 EST266767 tomato ovary, TAMU Lycopersicon 90 5e-17
	13.777.(0000.0).177.(0000.0).777.00
	emb[A W 688235] A W 688235 NF005A07ST1F1000 Developing stem Medicago 89 1e-16
	emb AW694992 AW694992 NF082D01ST1F1012 Developing stem Medicago 83 2e-16
	emb AW432582 AW432582 sh76d03.yl Gm-c1015 Glycine max cDNA clone 89 2e-16
	emb AW399097 AW399097 EST309597 L. pennellii trichome, Cornell U 69 2e-16
55	emb AI443128 AI443128 sa84f10.yl Gm-c1004 Glycine max cDNA clone 81 2e-16
-	4 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	emb Y14600 SBRLK1 Sorghum bicolor mRNA for protein serine/threon 88 4e-16
	emb AA738545 AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg 87 5e-16
	emb AW033367 AW033367 EST276938 tomato callus, TAMU Lycopersicon 87 5e-16
50	emb AV419297 AV419297 AV419297 Lotus japonicus young plants (two 63 7e-16
	emb AW689888 AW689888 NF025H09ST1F1000 Developing stem Medicago 86 1e-15

```
emb|AA557055|AA557055 897 Loblolly pine N Pinus taeda cDNA clone... 86 1e-15
       emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 80 1e-15
       emb|AW399471|AW399471 EST309971 L. pennellii trichome, Cornell U... 55 1e-15
       gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 85 2e-15
 5
       emb|AW164782|AW164782 se77g01.yl Gm-c1023 Glycine max cDNA clone...
       emb|A67797|A67797 Sequence 2 from Patent WO9743427.
       emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 80 2e-15
       emb|AI730245|AI730245 BNLGHi6465 Six-day Cotton fiber Gossypium ... 64 2e-15
       emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 80 3e-15
10
       emb|AV408986|AV408986 AV408986 Lotus japonicus young plants (two... 84 5e-15
       emb|AW671867|AW671867 LG1_352_F06.b1_A002 Light Grown 1 (LG1) So... 84 5e-15
       emb|AI488023|AI488023 EST246345 tomato ovary, TAMU Lycopersicon ... 84 5e-15
       emblAI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 84 6e-15
       emb|AV428126|AV428126 AV428126 Lotus japonicus young plants (two... 84 6e-15
15
       emb|AW695797|AW695797 NF098F06ST1F1058 Developing stem Medicago ... 84 6e-15
       emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 66_9e-15
       emb|AI856215|AI856215 sb39c10.x1 Gm-c1014 Glycine max cDNA clone... 83 9e-15
       emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 83 9e-15
       emb[AW616567]AW616567 EST322978 L. hirsutum trichome, Cornell Un... 83 9e-15
20
       emb|AW697060|AW697060 NF111H11ST1F1095 Developing stem Medicago ... 77 1e-14
       emb|X81369|TAAWJL218 T.aestivumn (subclone pAWJL218) AWJL218 gene. 83 1e-14
       emb|AI776963|AI776963 EST251989 tomato callus, TAMU Lycopersicon... 83 1e-14
       emb|AW443205|AW443205 EST308135 tomato mixed elicitor, BTI Lycop... 83 1e-14
       emb|AW696757|AW696757 NF110F02ST1F1025 Developing stem Medicago ... 83 1e-14
25
       Query= AL035528.279 s at 14111 s at /id_source genbank /description
       emb|cab36854.1| (al035528) putative disease resistance protein
       [arabidopsis thaliana] /blast_score 0 /ec number /family /chip nova
30
      /gb link /ncgi
          · (2508 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
35
      Searching.....done
                                           Score E
      Sequences producing significant alignments:
                                                          (bits) Value
40
      emb|AF119041|AF119041 Lycopersicon esculentum haplotype Southern... 105 4e-61
      emb|AF119040|AF119040 Lycopersicon esculentum haplotype Northern... 112 1e-59
      emb|AJ002235|LHJ002235 Lycopersicon hirsutum Cf-4 resistance gen... 103 1e-59
      emb|AJ002236|LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist... 103 2e-57
45
      gb[U42444|U42444 Lycopersicon pimpinellifolium leucine rich repe... 122 4e-57
      emb|A57130|A57130 Sequence 1 from Patent WO9531564.
                                                                     122 4e-57
      gb|U42445|U42445 Lycopersicon pimpinellifolium leucine rich repe... 122 4e-57
      emb|A57133|A57133 Sequence 4 from Patent WO9531564.
                                                                     122 4e-57
      emb|AF053995|AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ... 121 2e-56
50
      emb|AF053997|AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ... 109 1e-52
      emb|A67432|A67432 Sequence 5 from Patent WO9743429.
                                                                    109 1e-52
      emb|AF053996|AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr... 101 5e-49
      emb|AF053998|AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ... 127 7e-49
      emb|A67434|A67434 Sequence 7 from Patent WO9743429.
                                                                     127 7e-49
55
      emb|AF053993|AF053993 Lycopersicon esculentum disease resistance... 127 7e-49
      emb|A67429|A67429 Sequence 2 from Patent WO9743429.
                                                                    127 7e-49
      emb|A67428|A67428 Sequence 1 from Patent WO9743429.
                                                                    127 7e-49
      emb|AB029327|AB029327 Nicotiana tabacum mRNA for elicitor-induci... 102 3e-48
      emb|AF053994|AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ... 103 2e-42
60
      emb|Y12640|LECF4A L.esculentum Cf-4A gene.
                                                                100 le-40
      emb|AJ002237|LEJ002237 Lycopersicon esculentum haplotype of the ... 100 8e-39
```

```
emb|A58270|A58270 Sequence 1 from Patent WO9635790.
                                                                     93 6e-37
      gb|U15936|LPU15936 Lycopersicon pimpinellifolium Cf-9 precursor ... 93 3e-36
      gb|U77888|INU77888 Ipomoea nil receptor-like protein kinase (inr... 99 4e-29
      emb|AI778581|AI778581 EST259460 tomato susceptible, Cornell Lyco... 99 3e-26
 5
      emb|AI486572|AI486572 EST244893 tomato ovary, TAMU Lycopersicon ... 88 5e-26
      emb|AI898269|AI898269 EST267712 tomato ovary, TAMU Lycopersicon ... 88 5e-26
      emb|AW267955|AW267955 EST306297 DSIR Medicago truncatula cDNA cl... 81 3e-25
      emb|AF053127|AF053127 Malus domestica leucine-rich receptor-like... 84 1e-24
      emb|AQ367638|AQ367638 toxb0002D20f CUGI Tomato BAC Library Lycop... 81 8e-24
10
      emb|AW306675|AW306675 se53h08.yl Gm-c1017 Glycine max cDNA clone... 90 6e-23
      emb|AW299082|AW299082 EST305756 KV2 Medicago truncatula cDNA clo... 83 1e-22
      emb|AW980804|AW980804 EST391957 GVN Medicago truncatula cDNA clo... 86 3e-22
      emb|AW616452|AW616452 EST322863 L. hirsutum trichome, Cornell Un... 86 8e-22
      emb|AZ044600|AZ044600 Gm_UMb001_116_G01.R UMN Soybean BAC Librar... 106 8e-22
15
      emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 85 1e-21
      emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 82 1e-21
      emb|AW775087|AW775087 EST334238 KV3 Medicago truncatula cDNA clo... 85 2e-21
      emb|AW033129|AW033129 EST276688 tomato callus, TAMU Lycopersicon... 86 5e-21
      emb[X81367]TAAWJL172 T.aestivumn (subclone pAWJL172) AWJL172 gene. 71 9e-21
20
      emb|AW398661|AW398661 EST309161 L. pennellii trichome, Cornell U... 85 2e-20
      emb|AW398651|AW398651 EST309151 L. pennellii trichome, Cornell U... 85 2e-20
      emb|AW217935|AW217935 EST296649 tomato flower buds, anthesis, Co... 79 4e-20
      emb|AI726155|AI726155 BNLGHi5095 Six-day Cotton fiber Gossypium ... 78 5e-20
      emb|AF159296|AF159296 Lycopersicon esculentum pollen extensin-li... 70 1e-19
25
      emb|AW267958|AW267958 EST306300 DSIR Medicago truncatula cDNA cl... 97 6e-19
      emb|Y10816|LIY10816 L.infantum psa gene.
                                                              70 7e-19
      gb|U77041|MDU77041 Malus domestica polygalacturonase-inhibiting ... 76 7e-19
      emb|AI898226|AI898226 EST267669 tomato ovary, TAMU Lycopersicon ... 95 2e-18
      emb|AW030004|AW030004 EST273259 tomato callus, TAMU Lycopersicon... 95 2e-18
30
      emb|AF159171|AF159171 Eucalyptus nitens polygalacturonase-inhibi... 74 3e-18
      emb|AF159170|AF159170 Eucalyptus saligna polygalacturonase-inhib... 74 3e-18
      emb|AF159167|AF159167 Eucalyptus grandis polygalacturonase-inhib... 74 3e-18
      emb|AI352869|AI352869 MB70-4A PZ204.BNlib Brassica napus cDNA cl... 89 3e-18
      emb|X81370|TAAWJL236 T.aestivumn (subclone pAWJL236) AWJL236 gene. 78 4e-18
35
      emb|Z49063|ADPGIP A.deliciosa pgip mRNA for polygalacturonase in... 74 5e-18
      emb|AF159169|AF159169 Eucalyptus urophylla polygalacturonase-inh... 74 7e-18
      gb[U62279|SBU62279 Sorghum bicolor leucine-rich repeat-containin... 93 8e-18
      emblAW738046|AW738046 EST339473 tomato flower buds, anthesis, Co... 93 1e-17
      emb|AW307311|AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone... 80 1e-17
40
      gb|L09264|PYPPGI Pyrus communis polygalacturonase inhibitor mRNA... 71 2e-17
      emb|AF159168|AF159168 Eucalyptus camaldulensis polygalacturonase... 74 2e-17
      emb|AW689207|AW689207 NF016F04ST1F1000 Developing stem Medicago ... 78 2e-17
      emb|AA738549|AA738549 SbRLK7 Sorghum bicolor cv. TX430 leaf Sorg... 90 5e-17
      emb|AI897228|AI897228 EST266767 tomato ovary, TAMU Lycopersicon ... 90 5e-17
      emblAW688235|AW688235 NF005A07ST1F1000 Developing stem Medicago ... 89 1e-16
45
      emb|AW694992|AW694992 NF082D01ST1F1012 Developing stem Medicago ... 83 2e-16
      emb|AW432582|AW432582 sh76d03.yl Gm-c1015 Glycine max cDNA clone... 89 2e-16
      emb|AW399097|AW399097 EST309597 L. pennellii trichome, Cornell U... 69 2e-16
      emb|AI443128|AI443128 sa84f10.yl Gm-c1004 Glycine max cDNA clone... 81 2e-16
50
      emb|AI899284|AI899284 EST268727 tomato ovary, TAMU Lycopersicon ... 88 3e-16
      emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 88 4e-16
      emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 87 5e-16
      emb|AW033367|AW033367 EST276938 tomato callus, TAMU Lycopersicon... 87 5e-16
      emb|AV419297|AV419297 AV419297 Lotus japonicus young plants (two... 63 7e-16
55
      emb|AW689888|AW689888 NF025H09ST1F1000 Developing stem Medicago ... 86 1e-15
      emb|AA557055|AA557055 897 Loblolly pine N Pinus taeda cDNA clone... 86 1e-15
      emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 80 1e-15
      emb|AW399471|AW399471 EST309971 L. pennellii trichome, Cornell U... 55 1e-15
      gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 85 2e-15
60
      emb|AW164782|AW164782 se77g01.yl Gm-c1023 Glycine max cDNA clone... 85 2e-15
      emb|A67797|A67797 Sequence 2 from Patent WO9743427.
                                                                    85 2e-15
```

	·
5	emb AW929780 AW929780 EST354050 tomato flower buds 8 mm to pre-a 80 2e-15 emb AI730245 AI730245 BNLGHi6465 Six-day Cotton fiber Gossypium 64 2e-15 emb AW929854 AW929854 EST354124 tomato flower buds 8 mm to pre-a 80 3e-15 emb AV408986 AV408986 AV408986 Lotus japonicus young plants (two 84 5e-15 emb AW671867 AW671867 LG1_352_F06.b1_A002 Light Grown 1 (LG1) So 84 5e-15 emb AI488023 AI488023 EST246345 tomato ovary, TAMU Lycopersicon 84 5e-15
	emb AI488023 AI488023 EST246345 tomato ovary, TAMU Lycopersicon 84 5e-15 emb AI782076 AI782076 EST262955 tomato susceptible, Cornell Lyco 84 6e-15
10	emb AV428126 AV428126 AV428126 Lotus japonicus young plants (two 84 6e-15 emb AW695797 AW695797 NF098F06ST1F1058 Developing stem Medicago 84 6e-15 emb AW869870 AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti 66 9e-15 emb AI856215 AI856215 sb39c10.x1 Gm-c1014 Glycine max cDNA clone 83 9e-15 emb AW929189 AW929189 EST337977 tomato flower buds 8 mm to pre-a 83 9e-15
15	emb AW616567 AW616567 EST322978 L. hirsutum trichome, Cornell Un 83 9e-15 emb AW697060 AW697060 NF111H11ST1F1095 Developing stem Medicago 77 1e-14 emb X81369 TAAWJL218 T.aestivumn (subclone pAWJL218) AWJL218 gene. 83 1e-14 emb AI776963 AI776963 EST251989 tomato callus, TAMU Lycopersicon 83 1e-14 emb AW443205 AW443205 EST308135 tomato mixed elicitor, BTI Lycop 83 1e-14 emb AW696757 AW696757 NF110F02ST1F1025 Developing stem Medicago 83 1e-14
20	
25	Query= AF077407.30_at 14116_at /id_source genbank /description "gb aac26243.1 (af077407) contains similarity to sugar transporters (pfam: sugar_tr.hmm, score: 395.39) [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link
23	http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af077407 /ncgi http://www.ncgr.org/cgi-bin/ff?af077407 (1581 letters)
30	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
35	Score E
33	Sequences producing significant alignments: (bits) Value
40	emb AJ132224 LES132224 Lycopersicon esculentum mRNA for hexose t 819 0.0 emb AJ010942 LES010942 Lycopersicon esculentum mRNA for hexose t 815 0.0 gb L21753 SCFGLUTRAB Saccharum hybrid cultivar H65-7052 glucose 222 e-176 gb U38651 MTU38651 Medicago truncatula sugar tranporter mRNA, co 354 e-174 gb L08196 RCCSCP Ricinus communis (clone PST293) sugar carrier p 371 e-173
	emb Y09590 VVHEXTRAN V.vinifera mRNA for hexose transporter. 356 e-170 emb AF061106 AF061106 Petunia x hybrida putative monosaccharide 255 e-170
45	gb L08188 RCCHCP Ricinus communis (clone ST330) hexose carrier p 203 e-163 emb Z83829 PAMST1 P.abies mRNA for monosaccharide transporter Ms 211 e-154 emb Z93775 VFZ93775 V.faba mRNA for hexose transporter. 362 e-129 emb X66856 NTMST1 N.tabacum MST1 mRNA. 215 e-129
50	gb L08197 RCCSCPS Ricinus communis (clone PST9) sugar carrier pr 210 e-114
50	emb AI775535 AI775535 EST256635 tomato resistant, Cornell Lycope 401 e-111 gb L21752 SCFGLUTRAA Saccharum hybrid cultivar H65-7052 glucose 193 2e-99 emb AI775204 AI775204 EST256304 tomato resistant, Cornell Lycope 352 7e-98 emb AI772312 AI772312 EST253412 tomato resistant, Cornell Lycope 214 6e-82
55	emb AJ132225 LES132225 Lycopersicon esculentum mRNA for hexose t 188 5e-79 emb AF173655 AF173655 Beta vulgaris clone GTRTUNI glucose transp 156 1e-73 emb AJ001061 VVHEXOSET Vitis vinifera hexose transporter gene. 276 3e-73 emb AJ778344 AJ778344 EST259223 tomato susceptible, Cornell Lyco 259 1e-70
60	emb AV407522 AV407522 AV407522 Lotus japonicus young plants (two 253 2e-66 gb L31352 RCCHEX9HC Ricinus communis hexose carrier (Hex9) mRNA, 253 2e-66 emb AW684560 AW684560 NF018C12NR1F1000 Nodulated root Medicago t 208 9e-61 emb AI727659 AI727659 BNLGHi8536 Six-day Cotton fiber Gossypium 229 5e-59

emb|AW737777|AW737777 EST339204 tomato flower buds, anthesis, Co... 223 3e-57 emb|AI772048|AI772048 EST253148 tomato resistant, Cornell Lycope... 206 1e-55 emb|AI772049|AI772049 EST253149 tomato resistant, Cornell Lycope... 206 1e-55 emb|AJ132223|LES132223 Lycopersicon esculentum mRNA for hexose t... 196 2e-54 emb|AI774617|AI774617 EST255717 tomato resistant, Cornell Lycope... 188 4e-52 emb|AI776698|AI776698 EST257786 tomato resistant, Cornell Lycope... 191 8e-52 gb|BE020128|BE020128 sm41e08.y1 Gm-c1028 Glycine max cDNA clone ... 149 1e-51 emb|AW684408|AW684408 NF016F05NR1F1000 Nodulated root Medicago t... 204 2e-51 emb|AW596416|AW596416 sj12b09.y1 Gm-c1032 Glycine max cDNA clone... 197 2e-51 10 emblAW349933|AW349933 GM210006A20H11R Gm-r1021 Glycine max cDNA ... 189 2eemb|AI460634|AI460634 sa71d03.y1 Gm-c1004 Glycine max cDNA clone... 189 2e-49 emb|AJ248339|AJ248339 AJ248339 Medicago sativa subsp. x varia yo... 196 3e-49 emb|AW458444|AW458444 sh09c11.yl Gm-c1016 Glycine max cDNA clone... 190 6e-49 15 emb|AW705527|AW705527 sk61c02.yl Gm-c1016 Glycine max cDNA clone... 193 1e-48 emb|AA660304|AA660304 00173 MtRHE Medicago truncatula cDNA 5' si... 133 3e-48 emb|AW704934|AW704934 sk56d08.yl Gm-c1019 Glycine max cDNA clone... 188 7e-47 emb|AV412511|AV412511 AV412511 Lotus japonicus young plants (two... 188 1e-46 gb|BE021812|BE021812 sm62g03.yl Gm-c1028 Glycine max cDNA clone ... 187 2e-46 20 emb|AW691511|AW691511 NF045G06ST1F1000 Developing stem Medicago ... 125 3e-46 emb|AW720443|AW720443 LjNEST19b1r Lotus japonicus nodule library... 158 3e-46 emblAW737506|AW737506 EST338933 tomato flower buds, anthesis, Co... 169 2e-45 emb|AI731272|AI731272 BNLGHi9072 Six-day Cotton fiber Gossypium ... 172 3e-45 emblAW092826|AW092826 EST286006 tomato mixed elicitor, BTI Lycop... 173 6e-45 25 emb|AI730904|AI730904 BNLGHi8171 Six-day Cotton fiber Gossypium ... 156 2e-43 emb|AW737195|AW737195 EST338622 tomato flower buds, anthesis, Co... 173 3e-42 gb|L31353|RCCHEX10HC Ricinus communis hexose carrier (Hex10) mRN... 173 4e-42 emb|AW680072|AW680072 WS1 _3_B09.g1 _A002 Water-stressed 1 (WS1) S... 170 2e-41 emb|AI938772|AI938772 sb58g08.yl Gm-c1018 Glycine max cDNA clone... 104 3e-41 30 emb|AI930883|AI930883 sb43g12.yl Gm-c1015 Glycine max cDNA clone... 117 4e-38 gb|L08189|RCCSCPB Ricinus communis (clone PDG15) sugar carrier p... 158 1e-37 gb|L08191|RCCSCPD Ricinus communis (clone PDG19) sugar carrier p... 157 2e-37 emb|AW774154|AW774154 EST333237 KV3 Medicago truncatula cDNA clo... 153 4e-37 gb|L08194|RCCSCPG Ricinus communis (clone PDGK4) sugar carrier p... 155 6e-37 35 gb[U22525]KLU22525 Kluyveromyces lactis high affinity glucose tr... 109 3e-36 emb|AW234900|AW234900 sf20e02.yl Gm-c1028 Glycine max cDNA clone... 152 8e-36 emb|AW455278|AW455278 EST311938 tomato root during/after fruit s... 152 8e-36 emb|AW040775|AW040775 EST283639 tomato mixed elicitor, BTI Lycop... 141 2e-35 emb|X96876|SCCHRIVFY S.cerevisiae DNA of cosmid from chromosome ... 81 2e-35 40 emb|Z74186|SCYDL138W S.cerevisiae chromosome IV reading frame OR... 81 2e-35 gb|BE059128|BE059128 sn25f09.yl Gm-c1016 Glycine max cDNA clone ... 146 3e-35 emb|AW687897|AW687897 NF014F11RT1F1094 Developing root Medicago ... 124 3e-35 emb|AW185053|AW185053 se86b03.y1 Gm-c1023 Glycine max cDNA clone... 149 4e-35 gb|L08193|RCCSCPF Ricinus communis (clone PDG58) sugar carrier p... 149 7e-35 45 emb|AI780094|AI780094 EST260973 tomato susceptible, Cornell Lyco... 139 7e-35 emb|AF149282|AF149282 Phaseolus vulgaris clone pBHEX2 hexose car... 148 1e-34 emblAW756300|AW756300 sl18g04.yl Gm-c1036 Glycine max cDNA clone... 140 2e-33 emb|AF168773|AF168773 Betula pendula hexose transport protein (H... 141 1e-32 gb|L08195|RCCSCPH Ricinus communis (clone PDGB14) sugar carrier ... 141 1e-32 50 gb|BE126141|BE126141 DG1_66_B09.b1_A002 Dark Grown 1 (DG1) Sorgh... 114 2e-32 emb|AW395888|AW395888 sh07a07.yl Gm-c1016 Glycine max cDNA clone... 130 4e-32 gb|L08190|RCCSCPC Ricinus communis (clone PDG16) sugar carrier p... 139 6e-32 emb|AI729864|AI729864 BNLGHi5432 Six-day Cotton fiber Gossypium ... 124 1e-31 emblAF168772|AF168772 Betula pendula hexose transport protein (H... 137 2e-31 emblAW432874lAW432874 sh99b03.yl Gm-c1016 Glycine max cDNA clone... 130 5e-31 55 emb|AW756360|AW756360 sl19g10.yl Gm-c1036 Glycine max cDNA clone... 128 9e-29 gb|L08192|RCCSCPE Ricinus communis (clone PDG40) sugar carrier p... 128 1e-28 emb|AW830453|AW830453 sm27c06.yl Gm-c1028 Glycine max cDNA clone... 125 8e-28 emb|AW934681|AW934681 EST353573 tomato flower buds 0-3 mm, Corne... 79 1e-27 60 emb|AV407618|AV407618 AV407618 Lotus japonicus young plants (two... 78 2e-24 emb|AW875010|AW875010 00131 leafy spurge Lambda HybriZAP 2.1 two... 113 4e-24

emb|AI728506|AI728506 BNLGHi10921 Six-day Cotton fiber Gossypium... 98 1e-23 gb|T41488|T41488 EST057 Soybean, M Bhattacharyya Glycine max cDN... 102 3e-23 emb|AF215852|AF215852 Nicotiana tabacum hexose transporter (pGlc... 69 3e-23 emb|AW255075|AW255075 ML137 peppermint glandular trichome Mentha... 95 7e-23 emb|AV425362|AV425362 AV425362 Lotus japonicus young plants (two... 109 7e-23 gb[U43629]BVU43629 Beta vulgaris integral membrane protein mRNA,... 68 1e-22 emb|AF000952|AF000952 Prunus armeniaca putative sugar transporte... 68 2e-21 emb|AW677475|AW677475 DG1_7_H05.g1_A002 Dark Grown 1 (DG1) Sorgh... 104 2e-21 emblAF215851|AF215851 Spinacia oleracea hexose transporter mRNA,... 71 6e-21 10 emb|AW255633|AW255633 ML692 peppermint glandular trichome Mentha... 101 1e-20 emb|Z98530|SPAC4F8 S.pombe chromosome I cosmid c4F8. 89 7e-20 emb|X98622|SPITR1 S.pombe itr1 gene. 89 7e-20 emb|AW684920|AW684920 NF023B01NR1F1000 Nodulated root Medicago t... 96 7e-20 emblAI778758|AI778758 EST259637 tomato susceptible, Cornell Lyco... 89 1e-19 15 emb|AI778757|AI778757 EST259636 tomato susceptible, Cornell Lyco... 89 1e-19 gb|BE060390|BE060390 HVSMEg0012C22f Hordeum vulgare pre-anthesis... 99 1e-19

Query= AC002340.147_at 14609 at /id source genbank /description 20 gb|aac02748.1| (ac002340) putative cytochrome p450 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002340| /ncgi http://www.ncgr.org/cgi-bin/ff?ac002340 25 (1612 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

30 Searching......done

Score

Sequences producing significant alignments: (bits) Value 35 gb[M32885]AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 137 e-103 emb|X70981|SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 127 6e-99 emb|Y09423|NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... 136 8e-98 emb|X71654|SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. dbj|D14990|POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... 124 9e-95 40 emb[Y10489]GMC450CP1 G.max mRNA for putative cytochrome P450, cl... 90 1e-84 emb[X70982|SMCYPEG3 S.melongena CYP71A3 mRNA for P450 hydroxylase. 126 3e-74 emb|Y09424|NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... 154 3e-65 dbi|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 71 9e-63 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 71 9e-63 45 emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 126 3e-61 emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 103 1e-53 emb|Y09920|HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... 94 1e-50 emb[Y10098]HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 94 1e-50 emb|AF022459|AF022459 Glycine max cytochrome P450 monooxygenase ... 105 4e-50 50 emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 89 2e-49 emb|AF029858|AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... 139 3e-49 gb|U48434|SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... 117 2e-48 emb|AF166332|AF166332 Nicotiana tabacum cytochrome P450 gene, co... 114 4e-47 emb|AW223719|AW223719 EST300530 tomato fruit red ripe, TAMU Lyco... 88 4e-46 55 emb|Y10490|GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 104 6e-46 emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 88 2e-45 emb|AF122821|AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... 118 4e-45 emb|Z33875|CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. 88 7e-45 emb|AI897763|AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... 84 1e-44 60 emb|AW830233|AW830233 sm24f03.yl Gm-c1028 Glycine max cDNA clone... 139 5e-44

gb U48435 SCU48435 Solanum chacoense putative cytochrome P450 ge... 95 2e-43

	emb AF029857 AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C 127 2e-43
	emb X71657 SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 87 3e-43
	emb AJ249799 CAR249799 Cicer arietinum partial mRNA for cytochro 79 8e-43
	emb X96784 NTP450GEN N.tabacum cytochrome P-450 gene. 105 1e-42
5	emb AW034502 AW034502 EST278118 tomato callus, TAMU Lycopersicon 107 2e-42
-	emb AF124815 AF124815 Mentha spicata cytochrome p450 mRNA, compl 81 3e-42
٠.	emb AI484957 AI484957 EST243220 tomato ovary, TAMU Lycopersicon 84 4e-42
	gb/L24438/THLCYP450A Thlaspi arvense germline cytochrome P450 mR 94 7e-42
-	emb AF124816 AF124816 Mentha x piperita cytochrome p450 isoform 87 3e-41
10	emb AW774664 AW774664 EST333815 KV3 Medicago truncatula cDNA clo 102 6e-41
10	emb AW234222 AW234222 sf22f08.yl Gm-c1028 Glycine max cDNA clone 88 1e-40
	emb AF155332 AF155332 Petunia x hybrida flavonoid 3'-hydroxylase 112 6e-40
	emb AW394470 AW394470 sh05e04.yl Gm-c1016 Glycine max cDNA clone 89 1e-39
15	
13	dbj D14590 D14590 Campanula medium mRNA for flavonoid 3',5'-hydr 82 2e-39
	gb BE054146 BE054146 GA_Ea0034H12f Gossypium arboreum 7-10 dpa 72 3e-39
	emb AI727092 AI727092 BNLGHi7313 Six-day Cotton fiber Gossypium 87 4e-39
	emb AW223657 AW223657 EST300468 tomato fruit red ripe, TAMU Lyco 122 4e-39
20	emb AW255477 AW255477 ML502 perpermint glandular trichome Mentha 82 5e-39
20	emb AI779370 AI779370 EST260249 tomato susceptible, Cornell Lyco 91 6e-39
	emb AI488646 AI488646 EST246985 tomato ovary, TAMU Lycopersicon 79 7e-39
	emb Y10493 GMC450CP7 G.max mRNA for putative cytochrome P450, cl 114 1e-38
	emb AF022458 AF022458 Glycine max cytochrome P450 monooxygenase 92 3e-38
25	emb AF124817 AF124817 Mentha x piperita cytochrome p450 isoform 89 4e-38
25	emb AW132351 AW132351 se03a02.y1 Gm-c1013 Glycine max cDNA clone 159 5e-38
	emb AW832652 AW832652 sm15g02.y1 Gm-c1027 Glycine max cDNA clone 159 5e-38
	emb AF156976 AF156976 Gerbera hybrida flavone synthase II (CYP93 68 9e-38
	emb AF022460 AF022460 Glycine max cytochrome P450 monooxygenase 113 1e-37
20	emb AF014800 AF014800 Eschscholzia californica (S)-N-methylcocla 75 2e-37
30	emb AF014801 AF014801 Eschscholzia californica (S)-N-methylcocla 75 2e-37
	emb AI897760 AI897760 EST267203 tomato ovary, TAMU Lycopersicon 71 2e-37
	emb AF135485 AF135485 Glycine max cytochrome P450 monooxygenaseC 104 3e-37
	emb AI730111 AI730111 BNLGHi6162 Six-day Cotton fiber Gossypium 84 4e-37
35	emb AI726383 AI726383 BNLGHi5702 Six-day Cotton fiber Gossypium 84 4e-37
33	emb AI896171 AI896171 EST265614 tomato callus, TAMU Lycopersicon 89 7e-37
	emb AW256010 AW256010 MW364 peppermint glandular trichome Mentha 89 7e-37
	emb AW832315 AW832315 sm07e11.yl Gm-c1027 Glycine max cDNA clone 116 1e-36 emb AW705746 AW705746 sk51c10.yl Gm-c1019 Glycine max cDNA clone 154 2e-36
	emb AW442182 AW442182 EST311578 tomato fruit red ripe, TAMU Lyco 88 4e-36
40	emb AW680602 AW680602 WS1_6_C01.b1_A002 Water-stressed 1 (WS1) S 102 4e-36
40	emb AF000403 AF000403 Lotus japonicus putative cytochorome P450 113 5e-36
	A CANADA A A CANADA A CANADA A CANADA A CANADA A CANADA A CANADA A CANADA A CANADA A CANADA A CANADA A CANADA C
	emb AI938505 AI938505 sb46e03.yl Gm-c1015 Glycine max cDNA clone 94 2e-35 emb AI779369 AI779369 EST260248 tomato susceptible, Cornell Lyco 91 3e-35
	dbj D86351 D86351 Glycine max CYP93A2 mRNA for cytochrome P-450, 68 3e-35
45	emb[AW255799]AW255799 ML868 peppermint glandular trichome Mentha 68 8e-35
7.7	emb AW617225 AW617225 EST323636 L. hirsutum trichome, Cornell Un 138 3e-34
	emb AW278865 AW278865 sf99g03.yl Gm-c1019 Glycine max cDNA clone 147 3e-34
	emb AF188612 AF188612 Callistephus chinensis flavone synthase II 72 3e-34
	emb[X95342]NTHSR515 N.tabacum mRNA for HSR515 protein. 91 4e-34
50	emb AW728587 AW728587 GAEa0017C12 Gossypium arboreum 7-10 dpa 82 5e-34
50	emb AW728802 AW728802 GA_ Ea0028112 Gossypium arboreum 7-10 dpa 80 5e-34
	emb AW038994 AW038994 EST280967 tomato mixed elicitor, BTI Lycop 91 7e-34
	gb BE125733 BE125733 DG1_54_G12.g1_A002 Dark Grown 1 (DG1) Sorgh 145 1e-33
	emb AW923050 AW923050 DG1_48_G09.g1_A002 Dark Grown 1 (DG1) Sorg 91 1e-33
55	emb AJ010324 PAJ10324 Populus trichocarpa cv trichobel mRNA for 95 2e-33
	emb AF150881 AF150881 Lycopersicon esculentum x Lycopersicon per 100 2e-33 emb AF014802 AF014802 Eschscholzia californica (S)-N-methylcocla 86 3e-33
	emb AW349428 AW349428 GM210007A20E11R Gm-r1021 Glycine max cDNA 85 3e-33
60	emb AW459662 AW459662 sh90c05.y1 Gm-c1016 Glycine max cDNA clone 89 3e-33 emb AB032833 AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom 77 4e-33
50	emb AW688786 AW688786 NF011F03ST1F1000 Developing stem Medicago 129 4e-33
	omore in occopiative occopiation and the occupant and the occupant and

emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 83 6e-33 emb|AW255181|AW255181 ML169 peppermint glandular trichome Mentha... 142 6e-33 emb|AF191772|AF191772 Papaver somniferum (S)-N-methylcoclaurine ... 82 1e-32 emb|AI777331|AI777331 EST263739 tomato seed, TAMU Lycopersicon e... 86 1e-32 5 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 72 2e-32 emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 67 2e-32 emb|AW733734|AW733734 sk77e06.yl Gm-c1016 Glycine max cDNA clone... 70 2e-32 emb|AW832405|AW832405 sm09e01.yl Gm-c1027 Glycine max cDNA clone... 88 2e-32 emb|AW254778|AW254778 ML1061 peppermint glandular trichome Menth... 141 2e-32 10 emb|AW255299|AW255299 ML307 peppermint glandular trichome Mentha... 88 2e-32 emb|AF195801|AF195801 Medicago sativa isoflavone synthase 2 (ifs... 64 3e-32 emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 66 3e-32 Query= AC004165.66 at 14614 at /id source genbank /description gb|aac16958.1| (ac004165) putative glucosyltransferase [arabidopsis 15 thaliana] /blast score 0 /ec number /family glucosyltransferase /chip nova/gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004165| /ncgi http://www.ncgr.org/cgi-bin/ff?ac004165 20 (1368 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 25 Searching.....done Score E Sequences producing significant alignments: (bits) Value 30 emb|AW256802|AW256802 EST304939 KV2 Medicago truncatula cDNA clo... 112 5e-46 emb|AW268009|AW268009 EST306231 DSIR Medicago truncatula cDNA cl... 102 3e-39 emb|AF190634|AF190634 Nicotiana tabacum UDP-glucose:salicylic ac... 101 3e-37 emb|AB000623|AB000623 Nicotiana tabacum mRNA for glucosyl transf... 101 3e-36 emb|AB012116|AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 82 2e-34 35 emb[AB013598]AB013598 Verbena hybrida HGT8 mRNA for UDP-glucose:... 104 2e-34 emb|AW776132|AW776132 EST335197 DSIL Medicago truncatula cDNA cl... 99 3e-33 emb|AW459541|AW459541 sh42h03.y1 Gm-c1017 Glycine max cDNA clone... 98 2e-32 emb|AV408145|AV408145 AV408145 Lotus japonicus young plants (two... 85 2e-32 emb|AW216808|AW216808 EST295522 tomato callus, TAMU Lycopersicon... 101 3e-32 40 emb|AW398421|AW398421 EST298268 L. pennellii trichome, Cornell U... 84 6e-32 emb|AW349414|AW349414 GM210007A20D2R Gm-r1021 Glycine max cDNA 3... 97 1e-31 emb|AW035896|AW035896 EST282403 tomato callus, TAMU Lycopersicon... 100 1e-31 gb|BE022282|BE022282 sm72b01.yl Gm-c1028 Glycine max cDNA clone ... 102 4e-31 emb|AB013596|AB013596 Perilla frutescens PF3R4 mRNA for UDP-gluc... 93 7e-31 45 emb|AB013597|AB013597 Perilla frutescens PF3R6 mRNA for UDP-gluc... 93 1e-30 emb|AI771830|AI771830 EST252930 tomato ovary, TAMU Lycopersicon ... 93 1e-30 emb|AB027455|AB027455 Petunia x hybrida PH1 mRNA for anthocyanin... 89 6e-30 emb|AW459258|AW459258 sh22f07.yl Gm-c1016 Glycine max cDNA clone... 69 4e-29 emb|AW928895|AW928895 EST337683 tomato flower buds 8 mm to pre-a... 90 4e-29 50 emb|X85138|LETWI1 L.esculentum twi1 mRNA. 81 1e-28 emb|AB033758|AB033758 Citrus unshiu LGTase mRNA for limonoid UDP... 89 2e-28 emb[X72729]LEERT1B L.esculentum (ERT 1b) ripening-related mRNA. 87 9e-28 emblA62529|A62529 Sequence 34 from Patent WO9716559. 96 1e-27 emb|X77461|MECGT2 M.esculenta Crantz CGT2 mRNA for UTP-glucose g... 78 1e-27 55 emb|AQ580287|AQ580287 T135903b shotgun sub-library of BAC clone ... 93 1e-27 emb[X77460]MECGT4 M.esculenta Crantz CGT4 mRNA for UTP-glucose g... 84 2e-27 emb|AW621210|AW621210 EST312008 tomato root during/after fruit s... 98 4e-27 emb|AW036493|AW036493 EST282992 tomato seed, TAMU Lycopersicon e... 92 5e-27 emb|AW695243|AW695243 NF093A08ST1F1056 Developing stem Medicago ... 74 6e-27 60 emb|AQ368131|AQ368131 toxb0001H06r CUGI Tomato BAC Library Lycop... 84 7e-27 emb|AF199453|AF199453 Sorghum bicolor UDP-glucose glucosyltransf... 76 9e-27

	emb AI488782 AI488782 EST247121 tomato ovary, TAMU Lycopersicon 80 1e-26
	emb AI729108 AI729108 BNLGHi12670 Six-day Cotton fiber Gossypium 82 1e-26
	gb BE126076 BE126076 DG1_65_E03.g1_A002 Dark Grown 1 (DG1) Sorgh 106 1e-26
	dbj D85186 D85186 Gentiana triflora mRNA for UDP-glucose:flavono 86 3e-26
5	emb X77369 SMGT S.melongena GT mRNA for glycosyltransferase. 97 5e-26
	dbj E12713 E12713 Solanum melongena cDNA encoding flavonoid-3-gl 97 5e-26
	emb AW223197 AW223197 EST300008 tomato fruit red ripe, TAMU Lyco 79 6e-26
	emb AI485027 AI485027 EST243307 tomato ovary, TAMU Lycopersicon 84 6e-26
	emb AF127218 AF127218 Forsythia x intermedia flavonoid 3-O-gluco 95 1e-25
10	emb AF101972 AF101972 Phaseolus lunatus zeatin O-glucosyltransfe 87 2e-25
	emb X77462 MECGT5 M.esculenta Crantz CGT5 mRNA for UTP-glucose g 83 2e-25
	emb Y18871 DBE18871 Dorotheanthus bellidiformis mRNA for betanid 81 3e-25
	emb X15694 HVBRNZ1H Barley bronze 1 homologue for UDPglucose fla 80 5e-25
	emb AB027454 AB027454 Petunia x hybrida PGT8 mRNA for anthocyani 99 8e-25
15	emb AF116858 AF116858 Phaseolus vulgaris zeatin O-xylosyltransfe 84 8e-25
	emb AW573699 AW573699 EST316290 GVN Medicago truncatula cDNA clo 78 1e-24'
	emb AW442772 AW442772 EST307702 tomato mixed elicitor, BTI Lycop 84 1e-24
	emb AI898951 AI898951 EST268394 tomato ovary, TAMU Lycopersicon 83 1e-24
	emb AW040941 AW040941 EST283805 tomato mixed elicitor, BTI Lycop 83 1e-24
20	emb AW221893 AW221893 EST298704 tomato fruit red ripe, TAMU Lyco 84 2e-24
20	emb AW933199 AW933199 EST359042 tomato fruit mature green, TAMU 93 2e-24
	emb AW981156 AW981156 EST392350 DSIL Medicago truncatula cDNA cl 83 4e-24
	411
	Alberta table and a second and a second
25	
23	* i · m · m · m · m · m · m · m · m · m ·
	and the second state of th
30	emb AI780684 AI780684 EST261479 tomato susceptible, Cornell Lyco 79 2e-23
30	emb AI486974 AI486974 EST245296 tomato ovary, TAMU Lycopersicon 83 3e-23
	emb AI483783 AI483783 EST249654 tomato ovary, TAMU Lycopersicon 79 5e-23
	emb AW348549 AW348549 GM210002B12H12R Gm-r1021 Glycine max cDNA 82 5e-23
	emb AW649880 AW649880 EST328334 tomato germinating seedlings, TA 87 9e-23
35	emb AJ400861 CAR400861 Cicer arietinum partial mRNA for putative 80 1e-22
33	emb[X77463]MECGT6 M.esculenta Crantz CGT6 mRNA for UTP-glucose g 74 2e-22
	emb AI487582 AI487582 EST245904 tomato ovary, TAMU Lycopersicon 82 2e-22
	emb AW759836 AW759836 sl54f11.yl Gm-c1027 Glycine max cDNA clone 91 2e-22
	emb AW350921 AW350921 GM210010B10C8R Gm-r1021 Glycine max cDNA 3 82 3e-22
40	emb AF165148 AF165148 Petunia x hybrida UDP-galactose:flavonol 3 86 4e-22
40	emb AW394450 AW394450 sh05d10.yl Gm-c1016 Glycine max cDNA clone 75 8e-22
	emb AB009370 AB009370 Vigna mungo UF3GaT mRNA for flavonoid 3-O 80 1e-21
	emb AF000372 AF000372 Vitis vinifera UDP glucose:flavonoid 3-o-g 85 1e-21
	emb AF000371 AF000371 Vitis vinifera UDP glucose:flavonoid 3-o-g 85 1e-21
45	emb X77464 MECGT7 M.esculenta Crantz CGT7 mRNA for UTP-glucose g 88 1e-21
45	emb AB012114 AB012114 Vigna mungo UFGlyT mRNA for UDP-glycose:fl 73 2e-21
	emb AI894979 AI894979 EST264422 tomato callus, TAMU Lycopersicon 74 4e-21
	emb AW650189 AW650189 EST328643 tomato germinating seedlings, TA 90 5e-21
	emb AW127679 AW127679 M110425 DSLC Medicago truncatula cDNA clon 102 7e-21
50	gb U82367 STU82367 Solanum tuberosum UDP-glucose glucosyltransfe 73 9e-21
50	emb AW650188 AW650188 EST328642 tomato germinating seedlings, TA 89 9e-21
	emb AW617410 AW617410 EST323821 L. hirsutum trichome, Cornell Un 81 1e-20
	emb AF006081 AF006081 Solanum berthaultii UDPG glucosyltransfera 69 3e-20
	emb AI487484 AI487484 EST245806 tomato ovary, TAMU Lycopersicon 74 3e-20
	emb AW776615 AW776615 EST335680 DSIL Medicago truncatula cDNA cl 100 4e-20
55	emb AW687523 AW687523 NF010E07RT1F1054 Developing root Medicago 100 4e-20
	emb AI489089 AI489089 EST247428 tomato ovary, TAMU Lycopersicon 84 6e-20
	emb AW317745 AW317745 sg56g04.y1 Gm-c1007 Glycine max cDNA clone 57 8e-20
	emb AI780671 AI780671 EST261466 tomato susceptible, Cornell Lyco 62 1e-19
	emb AW092049 AW092049 EST285325 tomato mixed elicitor, BTI Lycop 88 4e-19
60	gb BE055475 BE055475 GA_Ea0035I12f Gossypium arboreum 7-10 dpa 69 5e-19
	emb AF117267 AF117267 Malus domestica UDP glucose:flavonoid 3-O 80 7e-19
	-

emb|AW781424|AW781424 s178a07.y1 Gm-c1037 Glycine max cDNA clone... 95 9e-19

emb|Z25802|PHUDPRHAX P.hybrida mRNA for UDP rhamnose: anthocyani... 68 9e-19 emb|AI967768|AI967768 Ljirnpest11-882-f3 Ljirnp Lambda HybriZap ... 95 1e-18 emb|AB002818|AB002818 Perilla frutescens mRNA for flavonoid 3-O-... 90 1e-18 5 emblAB012115|AB012115 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 89 1e-18 emb|AI485737|AI485737 EST244058 tomato ovary, TAMU Lycopersicon ... 71 2e-18 emb|AW677595|AW677595 DG1 8 E07.g1 A002 Dark Grown 1 (DG1) Sorgh... 94 2e-18 10 Query= AL021961.3 at 15042 at /id source genbank /description emb|caa17549.1| (al021961) cinnamyl alcohol dehydrogenase - like protein [arabidopsis thaliana] /blast score 1.00e-167 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbin-15 post/entrez/query?db=n&form=6&dopt=g&uid=gb|a1021961| /ncgi http://www.ncgr.org/cgi-bin/ff?al021961 (1074 letters) Database: plantfungal 20 661,018 sequences; 426,114,510 total letters Searching......done Score E 25 Sequences producing significant alignments: (bits) Value dbj|D13991|AAICAD A. cordata mRNA for cinnamyl alcohol dehydroge... 279 e-152 emb[X62343]NTCAD14MR N.tabacum CAD14 mRNA for cinnamyl alcohol d... 314 e-150 emb|Z19568|PDCIALDHA P.deltoides encoding cinnamyl alcohol dehyd... 310 e-146 30 emb|A24083|A24083 pPOPCAD1 cinnamyl alcohol dehydrogenase cDNA. emb|AF217957|AF217957 Populus tremuloides cinnamyl alcohol dehyd... 309 e-145 emb[X62344]NTCAD19MR N.tabacum CAD19 mRNA for cinnamyl alcohol d... 302 e-145 emblAF038561|AF038561 Eucalyptus globulus cinnamyl alcohol dehyd... 318 e-141 emb|X65631|EGCADMR E.gunnii mRNA cad for cinnamyl alcohol dehydr... 319 e-141 35 emb|A24084|A24084 pEUCAD1 cinnamyl alcohol dehydrogenase cDNA. 319 e-141 emb|AF083332|AF083332 Medicago sativa cinnamyl-alcohol dehydroge... 326 e-140 emb|Z19573|MSCIALDHA M.sativa encoding cinnamyl alcohol dehydrog... 325 e-140 emb|AJ231135|SOF231135 Saccharum officinarum mRNA for cinnamyl a... 384 e-134 emb|AF010290|AF010290 Lolium perenne cinnamyl alcohol dehydrogen... 262 e-133 40 emb[X72675]PACINALDA P.abies mRNA for cinnamyl alcohol dehydroge... 240 e-124 dbj|D86590|D86590 Zinnia elegans mRNA for cinnamyl alcohol dehyd... 264 e-123 gb|U62394|PRU62394 Pinus radiata cinnamyl alcohol dehydrogenase ... 242 e-122 emb|Z37992|PTCADBMR P.taeda mRNA for cinnamyl alcohol dehydrogen... 237 e-121 emb|Z37991|PTCADAMR P.taeda mRNA for cinnamyl alcohol dehydrogen... 237 e-121 45 gb|U63534|FXU63534 Fragaria x ananassa cinnamyl alcohol dehydrog... 251 9e-89 emb|AF083333|AF083333 Medicago sativa cinnamyl-alcohol dehydroge... 225 5e-84 gb|L36823|SSNCAD1A Stylosanthes humilis cinnamyl alcohol dehydro... 226 9e-84 gb|U24561|AGU24561 Apium graveolens mannitol dehydrogenase (Mtd)... 237 3e-79 emb|X67817|PCELI3 P.crispum mRNA for Eli3. 240 3e-77 50 emb|X92855|LEMTD L.esculentum exon 1 of MTD gene. 130 6e-77 emb|AW255506|AW255506 ML532 peppermint glandular trichome Mentha... 275 6e-73 emb|AI487388|AI487388 EST245710 tomato ovary, TAMU Lycopersicon ... 274 8e-73 emb|AF207552|AF207552 Brassica napus cinnamyl alcohol dehydrogen... 155 2e-72 emb|AF207553|AF207553 Brassica napus cinnamyl alcohol dehydrogen... 156 5e-72 emblAF207555|AF207555 Brassica rapa cinnamyl alcohol dehydrogena... 155 1e-71 55 emb|AF207554|AF207554 Brassica oleracea cinnamyl alcohol dehydro... 156 1e-71 emb|X92754|HVCADMRNA H.vulgare mRNA for cinnamyl alcohol dehydro... 270 2e-71 emb|AI489728|AI489728 EST248067 tomato ovary, TAMU Lycopersicon ... 269 3e-71 emb|AW830216|AW830216 sm24b12.yl Gm-c1028 Glycine max cDNA clone... 264 6e-70 emb|AW350274|AW350274 GM210007B20B7R Gm-r1021 Glycine max cDNA 3... 262 1e-69 60 gb|U79770|MCU79770 Mesembryanthemum crystallinum cinnamyl-alcoho... 255 4e-69

emb|AW031628|AW031628 EST275082 tomato callus, TAMU Lycopersicon... 182 7e-69 gb|BE021646|BE021646 sm60f08.yl Gm-c1028 Glycine max cDNA clone ... 259 4e-68 gb|BE123932|BE123932 EST394057 DSIL Medicago truncatula cDNA clo... 185 7e-65 emb|AW560160|AW560160 EST315208 DSIR Medicago truncatula cDNA cl... 169 3e-64 5 emb|AW684815|AW684815 NF021D07NR1F1000 Nodulated root Medicago t... 230 le-62 emb|AI162401|AI162401 A017P09U Hybrid aspen plasmid library Popu... 178 5e-62 emb|AI900147|AI900147 sc01e08.yl Gm-c1012 Glycine max cDNA clone... 142 2e-61 emb|AW101492|AW101492 sd78h08.yl Gm-c1009 Glycine max cDNA clone... 176 3e-61 emb|AW568106|AW568106 si68e05.yl Gm-r1030 Glycine max cDNA clone... 136 3e-59 10 emblAF146691|AF146691 Lycopersicon esculentum cultivar Rio Grand... 194 1e-58 emb|AI443116|AI443116 sa84e07.yl Gm-c1004 Glycine max cDNA clone... 170 1e-54 emb|AJ001925|PAAJ1925 Picea abies cad7 gene. 115 le-53 emb|AJ001926|PAAJ1926 Picea abies cad8 gene. 115 1e-53 emb|AJ001924|PAAJ1924 Picea abies cad2 gene. 114 le-53 15 emb|AI488134|AI488134 EST246456 tomato ovary, TAMU Lycopersicon ... 210 2e-53 emb|AW981164|AW981164 EST392358 DSIL Medicago truncatula cDNA cl... 133 3e-53 emb|AI965672|AI965672 sc76g06.yl Gm-c1018 Glycine max cDNA clone... 209 4e-53 emb|AW981208|AW981208 EST392298 DSIL Medicago truncatula cDNA cl... 149 3e-52 emb|AW692803|AW692803 NF059G11ST1F1087 Developing stem Medicago ... 125 4e-52 20 gb|BE123743|BE123743 NXNV 153 E12 F Nsf Xylem Normal wood Vertic... 187 4e-49 emb|AL121862|LMFL1063 Leishmania major Friedlin chromosome 23 co... 73 8e-48 emb|AF109157|AF109157 Eucalyptus globulus cinnamyl alcohol dehyd... 138 2e-46 emb|X75480|EGCAD E.gunnii CAD gene. 139 3e-46 dbj|D16624|EGCCAD Eucalyptus botryoides DNA for cinnamyl alcohol... 138 2e-45 25 emb|AW775567|AW775567 EST334632 DSIL Medicago truncatula cDNA cl... 105 7e-45 gb|L36456|SSNCAD3 Stylosanthes humilis cinnamyl alcohol dehydrog... 134 le-44. emb|AW706922|AW706922 sk08c02.y1 Gm-c1023 Glycine max cDNA clone... 113 1e-43 gb|BE123884|BE123884 EST394009 DSIL Medicago truncatula cDNA clo... 110 2e-43 emb[AW201173]AW201173 se98g05.yl Gm-c1027 Glycine max cDNA clone... 135 3e-43 30 emb|AI729035|AI729035 BNLGHi12406 Six-day Cotton fiber Gossypium... 174 9e-43 emb|AW666266|AW666266 sk34e03.y1 Gm-c1028 Glycine max cDNA clone... 108 2e-42 emb|AW218543|AW218543 EST303726 tomato radicle, 5 d post-imbibit... 88 6e-42 emb|AW100321|AW100321 sd23a02.yl Gm-c1012 Glycine max cDNA clone... 130 2e-41 emb|AI727983|AI727983 BNLGHi9898 Six-day Cotton fiber Gossypium ... 95 2e-40 35 emb|AV412798|AV412798 AV412798 Lotus japonicus young plants (two... 137 6e-40 emblAI731536|AI731536 BNLGHi9665 Six-day Cotton fiber Gossypium ... 94 8e-40 emb|AW775594|AW775594 EST334659 DSIL Medicago truncatula cDNA cl... 98 8e-40 emb|AI726959|AI726959 BNLGHi6955 Six-day Cotton fiber Gossypium ... 93 4e-39 gb|BE124304|BE124304 EST394429 DSIL Medicago truncatula cDNA clo... 94 7e-39 emb|AW776649|AW776649 EST335714 DSIL Medicago truncatula cDNA cl... 94 1e-38 40 emb|AI728121|AI728121 BNLGHi9734 Six-day Cotton fiber Gossypium ... 93 2e-38 emb|AF060491|AF060491 Pinus radiata cinnamyl alcohol dehydrogena... 118 2e-38 gb|BE036055|BE036055 MO19B09 MO Mesembryanthemum crystallinum cD... 81 4e-38 emb|AI161452|AI161452 A001P14U Hybrid aspen plasmid library Popu... 125 7e-38 45 emb|AW648829|AW648829 EST327283 tomato germinating seedlings, TA... 89 3e-37 gb|BE124289|BE124289 EST394414 DSIL Medicago truncatula cDNA clo... 154 1e-36 emb|AW348888|AW348888 GM210010A10H2R Gm-r1021 Glycine max cDNA 3... 154 1e-36 emb|AI496395|AI496395 sb04b10.y1 Gm-c1004 Glycine max cDNA clone... 154 1e-36 50 emb|AW684143|AW684143 NF012H08NR1F1000 Nodulated root Medicago t... 121 3e-36 emblAI899871|AI899871 sb94e03.y1 Gm-c1017 Glycine max cDNA clone... 100 3e-36 emb|AW650552|AW650552 EST329006 tomato germinating seedlings, TA... 148 4e-36 emb|AW928461|AW928461 EST337249 tomato flower buds 8 mm to pre-a... 89 3e-34 emb|AV417794|AV417794 AV417794 Lotus japonicus young plants (two... 140 1e-32 emb|AF067082|AF067082 Apium graveolens mannitol dehydrogenase (M... 127 9e-32 emb|AW234172|AW234172 sf22a12.yl Gm-c1028 Glycine max cDNA clone... 134 1e-30 emb|AI165779|AI165779 A091p26u Hybrid aspen plasmid library Popu... 94 2e-30 emblAW686753|AW686753 NF042C07NR1F1000 Nodulated root Medicago t... 93 2e-30 emb|AW256719|AW256719 EST304856 KV2 Medicago truncatula cDNA clo... 78 3e-30 60 emb|AW625821|AW625821 EST319728 tomato radicle, 5 d post-imbibit... 132 4e-30 emb|AI166747|AI166747 xylem.est.549 Poplar xylem Lambda ZAPII li... 94 5e-30

emb|AW218822|AW218822 EST301302 tomato root during/after fruit s... 84 2e-29

emb|AI960981|AI960981 sc93e08.y1 Gm-c1019 Glycine max cDNA clone... 85 4e-29 emb|AW617779|AW617779 EST324178 L. hirsutum trichome, Cornell Un... 89 1e-28 emb|AI165405|AI165405 A083p34u Hybrid aspen plasmid library Popu... 127 1e-28 5 emb|AW648072|AW648072 EST326526 tomato germinating seedlings, TA... 79 2e-27 Query= AL078637.213 s at 15523 s at /id source genbank /description emb|cab45071.1| (al078637) putative protein [arabidopsis thaliana] 10 /blast_score 8.00e-48 /ec_number /family /chip nova /gb_link /ncgi (336 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 15 Searching......done Score Ε Sequences producing significant alignments: (bits) Value 20 emb|AW394463|AW394463 sh32h06.yl Gm-c1017 Glycine max cDNA clone... 80 1e-17 gb|BE023782|BE023782 sm92d02.yl Gm-c1015 Glycine max cDNA clone ... 73 2e-15 emb|AW395908|AW395908 sh07c05.yl Gm-c1016 Glycine max cDNA clone... 80 7e-15 emb|AW733452|AW733452 sk73g05.y1 Gm-c1016 Glycine max cDNA clone... 77 4e-14 25 gb|BE058639|BE058639 sn18g09.y1 Gm-c1016 Glycine max cDNA clone ... 77 6e-14 emblAW156195|AW156195 se20g08.y1 Gm-c1015 Glycine max cDNA clone... 76 1e-13 emblAW563817|AW563817 LG1_261_C02.g1_A002 Light Grown 1 (LG1) So... 76 1e-13 emb|AW677327|AW677327 DG1_5_D03.g1_A002 Dark Grown 1 (DG1) Sorgh... 76 1e-13 emb|AW424028|AW424028 sh59f09.y1 Gm-c1015 Glycine max cDNA clone... 62 1e-12 30 gb|BE022753|BE022753 sm88a02.yl Gm-c1015 Glycine max cDNA clone ... 62 2e-12 emb|AW677332|AW677332 DG1_5 F03.g1 A002 Dark Grown 1 (DG1) Sorgh... 71 3e-12 gb|BE035944|BE035944 MO22E07 MO Mesembryanthemum crystallinum cD... 69 1e-11 emb|AW119934|AW119934 sd54g12.y1 Gm-c1016 Glycine max cDNA clone... 55 3e-10 gb|L20233|POPVEGSTRA P.trichocarpa x P.deltoides vegetative stor... 64 4e-10 35 emb|AW119941|AW119941 sd54h12.y1 Gm-c1016 Glycine max cDNA clone... 47 4e-08 emb|AW092074|AW092074 EST285350 tomato mixed elicitor, BTI Lycop... 57 4e-08 emb|AW127599|AW127599 M110330 DSLC Medicago truncatula cDNA clon... 43 5e-07 emb|AI822191|AI822191 L0-668T3 Ice plant Lambda Uni-Zap XR expre... 52 6e-07 gb|BE035204|BE035204 MO02A04 MO Mesembryanthemum crystallinum cD... 51 2e-06 40 gb|BE035225|BE035225 MO02E03 MO Mesembryanthemum crystallinum cD... 51 2e-06 gb|BE036341|BE036341 MO23E06 MO Mesembryanthemum crystallinum cD... 51 2e-06 gb|BE037208|BE037208 MP18A03 MP Mesembryanthemum crystallinum cD... 51 2e-06 gb|BE037538|BE037538 MP19G11 MP Mesembryanthemum crystallinum cD... 48 9e-06 gb|BE034872|BE034872 ML05E09 ML Mesembryanthemum crystallinum cD... 45 2e-04 45 emb|AW458345|AW458345 sh86h01.yl Gm-c1016 Glycine max cDNA clone... 31 9e-04 emb|AU036852|AU036852 AU036852 Cryptomeria japonica seedling lea... 41 0.003 gb|S59422|S59422 Populus x canadensis major storage protein mRNA... 41 0.003 gb|M77504|POPBSP Populus deltoides bark storage protein mRNA, co... 41 0.003 emb|AC000133|ENAC000133 Emericella nidulans cosmid SW06E08, comp... 33 0.77 50 emb|AW287856|AW287856 N100699e rootphos(-) Medicago truncatula c... 31 1.0 emb|AQ851083|AQ851083 LMAJFV1 lm38d08,y1 Leishmania major FV1 ra... 33 1.1 emb|AW329091|AW329091 N200297e rootphos(-) Medicago truncatula c... 31 1.2 emb|AW329193|AW329193 N200405e rootphos(-) Medicago truncatula c... 31 1.3 emb|AQ398028|AQ398028 mgxb0017N12f CUGI Rice Blast BAC Library P... 32 1.4 55 emb|AI068626|AI068626 mgae0003cD01f Magnaporthe grisea Appressor... 32 1.4 emb|AW981194|AW981194 EST392388 DSIL Medicago truncatula cDNA cl... 31 1.5 emb|AW695905|AW695905 NF100E05ST1F1038 Developing stem Medicago ... 31 1.5 dbj|D50414|D50414 Cannabis sativa male-associated DNA sequence. 29 1.7 emb|X70064|PDBSPA P.deltoides gene for poplar bark storage protein. 32 2.0 60 emb|Z64354|SPAC23D3 S.pombe chromosome I cosmid c23D3. 32 2.0 emb|X83853|NTPAR1A N.tabacum mRNA for PAR-1a. 32 2.0

	emb AW268020 AW268020 EST306242 DSIR Medicago truncatula cDNA cl 32 2.0 emb AA550547 AA550547 1710m3 gmbPfHB3.1, G. Roman Reddy Plasmodi 32 2.0 emb AL078627 SPBC365 S.pombe chromosome II cosmid c365. 31 2.7
5	gb[U05613 CBU05613 Crepidomanes birmanicum chloroplast large sub 31 3.7
3	emb AI050216 AI050216 TENU1464 T. cruzi epimastigote normalized 31 3.7
	emb AI065375 AI065375 TENU2262 T. cruzi epimastigote normalized 31 3.7 emb AI065371 AI065371 TENU2258 T. cruzi epimastigote normalized 31 3.7
	emb AT000167 AT000167 AT000167 Apple young fruit cDNA library Ma 29 4.0
	emb AJ388714 AJ388714 AJ388714 Medicago truncatula R108 Medicago 29 4.3
10	emb AQ361816 AQ361816 mgxb0005A07f CUGI Rice Blast BAC Library P 30 5.1
	emb AQ162953 AQ162953 mgxb0021G21r CUGI Rice Blast BAC Library P 30 5.1
	emb Z67998 SPAC1F7 S.pombe chromosome I cosmid c1F7. 30 5.1
	emb AF148676 AF148676 Zizaniopsis villanensis maturase (matK) ge 30 7.1
	emb AW684956 AW684956 NF023E05NR1F1000 Nodulated root Medicago t 30 7.1
15	emb AZ216404 AZ216404 Sheared DNA-121G9.TF Sheared DNA Trypanoso 30 7.1
,	emb AQ942697 AQ942697 Sheared DNA-42J8.TR Sheared DNA Trypanosom 30 7.1
	emb AI163063 AI163063 A031p30u Hybrid aspen plasmid library Popu 30 7.1
	gb BE058445 BE058445 sn16b09.yl Gm-c1016 Glycine max cDNA clone 30 7.1
• •	gb BE023592 BE023592 sm82e07.yl Gm-c1015 Glycine max cDNA clone 30 7.1
20	emb AZ220034 AZ220034 Sheared DNA-63D11.TR Sheared DNA Trypanoso 30 7.1
	emb AII10319 AII10319 TENU3289 T. cruzi epimastigote normalized 30 7.1
	emb AW870077 AW870077 NXNV_123_G11_F Nsf Xylem Normal wood Verti 30 7.1
	emb AI057841 AI057841 TENU1932 T. cruzi epimastigote normalized 30 7.1
25	emb X83851 NTPAR1B N.tabacum mRNA for PAR-1b. 30 7.1
23	gb M18538 POPPOP3A Populus balsamifera subsp. trichocarpa X Popu 30 7.1
	emb AW203632 AW203632 sf36d11.y1 Gm-c1028 Glycine max cDNA clone 30 7.1
	emb AQ640232 AQ640232 927P1-18B11.TV 927P1 Trypanosoma brucei ge 30 7.1 emb AI779122 AI779122 EST260001 tomato susceptible, Cornell Lyco 27 8.3
	emb AW096641 AW096641 EST289821 tomato mixed elicitor, BTI Lycop 27 8.9
30	gb[N98085]N98085 2245C3 czapPFDd2.1, Debopam Chakrabarti Plasmod 29 9.7
	emb AW929160 AW929160 EST337948 tomato flower buds 8 mm to pre-a 29 9.7
	emb AW037807 AW037807 EST279436 tomato mixed elicitor, BTI Lycop 29 9.7
	emb AW729409 AW729409 GA Ea0024O24 Gossypium arboreum 7-10 dpa 29 9.7
	emb AF193903 AF193903 Cafeteria roenbergensis mitochondrial DNA, 29 9.7
35	
	Query= AL078637.191 r at 15532 r at /id_source genbank /description
	emb cab45069.1 (al078637) putative protein [arabidopsis thaliana]
40	/blast score 0 /ec_number /family /chip nova /gb_link
1 U	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb al078637 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al078637
	(990 letters)
•	(222 1511110)
45	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
50	
ou	Score E
,	Sequences producing significant alignments: (bits) Value
	emb AW092074 AW092074 EST285350 tomato mixed elicitor, BTI Lycop 145 1e-69
	emb A1778762 A1778762 EST259641 tomato susceptible, Cornell Lyco 149 1e-49
55	gb BE035944 BE035944 MO22E07 MO Mesembryanthemum crystallinum cD 120 9e-49
	emb AW618184 AW618184 EST314234 L. pennellii trichome, Cornell U 138 2e-46
	emb AI778761 AI778761 EST259640 tomato susceptible, Cornell Lyco 133 6e-45
	emb AW618179 AW618179 EST314229 L. pennellii trichome, Cornell U 114 3e-39
	gb S59422 S59422 Populus x canadensis major storage protein mRNA 99 6e-32
50	gb M77504 POPBSP Populus deltoides bark storage protein mRNA, co 99 3e-30
	emb AW395908 AW395908 sh07c05.yl Gm-c1016 Glycine max cDNA clone 125 5e-28
	•

emb|AW733452|AW733452 sk73g05.y1 Gm-c1016 Glycine max cDNA clone... 122 3e-27 gb|BE058639|BE058639 sn18g09.y1 Gm-c1016 Glycine max cDNA clone ... 122 4e-27 emb|AW394463|AW394463 sh32h06.y1 Gm-c1017 Glycine max cDNA clone... 111 4e-26 emb|AW563817|AW563817 LG1 261 C02.g1 A002 Light Grown 1 (LG1) So... 104 4e-25 5 emblAI822191|AI822191 LO-668T3 Ice plant Lambda Uni-Zap XR expre... 114 1e-24 gb|BE036341|BE036341 MO23E06 MO Mesembryanthemum crystallinum cD... 112 3e-24 gb|BE035204|BE035204 MO02A04 MO Mesembryanthemum crystallinum cD... 112 3e-24 gb|BE037538|BE037538 MP19G11 MP Mesembryanthemum crystallinum cD... 112 3e-24 gb|BE035225|BE035225 MO02E03 MO Mesembryanthemum crystallinum cD... 112 3e-24 10 gb|BE059090|BE059090 sn25b08.y1 Gm-c1016 Glycine max cDNA clone ... 75 2e-23 emb|AW395168|AW395168 sh40g07.yl Gm-c1017 Glycine max cDNA clone... 68 3e-21 gb|BE037512|BE037512 MP04B06 MP Mesembryanthemum crystallinum cD... 95 4e-20 emb|AW623629|AW623629 EST321574 tomato flower buds 3-8 mm, Corne... 92 3e-19 emb|AW625587|AW625587 EST319494 tomato radicle, 5 d post-imbibit... 92 3e-19 15 emb|AW929488|AW929488 EST338276 tomato flower buds 8 mm to pre-a... 92 3e-19 emb|AI778197|AI778197 EST259076 tomato susceptible, Cornell Lyco... 92 3e-19 emb|AW648720|AW648720 EST327090 tomato germinating seedlings, TA... 92 3e-19 emb|AW625287|AW625287 EST319290 tomato radicle, 5 d post-imbibit... 92 3e-19 emb|AW648718|AW648718 EST327088 tomato germinating seedlings, TA... 92 3e-19 20 emb|AW928879|AW928879 EST337667 tomato flower buds 8 mm to pre-a... 92 3e-19 gb|L20233|POPVEGSTRA P.trichocarpa x P.deltoides vegetative stor... 94 2e-18 emb|AW733620|AW733620 sk75h08.y1 Gm-c1016 Glycine max cDNA clone... 86 3e-18 emb|AW677327|AW677327 DG1 5 D03.gl A002 Dark Grown 1 (DG1) Sorgh... 93 4e-18 emb|AI163910|AI163910 A051P26U Hybrid aspen plasmid library Popu... 56 1e-17 25 emb|AW156195|AW156195 se20g08.yl Gm-c1015 Glycine max cDNA clone... 90 2e-17 emb|AW775932|AW775932 EST334997 DSIL Medicago truncatula cDNA cl... 84 2e-17 emb|AW692820|AW692820 NF056A09ST1F1000 Developing stem Medicago ... 84 2e-17 emb|AW685340|AW685340 NF027C09NR1F1000 Nodulated root Medicago t... 83 4e-17 emblAW684469|AW684469 NF017C09NR1F1000 Nodulated root Medicago t... 75 1e-16 30 gb|BE037208|BE037208 MP18A03 MP Mesembryanthemum crystallinum cD... 84 2e-15 gb|BE023782|BE023782 sm92d02.y1 Gm-c1015 Glycine max cDNA clone ... 72 4e-14 gb|BE036234|BE036234 MO21C12 MO Mesembryanthemum crystallinum cD... 78 1e-13 emb|AW286123|AW286123 LG1_261_F11.b1 A002 Light Grown 1 (LG1) So... 64 5e-13 emb|AW626069|AW626069 EST319976 tomato radicle, 5 d post-imbibit... 69 1e-12 35 gb|BE095283|BE095283 00344 leafy spurge Lambda HybriZAP 2.1 two-... 62 1e-12 emb|AW677160|AW677160 DG1_5 D03.b1 A002 Dark Grown 1 (DG1) Sorgh... 62 2e-12 emb|AW677332|AW677332 DG1 5 F03.g1 A002 Dark Grown 1 (DG1) Sorgh... 70 2e-11 gb|BE022753|BE022753 sm88a02.y1 Gm-c1015 Glycine max cDNA clone ... 61 5e-11 emb|AW424028|AW424028 sh59f09.yl Gm-c1015 Glycine max cDNA clone... 62 8e-11 40 emb[X70064]PDBSPA P.deltoides gene for poplar bark storage protein. 63 3e-09 emb|AW119934|AW119934 sd54g12.yl Gm-c1016 Glycine max cDNA clone... 54 4e-09 emb|AW677125|AW677125 DG1_5_F03.b1_A002 Dark Grown 1 (DG1) Sorgh... 43 5e-07 gb|BE058421|BE058421 sn15h03.yl Gm-c1016 Glycine max cDNA clone ... 56 6e-07 emb|AW119941|AW119941 sd54h12.y1 Gm-c1016 Glycine max cDNA clone... 46 1e-06 45 gb|BE037054|BE037054 MP13H01 MP Mesembryanthemum crystallinum cD... 55 1e-06 gb|BE036004|BE036004 MO17H11 MO Mesembryanthemum crystallinum cD... 51 1e-06 gb|BE035382|BE035382 MO03G01 MO Mesembryanthemum crystallinum cD... 54 2e-06 emb[AW127599]AW127599 M110330 DSLC Medicago truncatula cDNA clon... 44 3e-06 gb|BE095282|BE095282 00343 leafy spurge Lambda HybriZAP 2.1 two-... 52 5e-06 50 emb|AW287592|AW287592 LG1_244_A09.b1_A002 Light Grown 1 (LG1) So... 40 6e-06 emb|AA557101|AA557101 943 Loblolly pine N Pinus taeda cDNA clone... 47 2e-04 gb|BE037091|BE037091 MP14F10 MP Mesembryanthemum crystallinum cD... 47 2e-04 gblM25340|POPCHIC Populus sp. chitinase mRNA fragment, clone 4. 46 6e-04 gb|BE036753|BE036753 MP04H07 MP Mesembryanthemum crystallinum cD... 46 6e-04 55 gb|BE037437|BE037437 MP21A08 MP Mesembryanthemum crystallinum cD... 34 8e-04 gb|BE037490|BE037490 MP21G12 MP Mesembryanthemum crystallinum cD... 45 9e-04 emb|AU036852|AU036852 AU036852 Cryptomeria japonica seedling lea... 41 0.015 emb|AA556425|AA556425 280 Loblolly pine C Pinus taeda cDNA clone... 41 0.015 gb|BE036626|BE036626 MP02H12 MP Mesembryanthemum crystallinum cD... 40 0.021 60 emb|AW458345|AW458345 sh86h01.yl Gm-c1016 Glycine max cDNA clone... 30 0.052 gb|BE034872|BE034872 ML05E09 ML Mesembryanthemum crystallinum cD... 38 0.10

	emb AW729858 AW729858 GAEa0026H02 Gossypium arboreum 7-10 dpa 36 0.3
	emb AQ953583 AQ953583 Sheared DNA-53H18.TF Sheared DNA Trypanoso 36 0.5
	gb BE036480 BE036480 MP03G10 MP Mesembryanthemum crystallinum cD 36 0.51
	emb Z00044 CHNTXX Nicotiana tabacum chloroplast genome DNA. 35 0.70
5	emb AL160939 L1356CX Leishmania major Friedlin cosmid L1356.3 t3 34 1.8
	gb BE036897 BE036897 MP08B09 MP Mesembryanthemum crystallinum cD 34 1.8
	emb AI730722 AI730722 BNLGHi7729 Six-day Cotton fiber Gossypium 34 1.8
	emb AB030726 AB030726 Nicotiana tabacum mRNA for DNA (cytosine-5 34 2.5
	emb AW397331 AW397331 sg77e08.y1 Gm-c1007 Glycine max cDNA clone 34 2.5
10	
10	emb AI210350 AI210350 i0c03a1.rl Aspergillus nidulans 24hr asexu 34 2.5
	emb AA786346 AA786346 13g09a1.fl Aspergillus nidulans 24hr asexu 34 2.5
	emb AW397063 AW397063 sg66e08.yl Gm-c1007 Glycine max cDNA clone 34 2.5
	emb AI327733 AI327733 i0c03a1.fl Aspergillus nidulans 24hr asexu 34 2.5
	emb[AW672119]AW672119 LG1_357_F07.b1_A002 Light Grown 1 (LG1) So 33 3.4
15	emb AJ270207 ECA270207 Entodinium caudatum partial mRNA fro puta 33 3.4
	emb AW672133 AW672133 LG1_357_D07.b1_A002 Light Grown 1 (LG1) So 33 3.4
	emb AQ847463 AQ847463 LMAJFV1_lm34c05.y1 Leishmania major FV1 ra 33 4.7
	emb AZ212142 AZ212142 Sheared DNA-70G10.TF Sheared DNA Trypanoso 32 6.4
•	emb AI163630 AI163630 A045p06u Hybrid aspen plasmid library Popu 32 6.4
20	emb AL354532 LMFL1177 Leishmania major Friedlin chromosome 21 co 30 6.9
	emb AJ243516 NCR243516 Neurospora crassa partial nca-3 gene for 32 8.8
	emb AL116648 CNS01DCG Botrytis cinerea strain T4 cDNA library un 27 9.3
	Query= X71794.2 s at 15970 s at /id source genbank /description
25	emb caa50677.1 (x71794) peroxidase [arabidopsis thaliana]
25	/blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
	(1236 letters)
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
30	
	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
35	
	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge 744 0.0
	emb A00741 A00741 A.rusticana synthetic gene (reverse complement 692 0.0
	emb A00740 A00740 A.rusticana synthetic gene for peroxidase. 692 0.0
	dbj E01651 E01651 cDNA encoding horseradish peroxidase. 692 0.0
40	gb[M37157]HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge 371 e-133
	emb X97349 PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P 473 e-132
	emb[X97350]PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P 469 e-131
	dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds. 468 e-131
	gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge 363 e-130
45	emb[X97348]PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P 463 e-129
7.7	dbilD20652IDODDA Bornbra kitakomiensia mDNA for massidana mata 441 - 102
	dbj[D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part 441 e-123
	emb X97351 PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P 383 e-120
	dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part 356 e-112
	emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor 227 e-107
50	gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple 229 e-107
	emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1) 229 e-106
	gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA 381 e-105
	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A. 211 e-105
	dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i 296 e-103
55 -	emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod 138 2e-97
-	emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor 142 4e-97
	* maa a a a la caracter de la caract
	A Mark Andrews Community C
	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C. 226 7e-94
50	gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 210 2e-89
317	PRINTED INTOX 4 //A INDIVIZIO AND/INDIVIZION A LA DE AL LA LA LA LA LA LA LA LA LA LA LA LA
• •	emb AI959837 AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone 228 6e-89 emb AF244924 AF244924 Spinacia oleracea peroxidase prr 15 precurs 208 9e-88

emb|AW559660|AW559660 EST314772 DSIR Medicago truncatula cDNA cl... 236 1e-87 emb|AW774581|AW774581 EST333732 KV3 Medicago truncatula cDNA clo... 236 7e-87 emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 215 2e-86 emb|AW981426|AW981426 EST392579 DSIL Medicago truncatula cDNA cl... 236 2e-85 5 emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 209 2e-85 emb|AF244923|AF244923 Spinacia oleracea peroxidase prx14 precurs... 205 9e-85 emb|AJ250121|PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... 253 1e-83 emb|AW775762|AW775762 EST334827 DSIL Medicago truncatula cDNA cl... 236 6e-83 emb[Y10466]SOPRXR5 S.oleracea mRNA for peroxidase, clone PC18. 10 emb|AW775425|AW775425 EST334490 DSIL Medicago truncatula cDNA cl... 208 1e-81 emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root Medicago t... 230 9e-80 emb|AB024439|AB024439 Scutellaria baicalensis mRNA for peroxidas... 209 2e-79 emb|AF244922|AF244922 Spinacia oleracea peroxidase prx13 precurs... 212 3e-79 emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 115 6e-78 emb|AW776273|AW776273 EST335338 DSIL Medicago truncatula cDNA cl... 222 1e-77 15 emb|AW267813|AW267813 EST305941 DSIR Medicago truncatula cDNA cl... 200 1e-76 emb|X91232|MARNAPRX M.annua mRNA for peroxidase. 196 5e-76 emb|AF049881|AF049881 Linum usitatissimum peroxidase FLXPER4 (PE... 207 7e-76 emb|AW256487|AW256487 EST304624 KV2 Medicago truncatula cDNA clo... 200 9e-76 emblAW775890lAW775890 EST334955 DSIL Medicago truncatula cDNA cl... 200 -3e-74 20 emb|AW257195|AW257195 EST305332 KV2 Medicago truncatula cDNA clo... 214 5e-74 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 86 2e-73 gb|U41657|GMU41657 Glycine max seed coat peroxidase isozyme (SPO... 159 3e-73 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 197 5e-73 25 gb|L36110|SSNPEROXIA Stylosanthes humilis peroxidase mRNA. 199 5e-73 gb|M37636|ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR... 204 7e-73 emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root Medicago t... 236 9e-73 emb[AW278775]AW278775 sf97d02.y1 Gm-c1019 Glycine max cDNA clone... 155 1e-72 emb|X71593|LECEVI1A L.esculentum CEVI-1 mRNA. 99 2e-72 30 gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 100 2e-72 emb|AW559945|AW559945 EST314993 DSIR Medicago truncatula cDNA cl... 233 2e-72 emb|AW980744|AW980744 EST391897 GVN Medicago truncatula cDNA clo... 235 5e-70 emb[Y10467|SOPRXR6 S.oleracea mRNA for peroxidase, clone PC23. 105 le-69 dbj|D83225|POPP02 Populus nigra peroxidase gene, complete cds. 35 gb[M74103]TOBANPER Nicotiana sylvestris anionic peroxidase mRNA,... 205 6e-69 emb|AF043234|AF043234 Striga asiatica ferriprotein porphyrin-con... 211 1e-68 gb|BE034991|BE034991 MM01A12 MM Mesembryanthemum crystallinum cD... 202 6e-68 emb|AW574244|AW574244 EST316835 GVN Medicago truncatula cDNA clo... 202 1e-67 emb|Y10465|SOPRXR4 S.oleracea mRNA for peroxidase, clone PC44. 40 emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root Medicago t... 236 5e-67 emb|AW561032|AW561032 EST316080 DSIR Medicago truncatula cDNA cl... 203 7e-67 emb[X56011]TAPERO Wheat mRNA for peroxidase. 111 2e-66 emb|AW185769|AW185769 se59d08.y1 Gm-c1019 Glycine max cDNA clone... 219 4e-65 emb[Y17192]CPY17192 Cucurbita pepo mRNA for peroxidase. 96 2e-64 45 gb|BE033422|BE033422 ME01E09 ME Mesembryanthemum crystallinum cD... 184 4e-64 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidas... 205 7e-64 gb[M91374]CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 76 2e-63 gb|L24120|LINFLXP Linum usitatissimum peroxidase precursor (FLXP... 167 2e-63 gb|M91372|CUSPREPERB Cucumis sativus peroxidase mRNA, complete cds. 134 2e-63 50 emb|AF043235|AF043235 Striga asiatica ferriprotein porphyrin-con... 199 3e-63 emb|AW288002|AW288002 N100846e rootphos(-) Medicago truncatula c... 182 7e-63 emb|AW126121|AW126121 N100318e rootphos(-) Medicago truncatula c... 216 1e-62 gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. emb|AW687443|AW687443 NF009F07RT1F1062 Developing root Medicago ... 235 1e-61 55 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem Medicago ... 236 3e-61 emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 163 3e-61 emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). emb|AI496388|AI496388 sb04a11.yl Gm-c1004 Glycine max cDNA clone... 224 6e-61 emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root Medicago t... 222 8e-61 60 dbj|D38050|POPP1 Aspen prxA3a gene for peroxidase, complete cds. emb|AW704659|AW704659 sk54h10.y1 Gm-c1019 Glycine max cDNA clone... 149 9e-61

emb[Y10464|SOPRXR3 S.oleracea mRNA for peroxidase, clone PC42. emb|AW705730|AW705730 sk51b02.yl Gm-c1019 Glycine max cDNA clone... 149 8e-60 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60 gb|U12314|CCU12314 Cenchrus ciliaris clone PX7 peroxidase mRNA. ... 105 9e-60 emb|AI938533|AI938533 sb46h09.yl Gm-c1015 Glycine max cDNA clone... 145 1e-59 emb|AW705617|AW705617 sk50d03.y1 Gm-c1019 Glycine max cDNA clone... 149 2e-59 emb|AI781859|AI781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59 emb|AF149278|AF149278 Phaseolus vulgaris peroxidase 3 precursor ... 90 3e-59 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 102 4e-59 10 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58 emb|AW705946|AW705946 sk52h07.yl Gm-c1019 Glycine max cDNA clone... 224 6e-58 15 Query= X68592.6_at 15978 at /id_source genbank /description emb|caa48579.1| (x68592) adenosine nucleotide translocator [arabidopsis thaliana] /blast_score 0 /ec_number_/family_translocase /chip nova /gb link 20 http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi http://www.ncgr.org/cgi-bin/ff?x68592 (1530 letters) 25 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 30 Score E Sequences producing significant alignments: (bits) Value emb|AF006489|AF006489 Gossypium hirsutum adenine nucleotide tran... 325 0.0 emb|X62123|STANTG S.tuberosum ant gene for ADP/ATP translocator. 35 gb|U89839|LEU89839 Lycopersicon esculentum ADP/ATP translocator ... 327 0.0 emb|X57557|STANT1 S.tuberosum PANT1 mRNA for adenine nucleotide ... 635 0.0 emb|AJ003197|LAAJ3197 Lupinus albus mRNA for adenine nucleotide ... 331 e-175 emb|X80023|TTADPATP T.turgidum mRNA for ADP/ATP carrier. emb|X65194|CRANT C.reinhardtii mRNA CRANT for mitochondrial ADP/... 348 e-149 40 emb|AL023634|SPBC530 S.pombe chromosome II cosmid c530. emb|Z49974|SPANC1GN S.pombe ANC1 gene for adenine nucleotide car... 265 e-139 emb|AF085429|AF085429 Candida parapsilosis ADP/ATP carrier prote... 311 e-134 dbi|D89102|D89102 Schizosaccharomyces pombe mRNA, partial cds, c... 265 e-133 gb|L33797|YSKAAC Kluyveromyces lactis ADP/ATP translocase (AAC) ... 259 e-132 45 emb|AF237675|AF237675 Yarrowia lipolytica ADP/ATP carrier protei... 247 e-132 emb|AJ277099|CUT277099 Candida utilis anc gene for mitochondrial... 253 e-131 emb|AJ277098|CUT277098 Candida utilis and gene for mitochondrial... 253 e-131 gb[M34075]YSCAAC3 S.cerevisiae ADP/ATP-translocator protein (AAC... 252 e-129 emb|X77291|SCIILDNA S.cerevisiae YBL0421, YBL0438, YBL0418, YBL0... 252 e-129 50 emb|Z35791|SCYBL030C S.cerevisiae chromosome II reading frame OR... 252 e-129 emb|X74427|SCADNUCA S.cerevisiae gene for adenine nucleotide car... 252 e-129 gb|J04021|YSCAAC2 S.cerevisiae ADP/ATP carrier protein (AAC2) ge... 252 e-129 emb|X00363|NCADPATP Neurospora crassa mRNA for mitochondrial ADP... 280 e-126 emb|Z49703|SC9796 S.cerevisiae chromosome XIII cosmid 9796. 248 e-125 55 gb|M12514|YSCPET9 S.cerevisiae ADP/ATP translocator protein (AAC... 248 e-125 emb|Z35954|SCYBR085W S.cerevisiae chromosome II reading frame OR... 247 e-125 gb|M34076|YSCAAC2A S.cerevisiae ADP/ATP-translocator protein (AA... 247 e-125 emb|AW774326|AW774326 EST333477 KV3 Medicago truncatula cDNA clo... 288 e-124 emb|AL111975|CNS019QN Botrytis cinerea strain T4 cDNA library un... 254 e-122 60 emb|AW647699|AW647699 EST307178 tomato germinating seedlings, TA... 299 e-120

emb|AW349848|AW349848 GM210006A11G9R Gm-r1021 Glycine max cDNA 3... 326 eemb|AW624842|AW624842 EST313671 tomato radicle, 5 d post-imbibit... 229 e-116 emb|X95863|TTANT1 T.turgidum ant gene (1549bp). 195 e-114 5 emb|AW041186|AW041186 EST284050 tomato mixed elicitor, BTI Lycop... 239 e-114 emb|X95864|TTANT2 T.turgidum ant gene (1494bp). 191 e-112 emb|AW706324|AW706324 sj54h05.yl Gm-c1033 Glycine max cDNA clone... 245 e-110 emb|AL157416|LMFL6066 Leishmania major Friedlin chromosome 19 co... 233 e-108 emb|AW160172|AW160172 EST290029 L. pennellii trichome, Cornell U... 328 e-108 10 emb|AW928728|AW928728 EST337516 tomato flower buds 8 mm to pre-a... 247 e-107 emb|AW218544|AW218544 EST303727 tomato radicle, 5 d post-imbibit... 325 e-105 emb|AW830381|AW830381 sm26a12.yl Gm-c1028 Glycine max cDNA clone... 268 e-105 emb|AW201674|AW201674 sf05h11.yl Gm-c1027 Glycine max cDNA clone... 309 e-104 emb AI812944 AI812944 22G12 Pine Lambda Zap Xylem library Pinus ... 251 e-103 15 emb|AI777865|AI777865 EST258744 tomato susceptible, Cornell Lyco... 284 e-102 emb|AW234033|AW234033 sf33d01.yl Gm-c1028 Glycine max cDNA clone... 237 e-101 emb[AW831587]AW831587 sm28b02.y1 Gm-c1028 Glycine max cDNA clone... 300 e-101 emb|AW668198|AW668198 GA__Ea0013C13 Gossypium arboreum 7-10 dpa ... 331 e-100 emb|AF049130|AF049130 Trypanosoma brucei brucei ADP/ATP carrier ... 238 1e-98 20 emb|AI898886|AI898886 EST268329 tomato ovary, TAMU Lycopersicon ... 213 2e-98 gb|U32987|TBU32987 Trypanosoma brucei rhodesiense ADP/ATP carrie... 238 3e-98 emb|AW223982|AW223982 EST300793 tomato fruit red ripe, TAMU Lyco... 327 1e-96 emb|AW624951|AW624951 EST313780 tomato radicle, 5 d post-imbibit... 327 1e-96 emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 328 2e-25 emb|AW441243|AW441243 EST310639 tomato fruit red ripe, TAMU Lyco... 324 1e-95 emb|AW223973|AW223973 EST300784 tomato fruit red ripe, TAMU Lyco... 321 7e-95 emb|AW931569|AW931569 EST357412 tomato fruit mature green, TAMU ... 328 2e-94 emb|AW218871|AW218871 EST301353 tomato root during/after fruit s... 327 8e-94 30 emb|AL116444|CNS01D6S Botrytis cinerea strain T4 cDNA library un... 267 4e-93 emb|AW831561|AW831561 sm34f06.y1 Gm-c1028 Glycine max cDNA clone... 312 2e-92 emb|AI484151|AI484151 EST248958 tomato resistant, Cornell Lycope... 264 3e-91 emb|AW925414|AW925414 HVSMEg0001L02 Hordeum vulgare pre-anthesis... 299 6e-91 emb|AI731594|AI731594 BNLGHi10182 Six-day Cotton fiber Gossypium... 335 7e-91 35 emb|AW647665|AW647665 EST307143 tomato germinating seedlings, TA... 317 1e-90 emb|AW395111|AW395111 sh40a06.yl Gm-c1017 Glycine max cDNA clone... 303 6e-90 emb|AI725588|AI725588 BNLGHi12376 Six-day Cotton fiber Gossypium... 288 1e-89 emb|AW934656|AW934656 EST353548 tomato flower buds 0-3 mm, Corne... 328 2e-89 40 emb|AW757478|AW757478 874001D11.y1 C. reinhardtii CC-1690, Lambd... 202 3e-89 emb|AW725897|AW725897 GA_Ea0020B06 Gossypium arboreum 7-10 dpa ... 328 8e-89 emb|AW647757|AW647757 EST326211 tomato germinating seedlings, TA... 301 1e-88 emb|AW509174|AW509174 sh92b04.y1 Gm-c1016 Glycine max cDNA clone... 297 4e-88 45 emb|AL114553|CNS01BQ9 Botrytis cinerea strain T4 cDNA library un... 231 3e-87 gb|BE021489|BE021489 sm59b05.y1 Gm-c1028 Glycine max cDNA clone ... 322 5e-87 emb|AW507801|AW507801 si45c02.yl Gm-r1030 Glycine max cDNA clone... 259 2e-86 emb|AW733916|AW733916 sk85a11.yl Gm-c1035 Glycine max cDNA clone... 306 2e-86 emb|AW096468|AW096468 EST289648 tomato mixed elicitor, BTI Lycop... 292 6e-86 50 emb|AW156741|AW156741 se30b08.y1 Gm-c1015 Glycine max cDNA clone... 184 1e-85 emb|AI729625|AI729625 BNLGHi13824 Six-day Cotton fiber Gossypium... 276 4e-85 emb|AW034214|AW034214 EST277785 tomato callus, TAMU Lycopersicon... 304 5e-85 emblAJ273864|AJ273864 AJ273864 Metarhizium anisopliae ARSEF 2575... 184 1e-84 emb|AI775647|AI775647 EST256747 tomato resistant, Cornell Lycope... 297 1e-84 emb|AI822682|AI822682 L0-1204T3 Ice plant Lambda Uni-Zap XR expr... 314 2e-84 emb|AW625107|AW625107 EST313924 tomato radicle, 5 d post-imbibit... 314 2e-84 emb|AI726147|AI726147 BNLGHi5085 Six-day Cotton fiber Gossypium ... 263 6e-83 emb|AW755396|AW755396 sl03d11.yl Gm-c1036 Glycine max cDNA clone... 306 3e-82 emb|AI728088|AI728088 BNLGHi9938 Six-day Cotton fiber Gossypium ... 259 5e-82 60 emb|AW979992|AW979992 EST310378 tomato root deficiency, Cornell ... 285 8e-82 emb|AW333018|AW333018 S16C3 AGS-1 Pneumocystis carinii f. sp. ca... 278 1e-81

emb|AI780394|AI780394 EST261273 tomato susceptible, Cornell Lyco... 284 2e-81 emb|AW691046|AW691046 NF037A12ST1F1000 Developing stem Medicago ... 266 2e-81 emb|AW924717|AW924717 WS1_71_A04.b1_A002 Water-stressed 1 (WS1) ... 303 3e-81 emb|AI731287|AI731287 BNLGHi9093 Six-day Cotton fiber Gossypium ... 262 5e-81 emb|AW760027|AW760027 sl57b04.y1 Gm-c1027 Glycine max cDNA clone... 301 1e-80 emb|AW667101|AW667101 GA_Ea0007F21 Gossypium arboreum 7-10 dpa ... 300 2e-80 emb|AW622023|AW622023 EST312821 tomato root during/after fruit s... 280 4e-80 emb|AV388663|AV388663 AV388663 Chlamydomonas reinhardtii C9 Chla... 284 8e-80 emb|AW650428|AW650428 EST328882 tomato germinating seedlings, TA... 278 4e-79 emb|AI775628|AI775628 EST256728 tomato resistant, Cornell Lycope... 295 7e-79 gb|BE024093|BE024093 sm96f04.y1 Gm-c1015 Glycine max cDNA clone ... 293 2e-78 emb|AJ273749|AJ273749 AJ273749 Metarhizium anisopliae ARSEF 2575... 256 1e-77 emb|AW737446|AW737446 EST338789 tomato flower buds, anthesis, Co... 290 2e-77

15

20

Query=Y14251.4_i_at 16053_i_at /id_source genbank /description emb|caa74639.1| (y14251) glutathione s-transferase [arabidopsis thaliana] /blast_score 1.00e-110 /ec_number /family transferase /chip nova /gb link

http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi http://www.ncgr.org/cgi-bin/ff?y14251 (630 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching.....done

30

35

40

45

50

Score E

Sequences producing significant alignments: (bits) Value emb|X78203|HMGST H.muticus mRNA for glutathione S-transferase. emb|AW727692|AW727692 GA_Ea0015I24 Gossypium arboreum 7-10 dpa ... 146 9e-71 emb|AF002692|AF002692 Solanum commersonii glutathione S-transfer... 264 3e-70 dbj|D10524|TOBPARB Nicotiana tabacum mRNA for glutathione S-tran... 262 2e-69 dbj|D29680|TOBAPI2B Tobacco api2 mRNA (which expression is induc... 261 4e-69 emb|AW220064|AW220064 EST302547 tomato root during/after fruit s... 260 5e-69 emb|Z71749|NPGSTMR N.plumbaginifolia mRNA for glutathione S-tran... 260 8e-69 emb|AI774583|AI774583 EST255683 tomato resistant, Cornell Lycope... 258 3e-68 emb|AW728413|AW728413 GA_Ea0016J18 Gossypium arboreum 7-10 dpa ... 142 7e-68 emb|AI725552|AI725552 BNLGHi12077 Six-day Cotton fiber Gossypium... 142 4e-67 emb|AI728937|AI728937 BNLGHi12090 Six-day Cotton fiber Gossypium... 142 4e-67 gb|BE033971|BE033971 MG02G09 MG Mesembryanthemum crystallinum cD... 228 2e-65 emb|AW735791|AW735791 EST336559 tomato flower buds 0-3 mm, Corne... 248 2e-65 emb|AF242309|AF242309 Euphorbia esula glutathione S-transferase ... 130 3e-62 emb|AI726215|AI726215 BNLGHi5300 Six-day Cotton fiber Gossypium ... 142 5e-61 emb|AW218151|AW218151 EST303332 tomato radicle, 5 d post-imbibit... 232 1e-60 gb|M84968|SIPGTSTF Silene cucubalus glutathione-S-transferase mR... 115 5e-59 emb|AF133894|AF133894 Persea americana glutathione S-transferase... 220 8e-57

emb|AI352770|AI352770 MB58-4B PZ204.BNIib Brassica napus cDNA cl... 174 7e-55
emb|AW040790|AW040790 EST283654 tomato mixed elicitor, BTI Lycop... 210 6e-54
emb|AW649890|AW649890 EST328344 tomato germinating seedlings, TA... 202 2e-51
emb|AW862639|AW862639 00097 leafy spurge Lambda HybriZAP 2.1 two... 128 2e-48
emb|AI943409|AI943409 MF02B7 MF Mesembryanthemum crystallinum cD... 190 1e-47
emb|AV411409|AV411409 AV411409 Lotus japonicus young plants (two... 187 6e-47
emb|AW684286|AW684286 NF015A06NR1F1000 Nodulated root Medicago t... 186 1e-46
emb|AW039384|AW039384 EST281641 tomato mixed elicitor, BTI Lycop... 185 2e-46

gb|BE033640|BE033640 MF05D04 MF Mesembryanthemum crystallinum cD... 185 2e-46 emb|AW777169|AW777169 Str3-D4 Sugar Beet germination cDNA librar... 185 3e-46 emb|AV414359|AV414359 AV414359 Lotus japonicus young plants (two... 182 2e-45 5 gb|BE034473|BE034473 MH05E04 MH Mesembryanthemum crystallinum cD... 181 4e-45 gb|BE033466|BE033466 ME02E04 ME Mesembryanthemum crystallimum cD... 170 7e-45 emb|AW623451|AW623451 EST321396 tomato flower buds 3-8 mm, Corne... 179 2e-44 emb|AV408851|AV408851 AV408851 Lotus japonicus young plants (two... 173 9e-43 emb|AV417287|AV417287 AV417287 Lotus japonicus young plants (two... 173 9e-43 10 emb|AI486597|AI486597 EST244918 tomato ovary, TAMU Lycopersicon ... 173 1e-42 emb|AV417605|AV417605 AV417605 Lotus japonicus young plants (two... 172 2e-42 emb|AW667380|AW667380 GA_Ea0009C08 Gossypium arboreum 7-10 dpa ... 147 2e-42 gb|C96149|C96149 C96149 Marchantia polymorpha immature sex organ... 145 1e-41 emb|AI054936|AI054936 coau0002J02 Cotton Boll Abscission Zone cD... 142 2e-40 15 dbj|D49526|TOBPARBA Tobacco chimeric parB promoter/beta-glucuron... 163 1e-39 emb|AI774099|AI774099 EST255199 tomato resistant, Cornell Lycope... 163 1e-39 emblAV418074|AV418074 AV418074 Lotus japonicus young plants (two... 160 6e-39 gb|BE020725|BE020725 sm52b05.yl Gm-c1028 Glycine max cDNA clone ... 148 5e-38 emb|AI162894|AI162894 A026P40U Hybrid aspen plasmid library Popu... 155 4e-37 20 emb|Y07721|PHGLSTRAN P.hybrida mRNA for glutathione S-transferase. 151 5e-36 gb|BE053268|BE053268 GA_Ea0035A09f Gossypium arboreum 7-10 dpa ... 137 7e-36 gb|M84969|SIPGTSTFA Silene cucubalus glutathione-S-transferase g... 78 1e-35 emb|AW507753|AW507753 si44f10.yl Gm-r1030 Glycine max cDNA clone... 149 2e-35 emb|AW596451|AW596451 sj12e11.y1 Gm-c1032 Glycine max cDNA clone... 149 2e-35 25 emblAW926756|AW926756 HVSMEg0008B23 Hordeum vulgare pre-anthesis... 92 3e-35 emb|AJ279691|BPE279691 Betula pendula partial mRNA for glutathio... 144 8e-34 emb|AV427165|AV427165 AV427165 Lotus japonicus young plants (two... 142 3e-33 emb|AJ010451|AMY010451 Alopecurus myosuroides mRNA for glutathio... 97 4e-33 emb|AF184059|AF184059 Triticum aestivum glutathione S-transferas... 81 5e-33 30 emb|AW164336|AW164336 se71b09.yl Gm-c1023 Glycine max cDNA clone... 139 1e-32 emb|AJ010454|AMY010454 Alopecurus myosuroides mRNA for glutathio... 95 2e-32 emb|AJ010452|AMY010452 Alopecurus myosuroides mRNA for glutathio... 94 3e-32 emb|AW678048|AW678048 WS1 13 A09.b1 A002 Water-stressed 1 (WS1) ... 84 3e-32 gb|BE021219|BE021219 sm56c09.yl Gm-c1028 Glycine max cDNA clone ... 99 7e-32 35 emb|AW561921|AW561921 IPPGHZ0010 Cotton fiber and embryo Lambda ... 137 7e-32 emb|AW458936|AW458936 sh16g07.yl Gm-c1016 Glycine max cDNA clone... 137 7e-32 emb|AW218152|AW218152 EST303333 tomato radicle, 5 d post-imbibit... 137 1e-31 emb|AV426478|AV426478 AV426478 Lotus japonicus young plants (two... 137 1e-31 emb|AI823144|AI823144 L30-1027T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31 40 emb|AI823131|AI823131 L30-1014T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31 gb|BE058603|BE058603 sn18c06.y1 Gm-c1016 Glycine max cDNA clone ... 134 5e-31 emb|AI773198|AI773198 EST254298 tomato resistant, Cornell Lycope... 133 1e-30 emb|AI778224|AI778224 EST259103 tomato susceptible, Cornell Lyco... 111 2e-30 emb|AW745644|AW745644 WS1_36_D11.b1_A002 Water-stressed 1 (WS1) ... 84 4e-30 45 emb|AW279568|AW279568 sf95d06.yl Gm-c1019 Glycine max cDNA clone... 131 4e-30 emb|AW054044|AW054044 L30-2014T3 Ice plant Lambda Uni-Zap XR exp... 106 3e-29 emb|AW202090|AW202090 sf11a03.y1 Gm-c1027 Glycine max cDNA clone... 106 1e-28 emb|AI440830|AI440830 sa86f05.yl Gm-c1004 Glycine max cDNA clone... 126 1e-28 emb|AW678628|AW678628 WS1 1 B05.b1 A002 Water-stressed 1 (WS1) S... 85 2e-28 50 emb|AW677650|AW677650 WS1 10 F04.b1 A002 Water-stressed 1 (WS1) ... 80 6e-28 emb|AW678706|AW678706 WS1_1_B05.b2_A002 Water-stressed 1 (WS1) S... 85 8e-28 emb|AW677798|AW677798 WS1_11_H05.b1_A002 Water-stressed 1 (WS1) ... 76 2e-27 emb|AW053375|AW053375 L30-1572T3 Ice plant Lambda Uni-Zap XR exp... 99 2e-27 emb|AV426523|AV426523 AV426523 Lotus japonicus young plants (two... 122 2e-27 55 emb|AV427075|AV427075 AV427075 Lotus japonicus young plants (two... 122 2e-27 emb|AV415440|AV415440 AV415440 Lotus japonicus young plants (two... 122 2e-27 emb|AT000441|AT000441 AT000441 Brassica rapa guard cell Brassica... 122 3e-27 emb|AI442436|AI442436 sa26h04.yl Gm-c1004 Glycine max cDNA clone... 111 4e-27 gb|BE034032|BE034032 MG03G03 MG Mesembryanthemum crystallinum cD... 90 6e-26 60 emb|AW689646|AW689646 NF022G04ST1F1000 Developing stem Medicago ... 66 3e-25 gb|BE060798|BE060798 HVSMEg0013G13f Hordeum vulgare pre-anthesis... 92 6e-25

gb|BE060847|BE060847 HVSMEg0013J11f Hordeum vulgare pre-anthesis... 64 3e-24 emb|AW171715|AW171715 N100609e rootphos(-) Medicago truncatula c... 112 3e-24 emb|AW348131|AW348131 GM210001A21A6R Gm-r1021 Glycine max cDNA 3... 98 4e-24 emb|AW680604|AW680604 WS1_6_C03.b1_A002 Water-stressed 1 (WS1) S... 84 4e-24 emb|AI352728|AI352728 MB47-17 PZ204.BNlib Brassica napus cDNA cl... 110 1e-23 emb|AW127163|AW127163 M110099 GVN Medicago truncatula cDNA clone... 110 1e-23 emb|AW924273|AW924273 WS1_51_A04.b1_A002 Water-stressed 1 (WS1) ... 95 1e-23 emb|AW680779|AW680779 WS1_7_D01.b1_A002 Water-stressed 1 (WS1) S... 97 1e-23 emb|AI444064|AI444064 sa31g12.y1 Gm-c1004 Glycine max cDNA clone... 109 2e-23 emb|AW459151|AW459151 sh21c07.y1 Gm-c1016 Glycine max cDNA clone... 66 6e-23

Query= X77500.2_at 16522_at /id_source genbank /description emb|caa54631.1| (x77500) amino acid transporter [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|x77500| /ncgi http://www.ncgr.org/cgi-bin/ff?x77500 (1619 letters)

20

Datābāse: plantfungal 661,018 sequences; 426,114,510 total letters

Searching.....done

25

Score E

Sequences producing significant alignments:

(bits) Value

emb|AJ007574|RCO7574 Ricinus communis mRNA for amino acid carrier. 410 0.0 30 emb|Y09591|VFAMACTRA V.faba mRNA for amino acid transporter. emb|AJ132228|RCO132228 Ricinus communis mRNA for amino acid carr... 342 0.0 emb|AF080543|AF080543 Nepenthes alata amino acid transporter (AA... 641 0.0 emb[Y09826]STAAP2 S.tuberosum mRNA for amino acid transporter AA... 354 0.0 emb|AF080544|AF080544 Nepenthes alata amino acid transporter (AA... 596 0.0 35 emb|Y09825|STAAP1 S.tuberosum mRNA for amino acid transporter AA... 288 e-158 emb|Z68759|RCAACMR R.communis mRNA for amino acid carrier. emb|AF080542|AF080542 Nepenthes alata amino acid transporter (AA... 239 e-145 emb|AF061435|AF061435 Vicia faba amino acid transporter b (AAPB)... 501 e-141 emb[Y11121]RCAACARR Ricinus communis mRNA for amino acid carrier... 264 e-123 40 emb|AF061434|AF061434 Vicia faba amino acid transporter a (AAPA)... 290 e-107 emblAF061436|AF061436 Vicia faba amino acid transporter c (AAPC)... 259 5e-95 emb|AW560155|AW560155 EST315203 DSIR Medicago truncatula cDNA cl... 293 4e-86 emb[AW203255]AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone... 312 4e-84 emb|AI166826|AI166826 xylem.est.62 Poplar xylem Lambda ZAPII lib... 188 2e-68 45 emb|AW648039|AW648039 EST326493 tomato germinating seedlings, TA... 226 2e-67 emb|AI974813|AI974813 T113295e KV2 Medicago truncatula cDNA clon... 153 2e-66 emb|AW926173|AW926173 HVSMEg0006I08 Hordeum vulgare pre-anthesis... 243 3e-66 emb|AW648857|AW648857 EST327311 tomato germinating seedlings, TA... 219 3e-65 emb|AV428014|AV428014 AV428014 Lotus japonicus young plants (two... 248 6e-65 50 emb|AW277711|AW277711 sf85f01.y1 Gm-c1019 Glycine max cDNA clone... 242 5e-63 emb|AW774110|AW774110 EST333340 KV3 Medicago truncatula cDNA clo... 238 7e-62 emb|AW720246|AW720246 LjNEST17f12r Lotus japonicus nodule librar... 235 6e-61 emb|AI930612|AI930612 sb37c02.y1 Gm-c1013 Glycine max cDNA clone... 167 5e-60 emb|AW399595|AW399595 EST310095 L. pennellii trichome, Cornell U... 192 8e-58 55 emb|AW737124|AW737124 EST338551 tomato flower buds, anthesis, Co... 217 2e-55 emb|AW691461|AW691461 NF045C01ST1F1000 Developing stem Medicago ... 206 7e-55 emb|AW432416|AW432416 sh73f10.yl Gm-c1015 Glycine max cDNA clone... 89 8e-51 emb|AW255060|AW255060 ML1355 peppermint glandular trichome Menth... 111 1e-50 emb|AW685782|AW685782 NF035B03NR1F1000 Nodulated root Medicago t... 201 1e-50 60 gb|BE125804|BE125804 DG1_57_F07.b1_A002 Dark Grown 1 (DG1) Sorgh... 178 3e-50

emb|AW307506|AW307506 sf57g11.yl Gm-c1009 Glycine max cDNA clone... 181 2e-49

```
emb|AW349599|AW349599 GM210005A21G12R Gm-r1021 Glycine max cDNA ... 140 5e-
       emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 122 2e-48
       emblAW737784|AW737784 EST339211 tomato flower buds, anthesis, Co... 192 6e-48
       emb|AW309945|AW309945 sf27a03.x1 Gm-c1028 Glycine max cDNA clone... 149 5e-47
       emb|AW738557|AW738557 EST339984 tomato flower buds, anthesis, Co... 188 8e-47
       emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 148 2e-44
       emblAF074703|AF074703 Glycine max pA381 marker, sequence tagged ... 149 1e-43
      emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 127 3e-43
10
      gb|BE022301|BE022301 sm73b09.yl Gm-c1028 Glycine max cDNA clone ... 176 4e-43
      emb|AW597381|AW597381 si92b03.yl Gm-c1031 Glycine max cDNA clone... 175 1e-42
      emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 172 5e-42
      emb|AW306512|AW306512 se51h04.y1 Gm-c1017 Glycine max cDNA clone... 140 1e-41
      emb|AW395873|AW395873 sh01d01.y1 Gm-c1026 Glycine max cDNA clone... 112 4e-41
15
      emb|AW201454|AW201454 sf03c12.yl Gm-c1027 Glycine max cDNA clone... 127 9e-41
      emb|AW684816|AW684816 NF021D09NR1F1000 Nodulated root Medicago t... 164 2e-39
      emb|AZ051221|AZ051221 Gm_UMb001_166_P11R UMN Soybean BAC Library... 159 7e-38
      emb AI779305 AI779305 EST260184 tomato susceptible, Cornell Lyco... 155 1e-36
      emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 155 1e-36
20
      emb|AW830977|AW830977 sm31a10.y1 Gm-c1028 Glycine max cDNA clone... 149 4e-35
      emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 147 3e-34
      emb|AJ004829|STAJ4829 Solanum tuberosum fdh3 pseudogene.
                                                                      110 3e-33
      emb|AQ841805|AQ841805 T134055 Soybean RFLP probe Glycine max gen... 140 2e-32
      emblAW736648lAW736648 EST333140 KV3 Medicago truncatula cDNA clo... 138 1e-31
25
      emb|AV418629|AV418629 AV418629 Lotus japonicus young plants (two... 130 3e-29
      emb|AW442349|AW442349 EST311745 tomato fruit red ripe, TAMU Lyco... 130 3e-29
      emb|AW738564|AW738564 EST339991 tomato flower buds, anthesis, Co... 104 7e-29
      emb|AW561095|AW561095 EST316143 DSIR Medicago truncatula cDNA cl... 126 6e-28
      emb|AW234791|AW234791 sf19c06.yl Gm-c1028 Glycine max cDNA clone... 124 2e-27
30.
      gb|U31932|NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 61 3e-27
      emb|AI441371|AI441371 sa64f02.yl Gm-c1004 Glycine max cDNA clone... 72 2e-26
      emb|AW438003|AW438003 ST83D04 Pine TriplEx shoot tip library Pin... 111 2e-23
      emb|AW056573|AW056573 ST52G03 Pine TriplEx shoot tip library Pin... 109 8e-23
      emb|AW923686|AW923686 DG1_57_F07.g1_A002 Dark Grown 1 (DG1) Sorg... 107 3e-22
35
      emb|AW924285|AW924285 WS1_52_F10.b1_A002 Water-stressed 1 (WS1) ... 106 5e-22
      emb|AJ238635|CPR238635 Chlorella protothecoides partial mRNA for... 75 4e-20
      emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 100 6e-20
      emb|AW102244|AW102244 sd85c02.y1 Gm-c1009 Glycine max cDNA clone... 92 1e-17
      emblAW620352|AW620352 sj04b02.yl Gm-c1032 Glycine max cDNA clone... 92 1e-17
40
      emb|AW288077|AW288077 N100921e rootphos(-) Medicago truncatula c... 84 2e-15
      emb|AW396191|AW396191 sh02e09.yl Gm-c1026 Glycine max cDNA clone... 57 2e-14
      emb|AI773761|AI773761 EST254861 tomato resistant, Cornell Lycope... 65 2e-12
      gb|BE020684|BE020684 sm45f08.yl Gm-c1028 Glycine max cDNA clone ... 74 3e-12
      emb|AF014810|AF014810 Lycopersicon esculentum proline transporte... 54 9e-12
45
      emb|AI728355|AI728355 BNLGHi10544 Six-day Cotton fiber Gossypium... 70 4e-11
      emb|AW780460|AW780460 sl71b05.yl Gm-c1027 Glycine max cDNA clone... 70 6e-11
      emblAF014808|AF014808 Lycopersicon esculentum proline transporte... 55 5e-09
      emb|AF014809|AF014809 Lycopersicon esculentum proline transporte... 52 2e-08
      emb|AW832495|AW832495 sm11e04.y1 Gm-c1027 Glycine max cDNA clone... 60 2e-08
50
      emb|AW563318|AW563318 LG1_228_A07.g1_A002 Light Grown 1 (LG1) So... 48 2e-07
      gb|U64823|NSU64823 Nicotiana sylvestris amino acid permease (nsa... 37 2e-06
      emb|AI489487|AI489487 EST247826 tomato ovary, TAMU Lycopersicon ... 52 1e-05
      emb|AV417239|AV417239 AV417239 Lotus japonicus young plants (two... 52 1e-05
      emb|AI772468|AI772468 EST253568 tomato resistant, Cornell Lycope... 52 1e-05
      gb|BE023644|BE023644 sm83e05.yl Gm-c1015 Glycine max cDNA clone ... 51 2e-05
55
      emb|AW102341|AW102341 sd86d12.yl Gm-c1009 Glycine max cDNA clone... 49 9e-05
      emb|AW560837|AW560837 EST315885 DSIR Medicago truncatula cDNA cl... 47 3e-04
      emb|AW720608|AW720608 LjNEST20d11rc Lotus japonicus nodule libra... 47 4e-04
      emb|AW720138|AW720138 LjNEST15d10r Lotus japonicus nodule librar... 47 4e-04
60
      emb|AV409658|AV409658 AV409658 Lotus japonicus young plants (two... 47 4e-04
      emb|AW691465|AW691465 NF045C04ST1F1000 Developing stem Medicago ... 44 8e-04
```

emb|AW428965|AW428965 EST306505 tomato flower buds 0-3 mm, Corne... 35 0.001 emb|AJ004959|CAA004959 Cicer arietinum mRNA for hypothetical pro... 45 0.002 emb|AW757005|AW757005 sl02a06.yl Gm-c1036 Glycine max cDNA clone... 45 0.002 emb|Z49501|SCYJR001W S.cerevisiae chromosome X reading frame ORF... 44 0.003 5 emb[X87611]SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). emblAW677443|AW677443 DG1 7 D10.b1 A002 Dark Grown 1 (DG1) Sorgh... 44 0.004 emb|AQ841996|AQ841996 T134282 Soybean RFLP probe Glycine max gen... 44 0.004 Query= AL049500.57_s_at 16914_s at /id source genbank /description 10 emb|cab39936.1| (al049500) osmotin precursor [arabidopsis thaliana] /blast score 1.00e-143 /ec number /family /chip nova /gb link /ncgi (735 letters) 15 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 20 Score E Sequences producing significant alignments: (bits) Value emb|AW685448|AW685448 NF029F08NR1F1000 Nodulated root Medicago t... 409 e-114 emb|AJ010501|CAR010501 Cicer arietinum L. mRNA for thaumatin-lik... 409 e-114 25 emb|AW573922|AW573922 EST316513 GVN Medicago truncatula cDNA clo... 409 e-113 emb|AW685184|AW685184 NF026H08NR1F1000 Nodulated root Medicago t... 338 e-105 emb|AW348587|AW348587 GM210002B22C8R Gm-r1021 Glycine max cDNA 3... 365 e-101 emb|AW685583|AW685583 NF029C04NR1F1000 Nodulated root Medicago t... 320 e-100 emb|X15224|NTE22TLP Tobacco E22 gene for a thaumatin-like protein. 201 4e-99 30 emb|X12739|NTPRRMAJ N. tabacum mRNA for pathogenesis-related pro... 201 4e-99 emb|AF003007|AF003007 Vitis vinifera thaumatin-like protein VVTL... 214 7e-98 emb[X15223]NTE2TLP Tobacco E2 gene for a thaumatin-like protein. 195 2e-97 emb[X03913]NTTHAUR Tobacco mRNA for TMV induced protein homologo... 195 2e-97 emb|AW684755|AW684755 NF021G01NR1F1000 Nodulated root Medicago t... 348 3e-95 35 emb|AV428977|AV428977 AV428977 Lotus japonicus young plants (two... 343 7e-94 emb[Y10992|VVOSM1 V.vinifera mRNA for osmotin-like protein. emb|AF199508|AF199508 Fragaria x ananassa osmotin-like protein (... 220 1e-89 emb|X72928|SC13OLP S.commersonii (pOSML13) gene for osmotin-like... 200 1e-88 emb[X67121]SCOSMLP S.commersonii mRNA for osmotin-like protein. 40 emb|X70787|LEPRPA L.esculentum pr p23 mRNA for pathogenesis-rela... 200 1e-88 emb|AW039873|AW039873 EST282346 tomato mixed elicitor, BTI Lycop... 200 1e-88 emb|X66416|LETPM1M L.esculentum tpm 1 mRNA. emb|AW218786|AW218786 EST301266 tomato root during/after fruit s... 197 9e-88 dbj|D76437|TOBNP5O Nicotiana sylvestris DNA for neutral PR-5 (os... 193 8e-87

emb|X95308|NTOSPR N.tabacum osmotin gene. 195 8e-87
gb|S40046|S40046 abscisic acid-activated [Nicotiana tabacum L.=t... 195 1e-86
emb|X65701|NTAP24G N.tabacum ap24 gene. 195 1e-86
emb|X65700|NTAP24 N.tabacum mRNA ap24. 195 1e-86
gb|S44889|S44889 osmotin=pathogenesis-related protein homolog [N... 195 1e-86

emb|A16782|A16782 osmotin-like protein gene without 20 C- termin... 195 1e-86 emb|A16780|A16780 osmotin-like protein gene seq ID No: 5. 195 1e-86 emb|A83550|A83550 Sequence 1 from Patent WO9849331. 195 1e-86 gb|M64081|TOBOLP Nicotania tabacum osmotin-like protein (OLP1) m... 193 1e-86

dbj|E03321|E03321 DNA encoding osmotin-like protein. 193 1e-86
emb|X72927|SC81OLP S.commersonii (pOSML81) gene for osmotin-like... 193 7e-86
emb|AW218785|AW218785 EST301265 tomato root during/after fruit s... 200 7e-86
emb|AF093743|AF093743 Lycopersicon esculentum pathogenesis-relat... 193 1e-85
gb|M21346|TOMNP24 Tomato NP24 protein mRNA, 3' end. 193 1e-85
emb|AW035171|AW035171 EST280433 tomato callus, TAMU Lycopersicon... 193 1e-85

60 emb|AW223970|AW223970 EST300781 tomato fruit red ripe, TAMU Lyco... 193 1e-85 emb|AW223507|AW223507 EST300318 tomato fruit red ripe, TAMU Lyco... 193 1e-85

emb|AW222204|AW222204 EST299015 tomato fruit red ripe, TAMU Lyco... 193 1e-85 emb|AW217005|AW217005 EST295719 tomato callus, TAMU Lycopersicon... 193 1e-85 emb|AW622159|AW622159 EST312957 tomato root during/after fruit s... 193 1e-85 emb|AW684839|AW684839 NF022B04NR1F1000 Nodulated root Medicago t... 316 1e-85 5 emb|AI855542|AI855542 sc20e11.yl Gm-c1013 Glycine max cDNA clone... 185 1e-85 emb|X67244|CSOSLP S.commersonii mRNA for osmotin-like protein. 193 2e-85 emb|AW216590|AW216590 EST295304 tomato callus, TAMU Lycopersicon... 193 3e-85 emb|X72926|SCA81OLP S.commersonii (pA81) mRNA for osmotin-like p... 189 6e-85 emb|AF001528|AF001528 Musa acuminata ripening-associated protein... 307 8e-85 10 emb|AW622107|AW622107 EST312905 tomato root during/after fruit s... 192 9e-85 emb|AW218972|AW218972 EST301454 tomato root during/after fruit s... 191 1e-84 emb|AW033829|AW033829 EST277400 tomato callus, TAMU Lycopersicon... 193 2e-84 emb|AW221921|AW221921 EST298732 tomato fruit red ripe, TAMU Lyco... 187 4e-84 emb|AF109653|AF109653 AF109653 Capsicum annuum root susceptible ... 192 9e-84 15 emb|AW621924|AW621924 EST312722 tomato root during/after fruit s... 192 2e-83 emb|AW650675|AW650675 EST329129 tomato germinating seedlings, TA... 193 1e-82 emb|AW034088|AW034088 EST277583 tomato callus, TAMU Lycopersicon... 193 1e-81 emb|AW219330|AW219330 EST301812 tomato root during/after fruit s... 193 1e-81 emb|AW034433|AW034433 EST278004 tomato callus, TAMU Lycopersicon... 175 2e-80 emb|AI895910|AI895910 EST265353 tomato callus, TAMU Lycopersicon... 177 3e-80 emb|AW625009|AW625009 EST313838 tomato radicle, 5 d post-imbibit... 193 4e-80 emb|AI896330|AI896330 EST265773 tomato callus, TAMU Lycopersicon... 193 4e-80 emb|AJ277064|LES277064 Lycopersicon esculentum PR-5 gene for pat... 192 3e-79 gb[M29279]TOBOSM N.tabacum osmotin mRNA, complete cds. 242 4e-79 25 emblAW029746|AW029746 EST273001 tomato callus, TAMU Lycopersicon... 168 2e-78 emb|AW029798|AW029798 EST273053 tomato callus, TAMU Lycopersicon... 168 2e-78 emb|AW650717|AW650717 EST329171 tomato germinating seedlings, TA... 165 2e-77 emb|AW094053|AW094053 EST287233 tomato mixed elicitor, BTI Lycop... 166 3e-77 emb|X61679|NTOSMOTIN N.tabacum mRNA for osmotin. 193 8e-77 30 emb|AW686653|AW686653 NF043G01NR1F1000 Nodulated root Medicago t... 265 1e-76 emb|AW220061|AW220061 EST302544 tomato root during/after fruit s... 193 1e-76 emb|AW830631|AW830631 sm04e12.yl Gm-c1027 Glycine max cDNA clone... 230 2e-76 emb|AW099440|AW099440 sd40e08.yl Gm-c1016 Glycine max cDNA clone... 227 2e-76 emb|AW458142|AW458142 sh78g09.y1 Gm-c1016 Glycine max cDNA clone... 185 2e-75 35 emb|AJ131731|PME131731 Pseudotsuga menziesii mRNA for Thaumatin-... 237 3e-74 gb|BE033983|BE033983 MG02H11 MG Mesembryanthemum crystallinum cD... 155 2e-73 gb[BE034303]BE034303 MH03A01 MH Mesembryanthemum crystallinum cD... 139 4e-73 emb|AW686245|AW686245 NF035F09NR1F1000 Nodulated root Medicago t... 274 7e-73 emb|A15671|A15671 proprothaumatine. 116 4e-72 40 gb|J01209|TDATHAU2 T.daniellii preprothaumatin-2 mRNA, complete ... 116 4e-72 emb|A15673|A15673 proprothaumatine and the coding strand of its ... 116 4e-72 emb|A15677|A15677 proprothaumatine and the coding stand of its s... 116 4e-72 emb|AF110151|AF110151 AF110151 Capsicum annuum root 1st-branched... 192 4e-72 emb|A15675|A15675 proprothaumatine and the coding strand of its ... 116 2e-71 45 emb|A15660|A15660 Mature thaumatin. 116 2e-71 emb|A46806|A46806 Sequence 3 from Patent EP0684312. emb|AF121776|AF121776 Juniperus ashei allergen Jun a 3 mRNA, com... 144 1e-70 emb|AF016327|AF016327 Hordeum vulgare Barperm1 (perm1) mRNA, par... 221 3e-70 emb|AW031249|AW031249 EST274624 tomato callus, TAMU Lycopersicon... 200 3e-70 50 emb|AI896554|AI896554 EST265997 tomato callus, TAMU Lycopersicon... 140 5e-70 emb|AF108890|AF108890 AF108890 Capsicum annuum root 1st-branched... 177 9e-70 emb|AV423642|AV423642 AV423642 Lotus japonicus young plants (two... 263 1e-69 emb|AI055586|AI055586 coau0004G15 Cotton Boll Abscission Zone cD... 262 2e-69 emb|AW032915|AW032915 EST276474 tomato callus, TAMU Lycopersicon... 200 2e-69 55 emb|A46810|A46810 Sequence 7 from Patent EP0684312. emb|AW441774|AW441774 EST311170 tomato fruit red ripe, TAMU Lyco... 193 1e-68 emb|AW223623|AW223623 EST300434 tomato fruit red ripe, TAMU Lyco... 193 1e-68 emb|AW032317|AW032317 EST275771 tomato callus, TAMU Lycopersicon... 193 1e-68 emb|AW224329|AW224329 EST301140 tomato fruit red ripe, TAMU Lyco... 193 1e-68 emb|AI895353|AI895353 EST264796 tomato callus, TAMU Lycopersicon... 193 1e-68 60 emb|AA824730|AA824730 CT028.SK Tomato Leaf cDNA from cv. VFNT ch... 193 1e-68

Query= U35829.2_s_at 16981_s_at /id_source genbank /description gb|aac49356.1| (u35829) thioredoxin h [arabidopsis thaliana] 5 /blast_score 4.00e-64 /ec_number /family /chip nova /gb_link /ncgi (357 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching.....done Score Sequences producing significant alignments: (bits) Value 15 emb[X89759]BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 2e-49 gblU59379|BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 2e-49 emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 9e-49 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 190 3e-48 20 emb|AW569018|AW569018 si74e02.yl Gm-c1031 Glycine max cDNA clone... 185 1e-46 emb|AI988470|AI988470 sd02f07.yl Gm-c1020 Glycine max cDNA clone... 185 1e-46 emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 182 9e-46 gb|BE053835|BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 9e-46 25 emb|AW677726|AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ... 181 2e-45 emb|AW924685|AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ... 181 2e-45 emb|AW565750|AW565750 LG1_349_G02.g1_A002 Light Grown 1 (LG1) So... 181 2e-45 emb|AW671668|AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So... 181 2e-45 emb|AW677651|AW677651 WS1 10 F03.b1 A002 Water-stressed 1 (WS1) ... 181 2e-45 30 emb|AW349345|AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 179 6eemb|AI938238|AI938238 sc41e05.yl Gm-c1014 Glycine max cDNA clone... 179 6e-45 emb|AI461219|AI461219 sa76f11.yl Gm-c1004 Glycine max cDNA clone... 179 6e-45 emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. 35 emb|AW164730|AW164730 se77a02.yl Gm-c1023 Glycine max cDNA clone... 179 9e-45 gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 3e-44 dbj|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 4e-44 emb|AW983331|AW983331 HVSMEg0010D20f Hordeum vulgare pre-anthesi... 177 4e-44 40 emb|AW329521|AW329521 N200767e rootphos(-) Medicago truncatula c... 176 6e-44 emblAW255195|AW255195 ML185 peppermint glandular trichome Mentha... 176 8e-44 emb|X69915|TATHIORDH T.aestivum mRNA for thioredoxine H. 175 1e-43 emb|AW164347|AW164347 se71c11.yl Gm-c1023 Glycine max cDNA clone... 175 1e-43 45 emb|AW781479|AW781479 sl79e04.yl Gm-c1037 Glycine max cDNA clone... 175 1e-43 emb|A48516|A48516 Sequence 4 from Patent WO9603505. 175 le-43 emb|AW705063|AW705063 sk57b09.yl Gm-c1019 Glycine max cDNA clone... 175 1e-43 emb|AW568753|AW568753 si72f07.yl Gm-c1031 Glycine max cDNA clone... 175 1e-43 emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 175 1e-43 50 emb|AJ001903|TDAJ1903 Triticum durum mRNA for thioredoxin H. 175 le-43 emb|A48520|A48520 Sequence 8 from Patent WO9603505. 175 le-43 emb|A48514|A48514 Sequence 2 from Patent WO9603505. 175 le-43 emb|A48519|A48519 Sequence 7 from Patent WO9603505. 175 1e-43 emb|AW329764|AW329764 N201033e rootphos(-) Medicago truncatula c... 174 2e-43 55 emb|AW983305|AW983305 HVSMEg0010C12f Hordeum vulgare pre-anthesi... 174 3e-43 emb|AW626018|AW626018 EST319925 tomato radicle, 5 d post-imbibit... 174 3e-43 emb|AW982237|AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi... 174 3e-43 emb|X58527|NTTRNA N.tabacum mRNA for thioredoxin. 173 5e-43 gb[U59380]BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 5e-43 60 gb|C95504|C95504 C95504 Citrus unshiu Miyagawa-wase maturation s... 172 7e-43

emb|AW277335|AW277335 sf80b02.yl Gm-c1019 Glycine max cDNA clone... 171 le-42

emb|AI441505|AI441505 sa87c03.y1 Gm-c1004 Glycine max cDNA clone... 171 1e-42 emb|AW349509|AW349509 GM210005A21B12R Gm-r1021 Glycine max cDNA ... 171 1eemb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 3e-42 5 emb|AI775760|AI775760 EST256860 tomato resistant, Cornell Lycope... 171 3e-42 emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycope... 171 3e-42 emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycope... 171 3e-42 emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 3e-42 emblAW040011|AW040011 EST282502 tomato mixed elicitor, BTI Lycop... 171 3e-42 10 emblAW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 3e-42 emb|AW621673|AW621673 EST312471 tomato root during/after fruit s... 171 3e-42 emb|AI780240|AI780240 EST261119 tomato susceptible, Cornell Lyco... 171 3e-42 emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 3e-42 emblAW038141|AW038141 EST279798 tomato mixed elicitor, BTI Lycop... 171 3e-42 15 emb|AW038924|AW038924 EST280880 tomato mixed elicitor, BTI Lycop... 171 3e-42 emblAW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 3e-42 emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 3e-42 emblAW625957|AW625957 EST319852 tomato radicle, 5 d post-imbibit... 171 3e-42 emb|AI781827|AI781827 EST262706 tomato susceptible, Cornell Lyco... 171 3e-42 20 emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 3e-42 emb|AW625331|AW625331 EST319154 tomato radicle, 5 d post-imbibit... 171 3e-42 emb|AW597424|AW597424 si92g01.yl Gm-c1031 Glycine max cDNA clone... 169 9e-42 emb|AW040201|AW040201 EST282700 tomato mixed elicitor, BTI Lycop... 168 1e-41 emb|AW040195|AW040195 EST282694 tomato mixed elicitor, BTI Lycop... 168 1e-41 25 emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 1e-41 gb|BE057793|BE057793 sn07c11.yl Gm-c1016 Glycine max cDNA clone ... 168 1e-41 emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 165 2e-40 emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 2e-40 emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 8e-40 30 emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 1e-39 emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 1e-39 emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 1e-39 emb|AW042699|AW042699 ST23E01 Pine TriplEx shoot tip library Pin... 162 1e-39 emb|AW043379|AW043379 ST32F12 Pine TriplEx shoot tip library Pin... 162 1e-39 35 emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 1e-39 emb|AW043171|AW043171 ST30B09 Pine TriplEx shoot tip library Pin... 162 1e-39 emb|AW497847|AW497847 PC02B02 Pine TriplEx pollen cone library P... 161 1e-39 emb|AW736931|AW736931 NXNV 081 G02 F Nsf Xylem Normal wood Verti... 161 1e-39 emb|AW680877|AW680877 WS1_7_D07.g1_A002 Water-stressed 1 (WS1) S... 161 2e-39 40 emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 2e-39 emb|AW011327|AW011327 ST19E02 Pine TriplEx shoot tip library Pin... 160 3e-39 emb|AW011046|AW011046 ST16A08 Pine TriplEx shoot tip library Pin... 160 4e-39 emb|AI736736|AI736736 sb32g12.yl Gm-c1012 Glycine max cDNA clone... 93 6e-39 emb|AW010836|AW010836 ST14F05 Pine TriplEx shoot tip library Pin... 159 7e-39 45 emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 1e-38 emblAW011498|AW011498 ST21E10 Pine TriplEx shoot tip library Pin... 158 2e-38 emb|AA740038|AA740038 803 PtIFG2 Pinus taeda cDNA clone 9266M 3'... 157 3e-38 emb|AW009991|AW009991 ST01A09 Pine TriplEx shoot tip library Pin... 157 3e-38 emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 3e-38 50 emb|AW706540|AW706540 sj57g11.yl Gm-c1033 Glycine max cDNA clone... 156 7e-38 emb|AI461254|AI461254 sa60f10.yl Gm-c1004 Glycine max cDNA clone... 155 9e-38 emb|AW745883|AW745883 WS1 38 B01.b1_A002 Water-stressed 1 (WS1) ... 154 2e-37 emb|AW923038|AW923038 DG1 48 B02.g1 A002 Dark Grown 1 (DG1) Sorg... 154 2e-37 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 2e-37 55 emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154_2e-37 emb|AW679524|AW679524 WS1 29 F05.g1 A002 Water-stressed 1 (WS1) ... 154 2e-37

Query= AC002391.188_at 16995_at /id_source genbank /description gb|aab87114.1| (ac002391) unknown protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova/gb link

http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002391| /ncgi http://www.ncgr.org/cgi-bin/ff?ac002391 (1896 letters)

5

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

10

Score E

Sequences producing significant alignments:

(bits) Value

emb|AF123503|AF123503 Nicotiana tabacum Nt-gh3 deduced protein m... 484 0.0 15 emb|X60033|GMGH3G G.max GH3 gene for auxin-regulated protein. emb|AI489187|AI489187 EST247526 tomato ovary, TAMU Lycopersicon ... 421 e-116 emb|AI489278|AI489278 EST247617 tomato ovary, TAMU Lycopersicon ... 410 e-113 emb|AW223544|AW223544 EST300355 tomato fruit red ripe, TAMU Lyco... 385 e-106 emb|AI729810|AI729810 BNLGHi5260 Six-day Cotton fiber Gossypium ... 225 e-103 20 emb|AW455302|AW455302 EST311840 tomato root during/after fruit s... 358 6e-98 emb|AW307114|AW307114 sf52h11.y1 Gm-c1009 Glycine max cDNA clone... 357 2e-97 emb|AW730905|AW730905 GA_ Ea0029G23 Gossypium arboreum 7-10 dpa ... 321 2e-95 emb|AW737090|AW737090 EST338517 tomato flower buds, anthesis, Co... 228 3e-94 gb|BE053589|BE053589 GA Ea0013N22f Gossypium arboreum 7-10 dpa ... 298 1e-79 25 emb|AW164615|AW164615 se74c04.y1 Gm-c1023 Glycine max cDNA clone... 169 1e-78 emb|AW686313|AW686313 NF040C09NR1F1000 Nodulated root Medicago t... 211 7e-78 emb|AW035201|AW035201 EST280463 tomato callus, TAMU Lycopersicon... 153 2e-77 emb|AW720296|AW720296 LjNEST20d3r Lotus japonicus nodule library... 290 3e-77 emb|AW559498|AW559498 EST314546 DSIR Medicago truncatula cDNA cl... 169 3e-76 30 emb|AW774169|AW774169 EST333252 KV3 Medicago truncatula cDNA clo... 169 1e-75 emb|AW125947|AW125947 N100142e rootphos(-) Medicago truncatula c... 274 1e-72 emb|AW668277|AW668277 GA__Ea0013G22 Gossypium arboreum 7-10 dpa ... 271 1e-71 emb|AW980820|AW980820 EST391973 GVN Medicago truncatula cDNA clo... 254 2e-66 emb|AW221739|AW221739 EST298550 tomato fruit red ripe, TAMU Lyco... 180 6e-63 35 emb|AW929039|AW929039 EST337743 tomato flower buds 8 mm to pre-a... 144 6e-62 emb|AV410002|AV410002 AV410002 Lotus japonicus young plants (two... 232 9e-61 emb|AW720379|AW720379 LjNEST22a11r Lotus japonicus nodule librar... 175 2e-59 emb|AW928468|AW928468 EST337256 tomato flower buds 8 mm to pre-a... 200 3e-59 emb|AW163964|AW163964 Ljirnpest17-383-g11 Ljirnp Lambda HybriZap... 198 6e-57 40 emb|AW185677|AW185677 se58c02.yl Gm-c1019 Glycine max cDNA clone... 219 5e-56 emb[AI773943]AI773943 EST255043 tomato resistant, Cornell Lycope... 133 5e-54 emb|AI054856|AI054856 coau0002F14 Cotton Boll Abscission Zone cD... 97 8e-53 emb|AV426547|AV426547 AV426547 Lotus japonicus young plants (two... 135 1e-51 emblAW684512|AW684512 NF017G09NR1F1000 Nodulated root Medicago t... 197 2e-49 45 emb|AW428928|AW428928 Ljirnpest25-068-h9 Ljirnp Lambda HybriZap ... 107 5e-49 emb|AI484627|AI484627 EST242888 tomato ovary, TAMU Lycopersicon ... 194 1e-48 emb|AW676760|AW676760 DG1_14_F09.g1_A002 Dark Grown 1 (DG1) Sorg... 167 2e-47 emb|AW647702|AW647702 EST307181 tomato germinating seedlings, TA... 130 2e-44 emb|AW160191|AW160191 EST290048 L. pennellii trichome, Cornell U... 137 6e-44 50 emb|AI775892|AI775892 EST256992 tomato resistant, Cornell Lycope... 177 2e-43 emb|AW031091|AW031091 EST274398 tomato callus, TAMU Lycopersicon... 104 4e-43 emb|AI437757|AI437757 sa39b12.yl Gm-c1004 Glycine max cDNA clone... 144 6e-43 emblAW647700|AW647700 EST307179 tomato germinating seedlings, TA... 129 7e-43 gb|BE122431|BE122431 Ljimpest26-072-a2 Ljimp Lambda HybriZap t... 107 1e-42 55 emb|AW349113|AW349113 GM210004B21A1R Gm-r1021 Glycine max cDNA 3... 131 4eemb|AI737532|AI737532 T110159e KV0 Medicago truncatula cDNA clon... 165 le-39 emb|AV420807|AV420807 AV420807 Lotus japonicus young plants (two... 154 7e-39 emb|AW622684|AW622684 EST306821 tomato flower buds 3-8 mm, Corne... 105 7e-38 60 emblAW217219|AW217219 EST295933 tomato callus, TAMU Lycopersicon... 157 2e-37

emb|AI771570|AI771570 EST252670 tomato ovary, TAMU Lycopersicon ... 112 3e-37

emb|AI483575|AI483575 EST249425 tomato ovary, TAMU Lycopersicon ... 112 3e-37 emb|AW781778|AW781778 sl92c01.yl Gm-c1037 Glycine max cDNA clone... 110 1e-35 emb|AW932607|AW932607 EST358450 tomato fruit mature green, TAMU ... 116 3e-35 emb|AW596402|AW596402 sj12a06.y1 Gm-c1032 Glycine max cDNA clone... 103 9e-35 5 emb|AI487477|AI487477 EST245799 tomato ovary, TAMU Lycopersicon ... 113 8e-34 emblAW568731|AW568731 si72d08.y1 Gm-c1031 Glycine max cDNA clone... 104 1e-33 emblAW037990|AW037990 EST279634 tomato mixed elicitor, BTI Lycop... 91 2e-31 emb|AW442518|AW442518 EST307448 tomato mixed elicitor, BTI Lycop... 92 1e-30 emb|AV408894|AV408894 AV408894 Lotus japonicus young plants (two... 132 1e-29 10 emb|AW597236|AW597236 si91a07.y1 Gm-c1031 Glycine max cDNA clone... 91 1e-29 emb|AB005877|AB005877 Nicotiana tabacum mRNA for BYJ14, partial ... 131 2e-29 emb|AI483752|AI483752 EST249623 tomato ovary, TAMU Lycopersicon ... 104 6e-29 emb|AW234030|AW234030 sf33c09.y1 Gm-c1028 Glycine max cDNA clone... 79 2e-28 emb[AW156137|AW156137 se20a04.y1 Gm-c1015 Glycine max cDNA clone... 125 1e-27 15 emb|AI900868|AI900868 sb95e02.yl Gm-c1012 Glycine max cDNA clone... 104 1e-26 emb|AI779963|AI779963 EST260842 tomato susceptible, Cornell Lyco... 122 1e-26 emb|AI898974|AI898974 EST268417 tomato ovary, TAMU Lycopersicon ... 99 3e-24 emb|AI778687|AI778687 EST259566 tomato susceptible, Cornell Lyco... 113 5e-24 emblAW981373|AW981373 EST392526 DSIL Medicago truncatula cDNA cl... 101 1e-23 20 emb|AI441355|AI441355 sa55f08.yl Gm-c1004 Glycine max cDNA clone... 59 8e-22 emb|AI974524|AI974524 T110474e KV0 Medicago truncatula cDNA clon... 105 2e-21 emb|AI899093|AI899093 EST268536 tomato ovary, TAMU Lycopersicon ... 104 2e-21 emb|AI777312|AI777312 EST258277 tomato resistant, Cornell Lycope... 103 6e-21 emb|AW398897|AW398897 EST309397 L. pennellii trichome, Cornell U... 74 1e-20 25 emb|AI166806|AI166806 xylem.est.601 Poplar xylem Lambda ZAPII li... 84 9e-20 emb|AW224185|AW224185 EST301092 tomato fruit red ripe, TAMU Lyco... 98 2e-19 emb|AA824951|AA824951 CT234.UNI Tomato Leaf cDNA from cv. VFNT c... 93 3e-19 emb[AW458783]AW458783 sh14c06.yl Gm-c1016 Glycine max cDNA clone... 95 1e-18 emb|AW038098|AW038098 EST279755 tomato mixed elicitor, BTI Lycop... 62 4e-16 30 emb|AW618367|AW618367 EST320353 L. pennellii trichome, Cornell U... 85 2e-15 emb|AI776968|AI776968 EST252060 tomato callus, TAMU Lycopersicon... 85 2e-15 emb|AW622772|AW622772 EST306758 tomato flower buds 3-8 mm. Corne... 55 3e-15 emb|AI777546|AI777546 EST258520 tomato susceptible, Cornell Lyco... 63 4e-15 emb|AW618243|AW618243 EST314293 L. pennellii trichome, Cornell U... 66 5e-15 35 emb|AW278756|AW278756 sf97b03.y1 Gm-c1019 Glycine max cDNA clone... 82 1e-14 emb[AW092080]AW092080 EST285356 tomato mixed elicitor, BTI Lycop... 71 8e-14 emb|AW282596|AW282596 LG1 310 F07.g1 A002 Light Grown 1 (LG1) So... 61 1e-13 emb|AW705294|AW705294 sk59b10.yl Gm-c1019 Glycine max cDNA clone... 78 3e-13 emb|AW738104|AW738104 EST339531 tomato flower buds, anthesis, Co... 77 4e-13 40 emb|AW459172|AW459172 sh21e10.y1 Gm-c1016 Glycine max cDNA clone... 77 6e-13 gb|BE035111|BE035111 MM03C07 MM Mesembryanthemum crystallinum cD... 66 6e-12 emb|AW442808|AW442808 EST307738 tomato mixed elicitor, BTI Lycop... 62 8e-12 emb|AW706842|AW706842 sk04g06.yl Gm-c1023 Glycine max cDNA clone... 72 1e-11 emb|AI773706|AI773706 EST254806 tomato resistant, Cornell Lycope... 49 2e-11 45 emb|AI897063|AI897063 EST266506 tomato ovary, TAMU Lycopersicon ... 66 8e-10 emb|AW032584|AW032584 EST276143 tomato callus, TAMU Lycopersicon... 64 3e-09 emb|AW683199|AW683199 NF008H01LF1F1014 Developing leaf Medicago ... 63 8e-09 gb|BE059206|BE059206 sn27f04.yl Gm-c1016 Glycine max cDNA clone ... 62 1e-08 emb|AW616334|AW616334 EST322745 L. hirsutum trichome, Cornell Un... 61 3e-08 50 emb|AI483553|AI483553 EST249402 tomato ovary, TAMU Lycopersicon ... 59 1e-07 emb|AI773748|AI773748 EST254848 tomato resistant, Cornell Lycope... 59 1e-07 emb|AW038769|AW038769 EST280630 tomato mixed elicitor, BTI Lycop... 56 9e-07 gb|L38057|L38057 BNAF0397E Mustard flower buds Brassica rapa cDN... 53 8e-06

55

Query= AC006585.212_at 17008_at /id_source genbank /description gb|aad23027.1|ac006585_22 (ac006585) putative tyrosine aminotransferase [arabidopsis thaliana] /blast_score 0 /ec_number /family transaminase /chip nova /gb_link

http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006585| /ncgi

http://www.ncgr.org/cgi-bin/ff?ac006585 (1582 letters)

Database: plantfungal 5 661,018 sequences; 426,114,510 total letters Searching.....done Score 10 Sequences producing significant alignments: dbj|D88273|D88273 Hordeum vulgare naat-A mRNA for nicotianamine ... 446 e-124 emb|AB005788|AB005788 Hordeum vulgare mRNA for nicotianamine ami... 433 e-120 15

(bits) Value

emb|AB024006|AB024006 Hordeum vulgare naat-B and naat-A genes fo... 184 3e-78 emb|AW760137|AW760137 sl58e07.yl Gm-c1027 Glycine max cDNA clone... 270 1e-72 emb|AW508844|AW508844 si41a10.yl Gm-r1030 Glycine max cDNA clone... 191 7e-61 emb|AW348839|AW348839 GM210003B11G12R Gm-r1021 Glycine max cDNA ... 233 2e-60

emb|AW832427|AW832427 sm10c03.yl Gm-c1027 Glycine max cDNA clone... 233 3e-60 20 emb|AW760284|AW760284 sl48d01.yl Gm-c1027 Glycine max cDNA clone... 206 6e-55 emb|AW620771|AW620771 sj09d03.yl Gm-c1032 Glycine max cDNA clone... 209 5e-53 emb|AW568831|AW568831 si61g09.yl Gm-r1030 Glycine max cDNA clone... 199 5e-50 emb|AW030722|AW030722 EST273977 tomato callus, TAMU Lycopersicon... 198 9e-50 emb|AW306460|AW306460 se51a02.yl Gm-c1017 Glycine max cDNA clone... 178 8e-44 25 emb|AW459166|AW459166 sh21e03.y1 Gm-c1016 Glycine max cDNA clone... 170 3e-41

emblAW030650|AW030650 EST273905 tomato callus, TAMU Lycopersicon... 96 4e-38 emb|AW202348|AW202348 sf14a04.yl Gm-c1027 Glycine max cDNA clone... 96 1e-33 emb|AW760709|AW760709 s136a11.y1 Gm-c1027 Glycine max cDNA clone... 138 8e-32 gb|BE020273|BE020273 sm42g02.yl Gm-c1028 Glycine max cDNA clone ... 91 3e-31

30 gb|L00673|TRBANTA Trypanosoma cruzi antigen tyrosine aminotransf... 97 1e-26 emb|AW102390|AW102390 sd87b05.yl Gm-c1009 Glycine max cDNA clone... 119 5e-26 emb|AW928492|AW928492 EST337280 tomato flower buds 8 mm to pre-a... 78 9e-25 emb|AI930964|AI930964 sb45d08.y1 Gm-c1015 Glycine max cDNA clone... 115 1e-24 emb|AW678964|AW678964 WS1_21_A12.g1_A002 Water-stressed 1 (WS1) ... 115 1e-24

35 emb|AW928458|AW928458 EST337246 tomato flower buds 8 mm to pre-a... 85 3e-23 emb|AI487927|AI487927 EST246249 tomato ovary, TAMU Lycopersicon ... 70 7e-23 emb|AW737817|AW737817 EST339244 tomato flower buds, anthesis, Co... 79 2e-22 emb|AW924630|AW924630 WS1_70_A07.g1_A002 Water-stressed 1 (WS1) ... 106 5e-22 emb|AW832131|AW832131 sm20a05.yl Gm-c1027 Glycine max cDNA clone... 105 9e-22

emb|AW221912|AW221912 EST298723 tomato fruit red ripe, TAMU Lyco... 70 9e-19 emb|AI562691|AI562691 TENS2678 T. cruzi epimastigote normalized ... 92 1e-18 emb|AI562604|AI562604 TENS2761 T. cruzi epimastigote normalized ... 95 2e-18 emb|AW782202|AW782202 sm02g12.y1 Gm-c1027 Glycine max cDNA clone... 70 1e-16 emb|Z48758|SC9727 S.cerevisiae chromosome IV cosmid 9727. 54 2e-16

45 emblAV421843|AV421843 AV421843 Lotus japonicus young plants (two... 86 6e-16 emb|Z69909|SPAC19G10 S.pombe chromosome I cosmid c19G10. 57 le-15 emb|AL096788|SPBC582 S.pombe chromosome II cosmid c582. 57 le-15 emb|AW034806|AW034806 EST278842 tomato callus, TAMU Lycopersicon... 85 1e-15 gb[U53880|YSCL9449 Saccharomyces cerevisiae chromosome XII cosmi... 51 2e-14

50 emb|Z73261|SCYLR089C S.cerevisiae chromosome XII reading frame O... 51 2e-14 emb|AW100534|AW100534 sd56d09.y1 Gm-c1016 Glycine max cDNA clone... 79 7e-14 emb|AW776160|AW776160 EST335225 DSIL Medicago truncatula cDNA cl... 70 6e-13 emb|Z49335|SCYJL060W S.cerevisiae chromosome X reading frame ORF... 63 8e-13 emb|AW329712|AW329712 N200976e rootphos(-) Medicago truncatula c... 75 1e-12

55 emb|Z98531|SPAC6B12 S.pombe chromosome I cosmid c6B12. emb|AI057693|AI057693 TENU1783 T. cruzi epimastigote normalized ... 74 3e-12 emb|AV419799|AV419799 AV419799 Lotus japonicus young plants (two... 72 2e-11 emb|AW219060|AW219060 EST301542 tomato root during/after fruit s... 71 3e-11 emb|AW756163|AW756163 sl16f12.yl Gm-c1036 Glycine max cDNA clone... 62 2e-08

60 emb|AI667953|AI667953 TENG0919 T. Cruzi epimastigote normalised ... 61 2e-08 emb|AQ911130|AQ911130 GSSTc02564 Trypanosome cruzi random genomi... 61 2e-08

emblAQ904747|AQ904747 GSSTc03969 Trypanosome cruzi random genomi... 61 2e-08 emb|AQ905153|AQ905153 GSSTc03744 Trypanosome cruzi random genomi... 61 2e-08 emb|AI068927|AI068927 mgae0004dB02f Magnaporthe grisea Appressor... 45 5e-08 emblAQ445624|AQ445624 GSSTc00112 Trypanosoma cruzi random genomi... 56 1e-06 5 emb|AII10334|AII10334 TENU3304 T. cruzi epimastigote normalized ... 39 1e-06 emb|AI055475|AI055475 coau0004B14 Cotton Boll Abscission Zone cD... 55 2e-06 gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 50 2e-06 dbj|D01033|CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane... 50 2e-06 emb|AF083816|AF083816 Antirrhinum majus ACC synthase 3 (ACS3) mR... 46 2e-06 10 emb|AI080889|AI080889 TENU3747 T. cruzi epimastigote normalized ... 52 9e-06 emb|AB006805|AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth... 48 1e-05 gb[U59813|CSU59813 Cucumis sativus 1-aminocyclopropane-1-carboxy... 48 1e-05 emb|AW934295|AW934295 EST360138 tomato fruit mature green, TAMU ... 52 1e-05 emb|AW101681|AW101681 sd68f11.y1 Gm-c1008 Glycine max cDNA clone... 51 2e-05 15 emb|AW691076|AW691076 NF041A07ST1F1000 Developing stem Medicago ... 44 2e-05 emb|AW477177|AW477177 ga42h10.y1 Moss EST library PPU Physcomitr... 44 2e-05 emblAV424265|AV424265 AV424265 Lotus japonicus young plants (two... 51 2e-05 emb|AF074929|AF074929 Sinapis arvensis 1-aminocyclopropane-1-car... 46 3e-05 emb|AW033989|AW033989 EST277651 tomato callus, TAMU Lycopersicon... 51 3e-05 20 emb|AF074931|AF074931 Sinapis arvensis 1-aminocyclopropane-1-car... 46 3e-05 emb|AI896625|AI896625 EST266068 tomato callus, TAMU Lycopersicon... 50 5e-05 emb|AW695981|AW695981 NF100F04ST1F1042 Developing stem Medicago ... 50 5e-05 emblAI483496lAI483496 EST249317 tomato ovary, TAMU Lycopersicon ... 41 5e-05 emb|AI487017|AI487017 EST245339 tomato ovary, TAMU Lycopersicon ... 41 5e-05 25 emb[AW032141]AW032141 EST275595 tomato callus, TAMU Lycopersicon... 50 6e-05 emb|AQ906278|AQ906278 GSSTc02322 Trypanosome cruzi random genomi... 50 6e-05 emb|AF074930|AF074930 Sinapis arvensis 1-aminocyclopropane-1-car... 45 9e-05 emb|AI896469|AI896469 EST265900 tomato callus, TAMU Lycopersicon... 49 9e-05 emb|AW033411|AW033411 EST276982 tomato callus, TAMU Lycopersicon... 49 9e-05 30 emb|AW685223|AW685223 NF027D03NR1F1000 Nodulated root Medicago t... emb|AI896781|AI896781 EST266224 tomato callus, TAMU Lycopersicon... 49 9e-05 emb|AV426435|AV426435 AV426435 Lotus japonicus young plants (two... 49 1e-04 emb|AW690226|AW690226 NF030F01ST1F1000 Developing stem Medicago ... emb|AW093940|AW093940 EST287120 tomato mixed elicitor, BTI Lycop... 48 2e-04 35 emb|Z26322|HVALAAT H.vulgare mRNA for alanine aminotransferase. emb|AW727211|AW727211 GA Ea0023N19 Gossypium arboreum 7-10 dpa ... 48 2e-04 emb|AV411813|AV411813 AV411813 Lotus japonicus young plants (two... 48 2e-04 emb[X69421]PMPALAAT2 P. miliaceum mRNA for alanine aminotransfer... 48 2e-04 emb|AQ873648|AQ873648 V73B5 mTn-3xHA/lacZ Insertion Library, str... 48 2e-04 40 emb|AW217028|AW217028 EST295742 tomato callus, TAMU Lycopersicon... 48 2e-04 emb|AW093939|AW093939 EST287119 tomato mixed elicitor, BTI Lycop... 47 3e-04 emb|AZ217827|AZ217827 Sheared DNA-81E6.TF Sheared DNA Trypanosom... 47 3e-04 emb|AF049137|AF049137 Dianthus caryophyllus 1-aminocyclopropane-... 47 4e-04 emb|AI773775|AI773775 EST254875 tomato resistant, Cornell Lycope... 39 4e-04 45 emb|AF052832|AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 47 4e-04 emb|AF049711|AF049711 Petunia x hybrida pollen-specific 1-aminoc... 42 5e-04 emb|AB010102|AB010102 Malus domestica gene for 1-aminocyclopropa... 41 7e-04 gb|U89156|MDU89156 Malus domestica ACC synthase (MdACS-1) gene, ... 41 7e-04 gb|L31347|MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox... 41 7e-04 50 emb|AB015624|AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 41 7e-04 emb|AB007449|AB007449 Actinidia deliciosa mRNA for 1-aminocyclop... 42 7e-04

Query= AJ006961.4_s_at 17413_s_at /id_source genbank /description emb|caa67551.1| (x99097) peroxidase [arabidopsis thaliana] /blast_score 2.00e-84 /ec_number /family /chip nova /gb_link /ncgi (460 letters)

Database: plantfungal
60 661,018 sequences; 426,114,510 total letters

Searching.....

.....done Score E Sequences producing significant alignments: (bits) Value 5 emb|AW035239|AW035239 EST280501 tomato callus, TAMU Lycopersicon... 274 3e-73 emb|AW035958|AW035958 EST282817 tomato callus, TAMU Lycopersicon... 274 3e-73 emb[X94943]LECEVI16G L.esculentum mRNA for peroxidase. 274 3e-73 emb|AW032485|AW032485 EST276044 tomato callus, TAMU Lycopersicon... 272 le-72 10 gb|M37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 271 2e-72 emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 265 1e-70 emb|AI777064|AI777064 EST252031 tomato callus, TAMU Lycopersicon... 261 3e-69 emb|AW216562|AW216562 EST295276 tomato callus, TAMU Lycopersicon... 259 9e-69 emb|AW035446|AW035446 EST281184 tomato callus, TAMU Lycopersicon... 258 2e-68 15 emb|AB027753|AB027753 Nicotiana tabacum mRNA for peroxidase, com... 255 1e-67 emb|AW216873|AW216873 EST295587 tomato callus, TAMU Lycopersicon... 251 2e-66 ' emb|AV414074|AV414074 AV414074 Lotus japonicus young plants (two... 250 5e-66 emb|AI773788|AI773788 EST254888 tomato resistant, Cornell Lycope... 246 9e-65 gb|L36112|SSNPEROXIC Stylosanthes humilis peroxidase mRNA. 193 3e-64 20 emb|Y10468|SOPRXR7 S.oleracea mRNA for peroxidase, clone PC36. 242 8e-64 emblAW035207|AW035207 EST280469 tomato callus, TAMU Lycopersicon... 237 5e-62 emb|AV422753|AV422753 AV422753 Lotus japonicus young plants (two... 235 1e-61 emb|AW224630|AW224630 EST303073 tomato root, plants pre-anthesis... 235 2e-61 emb|AW224631|AW224631 EST303074 tomato root, plants pre-anthesis... 235 2e-61 25 emb|AW219926|AW219926 EST302409 tomato root during/after fruit s... 235 2e-61 emb|AW224632|AW224632 EST303075 tomato root, plants pre-anthesis... 235 2e-61 emb|AW759829|AW759829 sl54f01.yl Gm-c1027 Glycine max cDNA clone... 231 3e-60 emb|AW219312|AW219312 EST301794 tomato root during/after fruit s... 230 6e-60 emblAW219314|AW219314 EST301796 tomato root during/after fruit s... 229 1e-59 30 emb|AW219112|AW219112 EST301594 tomato root during/after fruit s... 227 3e-59 emb|AI772237|AI772237 EST253337 tomato resistant, Cornell Lycope... 223 5e-58 emb|AW035660|AW035660 EST281492 tomato callus, TAMU Lycopersicon... 223 7e-58 emb|AW035872|AW035872 EST282181 tomato callus, TAMU Lycopersicon... 221 4e-57 emb|AW621675|AW621675 EST312473 tomato root during/after fruit s... 220 7e-57 35 emb|AW666030|AW666030 sk31c04.yl Gm-c1028 Glycine max cDNA clone... 216 8e-56 emb|AI778513|AI778513 EST259392 tomato susceptible, Cornell Lyco... 213 6e-55 emb|AW224633|AW224633 EST303076 tomato root, plants pre-anthesis... 215 6e-55 gb|L77080|SSNCAPEA Stylosanthes humilis cationic peroxidase gene... 161 9e-55 emb|AW031362|AW031362 EST274816 tomato callus, TAMU Lycopersicon... 205 2e-52 40 emb|AV414872|AV414872 AV414872 Lotus japonicus young plants (two... 202 2e-51 emb|AW033820|AW033820 EST277391 tomato callus, TAMU Lycopersicon... 193 7e-49 emb|AW029850|AW029850 EST273105 tomato callus, TAMU Lycopersicon... 191 3e-48 emb|AI895550|AI895550 EST264993 tomato callus, TAMU Lycopersicon... 188 3e-47 emb|AW030052|AW030052 EST273307 tomato callus, TAMU Lycopersicon... 186 8e-47 45 emb|AF145349|AF145349 Glycine max peroxidase (Prx3) mRNA, partia... 143 2e-46 emb|AI774511|AI774511 EST255611 tomato resistant, Cornell Lycope... 184 4e-46 emb|X57564|ARNEUPERO A.rusticana mRNA for neutral peroxidase. 129 2e-45 emb|AW220442|AW220442 EST302925 tomato root during/after fruit s... 108 3e-44 emb|AW625509|AW625509 EST319416 tomato radicle, 5 d post-imbibit... 106 7e-44 50 emb|AW569733|AW569733 si79g02.yl Gm-c1031 Glycine max cDNA clone... 175 2e-43 emb|AW621545|AW621545 EST312343 tomato root during/after fruit s... 108 2e-43 emb|AW694946|AW694946 NF081G11ST1F1087 Developing stem Medicago ... 142 4e-43 emb|AW132575|AW132575 se05h10.yl Gm-c1013 Glycine max cDNA clone... 138 5e-43 emb|AF109663|AF109663 AF109663 Capsicum annuum root susceptible ... 161 2e-42 55 emb|AW622066|AW622066 EST312864 tomato root during/after fruit s... 111 4e-42 gb|U51194|GMU51194 Glycine max peroxidase (sEPb2) mRNA, partial ... 138 4e-42 gb|L13654|TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN... 112 5e-42 gb|U51193|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial ... 133 2e-41 emb|AW219925|AW219925 EST302408 tomato root during/after fruit s... 168 2e-41 60 emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 111 2e-41 emb|AW621198|AW621198 EST311996 tomato root during/after fruit s... 111 2e-41

```
emb|AW626302|AW626302 EST320209 tomato radicle, 5 d post-imbibit... 111 2e-41
      emb|AW720673|AW720673 LjNEST4b2rc Lotus japonicus nodule library... 123 2e-41
      emb|AW693737|AW693737 NF068E06ST1F1050 Developing stem Medicago ... 136 3e-41
      emb|AW621449|AW621449 EST312247 tomato root during/after fruit s... 110 5e-41
      emb|AW928514|AW928514 EST337302 tomato flower buds 8 mm to pre-a... 95 5e-41
 5
      emb|AW220017|AW220017 EST302500 tomato root during/after fruit s... 111 1e-40
      emb|AI771103|AI771103 EST252203 tomato ovary, TAMU Lycopersicon ... 111 1e-40
      emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 11:1 1e-40
      emb|AW219955|AW219955 EST302438 tomato root during/after fruit s... 111 1e-40
10
      emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 103 2e-40
      gb|L13653|TOMTPX2A Lycopersicon esculentum peroxidase (TPX2) mRN... 107 2e-40
      emb|AI773722|AI773722 EST254822 tomato resistant, Cornell Lycope... 165 2e-40
      emb|AW035007|AW035007 EST279236 tomato callus, TAMU Lycopersicon... 165 2e-40
      emb|AI729640|AI729640 BNLGHi13846 Six-day Cotton fiber Gossypium... 155 4e-40
15
      emb|AI725603|AI725603 BNLGHi12435 Six-day Cotton fiber Gossypium... 153 5e-40
      emb|AF155124|AF155124 Gossypium hirsutum bacterial-induced perox... 94 8e-40
      emb|AV426241|AV426241 AV426241 Lotus japonicus young plants (two... 163 9e-40
      emb|AW034987|AW034987 EST279216 tomato callus, TAMU Lycopersicon... 163 9e-40
      emb|AW561204|AW561204 ga76g12.y1 Moss EST library PPU Physcomitr... 148 1e-39
20
      emb|Y10470|SOPRXR9 S.oleracea mRNA for peroxidase, clone PC56.
      gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 124 2e-39
      emb|AW671673|AW671673 LG1_349_F09.b1_A002 Light Grown 1 (LG1) So... 147 2e-39
      emb|AI728549|AI728549 BNLGHi11012 Six-day Cotton fiber Gossypium... 153 2e-39
      emb|AW672124|AW672124 LG1 357_F02.b1_A002 Light Grown 1 (LG1) So... 147 2e-39
25
      emb|AW625780|AW625780 EST319687 tomato radicle, 5 d post-imbibit... 105 2e-39
      emb|AW621202|AW621202 EST312000 tomato root during/after fruit s... 105 2e-39
      emb|Y16778|SPY16778 Spinacia oleracea mRNA for peroxidase, prx11... 130 3e-39
      emb|AI522935|AI522935 sa92c07.yl Gm-c1004 Glycine max cDNA clone... 126 3e-39
      emb|AW219743|AW219743 EST302225 tomato root during/after fruit s... 111 4e-39
30
      emb|Y17192|CPY17192 Cucurbita pepo mRNA for peroxidase.
      emb|AW622593|AW622593 EST313393 tomato root during/after fruit s... 105 1e-38
      emb|AW220074|AW220074 EST302557 tomato root during/after fruit s... 113 1e-38
      emb|AW219160|AW219160 EST301642 tomato root during/after fruit s... 107 1e-38
      emb|AW625441|AW625441 EST319348 tomato radicle, 5 d post-imbibit... 107 1e-38
35
      emb|AW625860|AW625860 EST319767 tomato radicle, 5 d post-imbibit... 105 1e-38
      emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 112 2e-38
      emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 101 3e-38
      emb|AW647641|AW647641 EST307119 tomato germinating seedlings, TA... 107 3e-38
      emb|AI895098|AI895098 EST264541 tomato callus, TAMU Lycopersicon... 111 6e-38
40
      emb|AW032353|AW032353 EST275807 tomato callus, TAMU Lycopersicon... 156 7e-38
      emb|AW719266|AW719266 LjNEST1h8r Lotus japonicus nodule library,... 111 1e-37
      emb|AI055188|AI055188 coau0003E18 Cotton Boll Abscission Zone cD... 99 2e-37
      emb|AW689722|AW689722 NF023F03ST1F1000 Developing stem Medicago ... 123 2e-37
      emb|AW686882|AW686882 NF003E08RT1F1000 Developing root Medicago ... 105 3e-37
45
      Query= AC000132.72_at 17464_at /id_source genbank /description
      "gb|aab60752.1| (ac000132) similar to a. thaliana receptor-like
      protein kinase (gb|rlk5_arath). ests gb|atts0475,gb|atts4362 come from
      this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
50
      kinase /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000132|/ncgi
      http://www.ncgr.org/cgi-bin/ff?ac000132
           (2766 letters)
55
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
```

Searching.....done

60

Score E.

Sequences producing significant alignments:

(bits) Value

```
emb|AF053127|AF053127 Malus domestica leucine-rich receptor-like... 333 2e-91
       emb|AW036763|AW036763 EST252152 tomato ovary, TAMU Lycopersicon ... 175 3e-77
  5
       emb|AW036762|AW036762 EST252151 tomato ovary, TAMU Lycopersicon ... 173 3e-76
       gb|U42444|U42444 Lycopersicon pimpinellifolium leucine rich repe... 198 1e-70
       emb|A57130|A57130 Sequence 1 from Patent WO9531564.
                                                                     198 1e-70
       gb[U42445]U42445 Lycopersicon pimpinellifolium leucine rich repe... 198 1e-70
       emb|A57133|A57133 Sequence 4 from Patent WO9531564.
                                                                     198 1e-70
 10
       emb|AF053998|AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ... 194 3e-68
       emb|A67434|A67434 Sequence 7 from Patent WO9743429.
                                                                     194 3e-68
       gb|U77888|INU77888 Ipomoea nil receptor-like protein kinase (inr... 174 2e-66
       emb|AF053995|AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ... 195 1e-65
       emb|AF053993|AF053993 Lycopersicon esculentum disease resistance... 198 2e-65
 15
       emb|A67429|A67429 Sequence 2 from Patent WO9743429.
                                                                     198 2e-65
       emb|A67428|A67428 Sequence 1 from Patent WO9743429.
                                                                     198 2e-65
       emb|AI485090|AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 177 9e-64
       emb|AF053996|AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr... 180 8e-62
       gb|BE034258|BE034258 MH02C02 MH Mesembryanthemum crystallinum cD... 239 9e-62
20
       emb|AF053994|AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ... 180 1e-61
       emb|AI486438|AI486438 EST244759 tomato ovary, TAMU Lycopersicon ... 230 1e-61
       emb|AF053997|AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ... 183 1e-61
       emb|A67432|A67432 Sequence 5 from Patent WO9743429.
                                                                     183 1e-61
       emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 185 2e-59
25
       emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 144 2e-59
       emb|AI771841|AI771841 EST252941 tomato ovary, TAMU Lycopersicon ... 177 6e-57
       emb|AW726024|AW726024 GA_Ea0020G24 Gossypium arboreum 7-10 dpa ... 193 2e-55
       emb|AI485862|AI485862 EST244183 tomato ovary, TAMU Lycopersicon ... 177 3e-54
       emb|AW224642|AW224642 EST303085 tomato root, plants pre-anthesis... 123 6e-54
30
      emb|AI495469|AI495469 sa98d06.yl Gm-c1004 Glycine max cDNA clone... 209 1e-52
      emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 146 2e-52
      emb|AB029327|AB029327 Nicotiana tabacum mRNA for elicitor-induci... 181 9e-48
      emb|AI442177|AI442177 sa58c02.yl Gm-c1004 Glycine max cDNA clone... 158 3e-45
      emb|AW727470|AW727470 GA_Ea0012H16 Gossypium arboreum 7-10 dpa ... 86 5e-41
35
      emb|AW979740|AW979740 EST341365 tomato root deficiency, Cornell ... 151 2e-39
      emb|AW010219|AW010219 ST03E03 Pine TriplEx shoot tip library Pin... 164 '2e-39
      emb|AI487432|AI487432 EST245754 tomato ovary, TAMU Lycopersicon ... 150 7e-39
      emb|AI490531|AI490531 EST249065 tomato ovary, TAMU Lycopersicon ... 154 6e-38
      emb|AW668045|AW668045 GA_Ea0012G15 Gossypium arboreum 7-10 dpa ... 113 3e-37
40
      emb|AW287714|AW287714 LG1_271_E06.b1 A002 Light Grown 1 (LG1) So... 150 3e-37
      emb|AW693988|AW693988 NF071C05ST1F1037 Developing stem Medicago ... 149 8e-35
      emb|AW774582|AW774582 EST333733 KV3 Medicago truncatula cDNA clo... 131 8e-35
      emb|AW650851|AW650851 EST329305 tomato germinating seedlings, TA... 87 1e-34
      emb[AW185015]AW185015 se85e10.y1 Gm-c1023 Glycine max cDNA clone... 89 1e-34
45
      emb|AW267958|AW267958 EST306300 DSIR Medicago truncatula cDNA cl... 125 2e-34
      emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 117 1e-33
      emb|AI725692|AI725692 BNLGHi12653 Six-day Cotton fiber Gossypium... 142 1e-32
      emb|Z73295|CRPK1 C.roseus mRNA for receptor-like protein kinase.
      emb|AW618736|AW618736 EST320722 L. pennellii trichome, Cornell U... 141 2e-32
50
      emb|AA557073|AA557073 915 Loblolly pine N Pinus taeda cDNA clone... 85 6e-32
      emb|AI442338|AI442338 sa61b11.yl Gm-c1004 Glycine max cDNA clone... 138 8e-32
      emb|AI495862|AI495862 sb17b07.yl Gm-c1004 Glycine max cDNA clone... 138 2e-31
      emb|AW156187|AW156187 se20f08.y1 Gm-c1015 Glycine max cDNA clone... 137 5e-31
      emb|AI967314|AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two... 88, 9e-31
55
      emblAW034426|AW034426 EST277997 tomato callus, TAMU Lycopersicon... 119 1e-30
      emb|AW224303|AW224303 EST301030 tomato fruit red ripe, TAMU Lyco... 128 1e-30
      emb|AW035394|AW035394 EST281132 tomato callus, TAMU Lycopersicon... 136 1e-30
      emb|AW930866|AW930866 EST356709 tomato fruit mature green, TAMU ... 84 1e-30
      emb|AW932515|AW932515 EST358358 tomato fruit mature green, TAMU ... 78 1e-30
60
      emb|AI166936|AI166936 xylem.est.719 Poplar xylem Lambda ZAPII li... 85 1e-30
      emb|AV419736|AV419736 AV419736 Lotus japonicus young plants (two... 135 1e-30
```

	gb BE054944 BE054944 GA_Ea0032D07f Gossypium arboreum 7-10 dpa 91 2e-30 emb AW756743 AW756743 si26f10.yl Gm-c1027 Glycine max cDNA clone 83 9e-30 gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR 94 1e-29
5	emb AL354532 LMFL1177 Leishmania major Friedlin chromosome 21 co 98 1e-29 gb BE060551 BE060551 HVSMEg0012J19f Hordeum vulgare pre-anthesis 88 1e-29 emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial. 85 3e-29
	emb AW031255 AW031255 EST274630 tomato callus, TAMU Lycopersicon 86 3e-29 emb AW650232 AW650232 EST328686 tomato germinating seedlings, TA 85 3e-29 emb AW694732 AW694732 NF079D07ST1F1061 Developing stem Medicago 89 4e-29
10	emb AI729170 AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium 129 8e-29 emb AI967315 AI967315 Ljirnpest00-018 Ljirnp Lambda HybriZap two 105 2e-28
1.5	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein. 85 2e-28 emb AI731035 AI731035 BNLGHi8447 Six-day Cotton fiber Gossypium 75 3e-28 emb AW735867 AW735867 EST336635 tomato flower buds 0-3 mm, Corne 127 3e-28
15	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon 127 3e-28 emb AW774553 AW774553 EST333704 KV3 Medicago truncatula cDNA clo 90 3e-28 emb AW094468 AW094468 EST287648 tomato mixed elicitor, BTI Lycop 126 6e-28
20	emb AW203459 AW203459 sf30e03.y1 Gm-c1028 Glycine max cDNA clone 75 7e-28 emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k 85 8e-28 emb AI727547 AI727547 BNLGHi8389 Six-day Cotton fiber Gossypium 75 9e-28
	emb AI730872 AI730872 BNLGHi8131 Six-day Cotton fiber Gossypium 73 9e-28 gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp 80 1e-27 emb AW299082 AW299082 EST305756 KV2 Medicago truncatula cDNA clo 126 1e-27
25	emb AI937984 AI937984 sc06e07.yl Gm-c1012 Glycine max cDNA clone 81 le-27 emb AF220602 AF220602 Lycopersicon pimpinellifolium Rio Grande 7 73 2e-27 emb A58270 A58270 Sequence 1 from Patent WO9635790. 90 2e-27
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR 75 3e-27 emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo 105 3e-27 gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1 99 3e-27
30	emb AW587497 AW587497 IPPGHZ0085 Cotton fiber and embryo Lambda 123 3e-27 emb AW705130 AW705130 sk42a08.yl Gm-c1019 Glycine max cDNA clone 117 3e-27 emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 78 4e-27
35	emb AW684339 AW684339 NF015G04NR1F1000 Nodulated root Medicago t 80 4e-27 emb AW587493 AW587493 IPPGHZ0080 Cotton fiber and embryo Lambda 122 4e-27 gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine 77 5e-27 emb AW224643 AW224643 EST303086 tomato root, plants pre-anthesis 123 5e-27
	emb AW687233 AW687233 NF007D09RT1F1077 Developing root Medicago 75 7e-27 emb AW982539 AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi 121 8e-27 gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK 80 9e-27
40	emb AW685504 AW685504 NF030H04NR1F1000 Nodulated root Medicago t 122 1e-26 emb AW287734 AW287734 LG1_271_G05.b1_A002 Light Grown 1 (LG1) So 104 1e-26
45	Query= Z97340.345 s_at 17485 s_at /id_source genbank /description "emb cab10405.1 (z97340) beta-1, 3-glucanase class i precursor
	[arabidopsis thaliana]" /blast_score 1.00e-169 /ec_number /family /chip nova /gb_link /ncgi (921 letters)
50	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
55	Score E Sequences producing significant alignments: (bits) Value
60	gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) 279 e-123 emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-gluc 276 e-123 emb A26453 A26453 Recombinant soya beta-1,3-glucanase plasmid. 259 e-117 emb A26449 A26449 Soya mutant beta-1,3-glucanase cDNA. 259 e-117

	emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f 259 e-117
	emb A26451 A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin 259 e-117
	emb X53129 PV13BDGL P. vulgaris mRNA for 1,3-beta-D-glucanase. 244 e-111
	emb X89717 PVB13GLUC P.vulgaris beta-1,3-glucanase gene. 247 e-110
5	emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-gluca 245 e-108
9	hM22120FORCHICD2 Tabassa Ol alimbaginish in hara busan 245 6-106
	gb[M23120]TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m 245 e-108
	emb AJ131047 CAR131047 Cicer arietinum mRNA for glucan-endo-1,3 251 e-107
	gb L02212 PEABETAGLU Pea beta-1,3-glucanase gene, complete cds. 246 e-106
	gb S51479 S51479 beta-1,3-glucanase [Pisum sativum=peas, cultiva 246 e-106
10	gb U27179 MSU27179 Medicago sativa acidic glucanase mRNA, comple 232 e-104
	emb AF034109 AF034109 Glycine max beta-1,3-glucanase 4 (SGlu4) g 225 4e-99
	gb[M80608]TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase 237 9e-99
	emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh 238 7e-97
15	gb[U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan 235 1e-96
15	emb X54742 NPB13GG Nicotiana plumbaginifolia beta-(1,3)-glucanas 240 2e-96
•	gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan 236 3e-96
	gb M60402 TOBGLA13B Nicotiana tabacum glucan beta-1,3-glucanase 240 6e-95
	emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase. 240 6e-95
	emb AF001523 AF001523 Musa acuminata beta-1, 3-glucananse mRNA, 205 8e-95
20	emb AF004838 AF004838 Musa acuminata beta-1,3-glucanase mRNA, pa 205 8e-95
	gb M60403 TOBGLB13B-Nicotiana tabacum glucan beta-1,3-glucosidas 238 2e-94
	emb AF034117 AF034117 Glycine max beta-1,3-glucanase 12 (SGlu12) 180 3e-94
	gb M59442 TOBGLUCA N.tabacum basic-1,3-glucanse gene, complete cds. 236 7e-94
25	emb A16121 A16121 Intracellular Beta-1, 3 glucanase gene (SEQ ID 236 7e-94
25	gb M59443 TOBGLUCB N.tabacum acidic beta-1,3-glucanase gene, com 150 2e-92
	emb A16120 A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID 150 2e-92
	gb M60460 TOBPR2A Tobacco PR2 protein mRNA, complete cds. 149 4e-91
	emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas 221 8e-91
	gb U01902 U01902 Solanum tuberosum Datura endo-1,3-beta-D-glucan 238 3e-90
30	gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene 211 2e-89
	emb AF227953 AF227953 Capsicum annuum basic beta-1,3-glucanase (224 4e-89
	emb AF034106 AF034106 Glycine max beta-1,3-glucanase 1 (SGlu1) g 221 2e-88
	emb[AF141654]AF141654 Nicotiana tabacum beta-1,3-glucanase (GGL4 139 3e-88
35	gb[M60463]TOBGL153A Tobacco GL153 protein mRNA, complete cds. 139 3e-88
))	gb[M20620]TOBGLUBC N.tabacum beta-1,3-glucanase mRNA, clone pGL43. 238 4e-88
	emb AF034113 AF034113 Glycine max beta-1,3-glucanase 8 (SGlu8) g 222 1e-87
	emb[X54431]NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 136 6e-87
	emb AF141653 AF141653 Nicotiana tabacum beta-1,3-glucanase (GGL1 136 1e-86
	gb[M60464]TOBB13G Tobacco beta-1,3-glucanase mRNA, complete cds. 136 1e-86
40	emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 113 2e-86
	emb[X81560]NTSP41AGN N.tabacum Sp41a gene. 136 4e-86
	emb X54430 NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 135 8e-86
	dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. 167 3e-84
	dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. 167 3e-84
45	gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple 167 3e-84
	emb AJ009932 STAJ9932 Solanum tuberosum mRNA for beta-1,3-glucan 144 4e-84
	chib A30037322 31A37532 303alulii tuotiosumi hikviva lot beta-1,3-giucan 144 46-84
	emb AW034632 AW034632 EST278316 tomato callus, TAMU Lycopersicon 188 1e-82
	gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c 169 3e-82
	emb AW033770 AW033770 EST277341 tomato callus, TAMU Lycopersicon 186 5e-82
50	gb M80604 TOMB13GLUA Lycopersicon esculentum beta-1,3-glucanase 142 5e-82
	emb[X74905]LEQA L.esculentum TomQ'a mRNA for beta(1,3)glucanase. 128 4e-79
	emb AI896001 AI896001 EST265444 tomato callus, TAMU Lycopersicon 175 9e-79
	emb AW034584 AW034584 EST278268 tomato callus, TAMU Lycopersicon 226 9e-79
	emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana 127 2e-78
55	emb AJ012751 CAR012751 Cicer arietinum mRNA for glucan endo-beta 126 2e-78
	emb AW034478 AW034478 EST278049 tomato callus, TAMU Lycopersicon 227 8e-78
	emb AW031078 AW031078 EST274385 tomato callus, TAMU Lycopersicon 169 4e-77
	emb AW035235 AW035235 EST280497 tomato callus, TAMU Lycopersicon 179 5e-77
	gb M60462 TOBPRNA Tobacco PRN protein mRNA, 3' end. 117 5e-76
50	emb AW775271 AW775271 EST334336 DSIL Medicago truncatula cDNA cl 163 6e-76
	emblAW776932IAW776932 FST335997 DSII Medicago trancatula cDNA cl. 156, 7c, 76

	•
	emb AW216637 AW216637 EST295351 tomato callus, TAMU Lycopersicon 164 2e-75 emb AW032447 AW032447 EST276006 tomato callus, TAMU Lycopersicon 227 2e-74 emb AW156463 AW156463 se26e04.yl Gm-c1015 Glycine max cDNA clone 256 3e-74
5	emb Z68154 GHBGLUCS G.hirsutum mRNA for 1,3-beta-glucanase. 152 1e-73 gb M63634 TOBGCBREG Nicotiana plumbaginifolia beta(1,3)-glucanas 250 9e-73 emb AW032644 AW032644 EST276203 tomato callus, TAMU Lycopersicon 189 1e-71
	emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl 173 3e-71 gb M20618 TOBGLUBA N.tabacum beta-1,3-glucanase mRNA, clones pGL 238 3e-71
10	emb AI894445 AI894445 EST263900 tomato callus, TAMU Lycopersicon 231 3e-71 emb AF034107 AF034107 Glycine max beta-1,3-glucanase 2 (SGlu2) g 142 7e-71 emb AW031387 AW031387 EST274841 tomato callus, TAMU Lycopersicon 237 7e-71
	emb AW035366 AW035366 EST280928 tomato callus, TAMU Lycopersicon 237 7e-71 emb AI896035 AI896035 EST265478 tomato callus, TAMU Lycopersicon 237 7e-71 emb AW031155 AW031155 EST274589 tomato callus, TAMU Lycopersicon 237 7e-71
15	emb AW030447 AW030447 EST273702 tomato callus, TAMU Lycopersicon 236 3e-70 emb AF034116 AF034116 Glycine max beta-1,3-glucanase 11 (SGlu11) 124 9e-70
	emb AW030277 AW030277 EST273532 tomato callus, TAMU Lycopersicon 144 2e-69 emb AF034110 AF034110 Glycine max beta-1,3-glucanase 5 (SGlu5) g 122 3e-69 emb AW035160 AW035160 EST280422 tomato callus, TAMU Lycopersicon 142 6e-69
20 -	emb AW032444 AW032444 EST276003 tomato callus, TAMU Lycopersicon 142 6e-69 -emb X74906 LEQB L.esculentum TomQ'b mRNA for beta(1,3)glucanase. 101 1e-68 emb AJ011769 CIN011769 Cichorium intybus X Cichorium endivia sub 97 1e-68
25	emb AW030283 AW030283 EST273538 tomato callus, TAMU Lycopersicon 140 2e-68 gb M13237 BLYGLUCB Barley beta glucanase mRNA. 158 7e-68 emb Z15131 ASBGLUCAN A.sativa mRNA for beta glucanase. 158 9e-68
23	emb AI896042 AI896042 EST265485 tomato callus, TAMU Lycopersicon 237 1e-67 gb M62740 BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan 158 2e-67
30	emb AW031259 AW031259 EST274634 tomato callus, TAMU Lycopersicon 136 3e-67 emb AW035840 AW035840 EST281994 tomato callus, TAMU Lycopersicon 136 3e-67 emb AW032451 AW032451 EST276010 tomato callus, TAMU Lycopersicon 136 3e-67
	emb AW031353 AW031353 EST274807 tomato callus, TAMU Lycopersicon 136 3e-67 emb AI895981 AI895981 EST265424 tomato callus, TAMU Lycopersicon 136 3e-67 gb U73709 VVU73709 Vitis vinifera beta-1,3-glucanase mRNA, parti 244 3e-67
35	emb Z22874 TABETGLUB T.aestivum (1,3;1,4) beta glucanase mRNA, c 160 3e-67 emb AF034114 AF034114 Glycine max beta-1,3-glucanase 9 (SGlu9) p 119 7e-67
	Query= U18993.2 s_at 17487_s_at /id_source genbank /description gb aac49117.1 (u18993) tryptophan synthase alpha chain [arabidopsis
40	thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova /gb_link /ncgi (939 letters)
	Database: plantfungal
45	661,018 sequences; 426,114,510 total letters Searchingdone
50	Score E Sequences producing significant alignments: (bits) Value
55	emb AW730233 AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa 352 5e-98 emb AW649960 AW649960 EST328414 tomato germinating seedlings, TA 308 4e-83 emb AW621664 AW621664 EST312462 tomato root during/after fruit s 290 1e-77 emb AW031327 AW031327 EST274781 tomato callus, TAMU Lycopersicon 282 3e-75 gb U38804 PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72 emb AW775853 AW775853 EST334918 DSIL Medicago truncatula cDNA cl 264 9e-70
60	emb Z21642 CHASTRNAA Antithamnion sp. Chloroplast trnK,trnE,trpA 255 4e-67 gb BE124387 BE124387 EST393422 GVN Medicago truncatula cDNA clon 227 9e-59 gb BE121873 BE121873 894015F07.y1 C. reinhardtii CC-1690, normal 227 1e-58 emb AF022186 AF022186 Cyanidium caldarium strain RK1 chloroplast 220 1e-56

```
emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
      emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
      dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
      emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 5
      emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
      dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
      emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
      dbj D63676 D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
      gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
10
      emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase.
                                                                    86 9e-42
      emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
      emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
      emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
      emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
15
      emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycope... 138 5e-32
      emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8.
                                                                      74 3e-30
      emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
      emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
      emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
20
      gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
      emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
      emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
      emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
      emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptopha... 64 1e-09
25
      emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
      emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09
      emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09
      emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
      emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09
30
      gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
      emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06
      emb|AW693052|AW693052 NF059C08ST1F1065 Developing stem Medicago ... 51 1e-05
      emb|AV390244|AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla... 49 4e-05
      emb|AW616467|AW616467 EST322878 L. hirsutum trichome, Cornell Un... 48 7e-05
35
      emb|AL354022|P761R Leishmania major Friedlin PAC P761 right end-... 44 0.002
      gb|M91656|CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1... 43 0.005
      emb|AQ903789|AQ903789 GSSTc04230 Trypanosome cruzi random genomi... 35 0.24
      gb|M91654|CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1... 36 0.52
40
      emb|AL139794|LMFP1105 Leishmania major Friedlin chromosome 4 PAC... 35 0.87
      emb|AW926438|AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis... 34 1.2
      emb|AA965348|AA965348 e9d04a1.rl Aspergillus nidulans 24hr asexu... 34 1.3
      gb[U12630|ENU12630 Emericella nidulans R153 core histone H3 (H3)... 34 1.3
45
      emb|AI007494|AI007494 e9c09a1.rl Aspergillus nidulans 24hr asexu... 34 1.3
      emb|AA787433|AA787433 n3d04a1.rl Aspergillus nidulans 24hr asexu... 34 1.3
      emb|X55548|ANH3GENE A.nidulans gene for core histone for H3.
                                                                    34 1.3
      emb|AQ396426|AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P... 34 1.6
      emb|AF262997|AF262997 Ricinus communis NADP-dependent malic prot... 34 1.6
50
      gb|M19025|CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c... 34 1.6
      emblAF084888|AF084888 Neurospora crassa 656-2A mutant tryptophan... 31 1.7
      emb|AF084887|AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta... 31 1.7
      emb|AW694774|AW694774 NF080A05ST1F1036 Developing stem Medicago ... 34 1.8
      emb|Y18012|TVE18012 Trametes versicolor mRNA for laccase.
55
      emb|AQ500614|AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 2.5
      emb|AW187498|AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ... 33 3.1
      emb|AW187530|AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ... 33 3.1
      emb|AW694072|AW694072 NF072B12ST1F1096 Developing stem Medicago ... 33 3.1
      emb|AW186883|AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ... 33 3.1
60
      emb|AW187537|AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ... 33 3.1
      emb|AW187474|AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ... 33 3.1
```

	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor 33 3.5 emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two 33 4.3 emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp 33 4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un 33 4.7
5	gb BE028433 BE028433 EtESTea78d07.yl Eimeria M5-6 Merozoite stag 32 5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li 32 5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom 32 5.9
	emb AW728623 AW728623 GA_Ea0017G06 Gossypium arboreum 7-10 dpa 32 5.9
	gb BE027723 BE027723 EtESTea86c08.yl Eimeria M5-6 Merozoite stag 32 5.9
10	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st 32 5.9
	gb BE027843 BE027843 EtESTea88c05.yl Eimeria M5-6 Merozoite stag 32 5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone 32 5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit 32 5.9
1.5	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit 32 5.9
15	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom 32 6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XTV reading frame O 32 6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien 28 7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop 32 8.1
20	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two 32 8.1
20	emb AW703740 AW703740 sk23g09.yl Gm-c1028 Glycine max cDNA clone 32 8.1
	emb AW703739 AW703739 sk23g08.yl-Gm-c1028 Glycine max cDNA clone 32-8.1
	emb AV419698 AV419698 AV419698 Lotus japonicus young plants (two 32 8.1
	emb AV419299 AV419299 AV419299 Lotus japonicus young plants (two 32 8.1
25	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two 32 8.1
23	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two 32 8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two 32 8.1 emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two 32 8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library 32 8.1 emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron. 32 8.1
30	omopia 7000 of 101020 orbitalica emotopiasi unit gene miton. 32 6.1
-	
	Query= Z97339.197_at 17899_at /id source genbank /description
	emb cab10339.1 (z97339) hypothetical protein [arabidopsis thaliana]
	/blast_score 5.00e-55 /ec_number /family /chip nova /gb_link
35	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb z97339 /ncgi
	http://www.ncgr.org/cgi-bin/ff?z97339
	(441 letters)
40	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
45	
43	Score E
	Sequences producing significant alignments: (bits) Value
	embl \ \\\\ 695774 \ \\\\\ 695774 \ \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
	emb AW685774 AW685774 NF035A03NR1F1000 Nodulated root Medicago t 123 6e-28 emb AW687017 AW687017 NF005A10RT1F1072 Developing root Medicago 123 6e-28
50	1 1 1777 CORRO (1 1 777 CORRO () PRO 4 0 PRO 4
50	emb AW687794 AW687794 NF013E08RT1F1066 Developing root Medicago 89 3e-23 emb AW310121 AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone 68 3e-19
	emb[AW704640]AW704640 sk54f05.yl Gm-c1019 Glycine max cDNA clone 68 3e-19
	emb AW395252 AW395252 sh45g06.y1 Gm-c1017 Glycine max cDNA clone 68 3e-19
	emb AW704612 AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone 68 3e-19
55	emb AT000508 AT000508 AT000508 Brassica rapa guard cell Brassica 50 2e-18
-	emb AW704218 AW704218 sk17c12.yl Gm-c1028 Glycine max cDNA clone 63 3e-17
	emb AW423428 AW423428 sh66f08.yl Gm-c1015 Glycine max cDNA clone 63 1e-16
	emb AW687188 AW687188 NF006H09RT1F1079 Developing root Medicago 82 3e-15
	emb AW684973 AW684973 NF023G04NR1F1000 Nodulated root Medicago t 68 1e-13
60	emb AW233878 AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone 69 3e-13
	emb AW687098 AW687098 NF006A02RT1F1007 Developing root Medicago 72 2e-12

```
emblAW686346|AW686346 NF040F08NR1F1000 Nodulated root Medicago t... 67 7e-12
      emb|AI437669|AI437669 sa38a11.yl Gm-c1004 Glycine max cDNA clone... 48 1e-11
      emb|AW348644|AW348644 GM210003A11A8R Gm-r1021 Glycine max cDNA 3... 48 2e-11
      emb|AW687565|AW687565 NF011A04RT1F1024 Developing root Medicago ... 48 2e-11
 5
      gb|BE033951|BE033951 MG02E05 MG Mesembryanthemum crystallinum cD... 44 3e-10
      emb|AW185776|AW185776 se59e03.y1 Gm-c1019 Glycine max cDNA clone... 51 2e-08
      emb|AI930953|AI930953 sb45c07.yl Gm-c1015 Glycine max cDNA clone... 48 4e-08
      emb|AI440599|AI440599 sa68c05.yl Gm-c1004 Glycine max cDNA clone... 48 6e-08
      emb|AW394608|AW394608 sh33e11.y1 Gm-c1017 Glycine max cDNA clone... 46 2e-07
      emblAW284126|AW284126 LG1_262_A05.g1_A002 Light Grown 1 (LG1) So... 55 3e-07
      emb|AI960446|AI960446 sc84a10.yl Gm-c1018 Glycine max cDNA clone... 48 4e-06
      emb|AI794716|AI794716 sb68b06.yl Gm-c1019 Glycine max cDNA clone... 48 5e-06
      gb|BE024111|BE024111 sm96h03.y1 Gm-c1015 Glycine max cDNA clone ... 48 9e-06
      emb|Z99969|MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl... 41 6e-05
15
      emb|AV412437|AV412437 AV412437 Lotus japonicus young plants (two... 47 9e-05
      emb|AV427297|AV427297 AV427297 Lotus japonicus young plants (two... 46 2e-04
      emb|AW666090|AW666090 sk32a11.yl Gm-c1028 Glycine max cDNA clone... 42 2e-04
      emb|AW277478|AW277478 sf82e11.yl Gm-c1019 Glycine max cDNA clone... 37 4e-04
      emb|AW775954|AW775954 EST335019 DSIL Medicago truncatula cDNA cl... 42 7e-04
20
      gb|BE122569|BE122569 Ljimpest29-344-g6 Ljimp Lambda HybriZap t... 43 0.001
      emb|AW299135|AW299135 EST305809 KV2 Medicago truncatula cDNA clo... 43 0.002
      emb|AW423359|AW423359 sh06g04.y1 Gm-c1016 Glycine max cDNA clone... 41 0.004
      emblAW171748|AW171748 N100642e rootphos(-) Medicago truncatula c... 40 0.014
      emb|AW285241|AW285241 LG1_236_C10.g1_A002 Light Grown 1 (LG1) So... 39 0.026
25
      emb|AW747074|AW747074 WS1_65_A07.g1_A002 Water-stressed 1 (WS1) ... 39 0.026
      emb|AW649685|AW649685 EST328139 tomato germinating seedlings, TA... 38 0.036
      emb|AW299176|AW299176 EST305986 KV2 Medicago truncatula cDNA clo... 38 0.036
      emb|AW220014|AW220014 EST302497 tomato root during/after fruit s... 38 0.050
      gb|C96140|C96140 C96140 Marchantia polymorpha immature sex organ... 38 0.050
30
      emb|AW625648|AW625648 EST319555 tomato radicle, 5 d post-imbibit... 38 0.050
      emb[AW926780]AW926780 HVSMEg0008D23 Hordeum vulgare pre-anthesis... 37 0.094
      gb|L05906|PMCMSGF Pneumocystis carinii (clone GP3) major surface... 36 0.18
      emb|AW333354|AW333354 S20F5 AGS-1 Pneumocystis carinii f. sp. ca... 36 0.18
      emb|Z98595|SPAC11E3 S.pombe chromosome I cosmid c11E3.
35
      gb|BE052896|BE052896 GA _ Ea0025106f Gossypium arboreum 7-10 dpa ... 35 0.46
      emb|AW309936|AW309936 sf26g12.x1 Gm-c1028 Glycine max cDNA clone... 35 0.46
      emblAW310120|AW310120 sf31d06.x1 Gm-c1028 Glycine max cDNA clone... 35 0.46
      emb|AW233798|AW233798 sf26g12.y1 Gm-c1028 Glycine max cDNA clone... 35 0.46
40
      gb|BE053040|BE053040 GA_Ea0015D14f Gossypium arboreum 7-10 dpa ... 35 0.46
      emb|AW310598|AW310598 sg21h03.x1 Gm-c1024 Glycine max cDNA clone... 35 0.46
     emb|AI731906|AI731906 BNLGHi11249 Six-day Cotton fiber Gossypium... 35 0.46
      emb|AW278505|AW278505 sf45c08.yl Gm-c1009 Glycine max cDNA clone... 35 0.46
45
     emb|AC013353|AC013353 Trypanosoma brucei chromosome VI clone RPC... 34 0.63
     emb|AI728996|AI728996 BNLGHi12315 Six-day Cotton fiber Gossypium... 34 0.63
     emb|AW691828|AW691828 NF044F04ST1F1000 Developing stem Medicago ... 34 0.63
     emb|AI729057|AI729057 BNLGHi12476 Six-day Cotton fiber Gossypium... 34 0.63
     emb|AI731500|AI731500 BNLGHi9982 Six-day Cotton fiber Gossypium ... 34 0.63
50
     emb|AQ660279|AQ660279 Sheared DNA-3L23.TF Sheared DNA Trypanosom...
     emb|AI729672|AI729672 BNLGHi13930 Six-day Cotton fiber Gossypium... 34 0.63
     emb|AI725456|AI725456 BNLGHi12219 Six-day Cotton fiber Gossypium... 34 0.63
     emb|AQ656131|AQ656131 Sheared DNA-27G20.TF Sheared DNA Trypanoso... 34 0.63
     emb|AI731231|AI731231 BNLGHi8954 Six-day Cotton fiber Gossypium ... 34 0.87
55
     emb|AL035477|PFMAL4P4 Plasmodium falciparum chromosome 4 strain ... 34 0.87
     gb|BE033791|BE033791 MF06E10 MF Mesembryanthemum crystallinum cD... 34 0.87
     gb|BE034803|BE034803 ML04E10 ML Mesembryanthemum crystallinum cD... 34 0.87
     emb|AI731464|AI731464 BNLGHi9855 Six-day Cotton fiber Gossypium ... 34 0.87
     emb|AI727451|AI727451 BNLGHi8020 Six-day Cotton fiber Gossypium ... 34 0.87
60
     emb|AW620830|AW620830 sj47b03.y1 Gm-c1033 Glycine max cDNA clone... 28 1.1
     dbj|D63449|YSCATF1A Yeast ATF1 gene for alcohol acetyltransferas... 33 1.2
```

	dbj E08050 E08050 cDNA encoding beer yeast alcohol acetyltransfe 33 1.2
	dbj E06817 E06817 DNA encoding alcohol acetyltransferase 1. 33 1.2
	dbj D26554 YSCATF1 Yeast ATF1 gene for alcohol acetyltransferase 33 1.2
	dbj E08049 E08049 cDNA encoding sake yeast alcohol acetyltransfe 33 1.2
5	dbj E06816 E06816 DNA encoding alcohol acetyltransferase 1. 33 1.2
_	emb Z75285 SCYOR377W S.cerevisiae chromosome XV reading frame OR 33 1.2
٠.	emb AW725476 AW725476 GAEa0018C14 Gossypium arboreum 7-10 dpa 33 1.6
	omblew 725470 AW 725470 CA Earot 101 COSSyptim arboreum 7-10 dpa 55 1.6
	emb AI812453 AI812453 11C3 Pine Lambda Zap Xylem library Pinus t 33 1.6
	emb AW459992 AW459992 si07c04.y1 Gm-c1029 Glycine max cDNA clone 33 1.6
10	emb X01777 HVB3HORD Barley mRNA fragment for B3-hordein. 33 1.6
	emb AQ449927 AQ449927 500006A04.x1 CpIOWAM13mp18gDNA1 Cryptospor 33 1
	emb AE001274 AE001274 Leishmania major chromosome 1, complete se 30 2.2
	emb AL031261 SPBC3H7 S.pombe chromosome II cosmid c3H7. 32 2.2
	emb AI812374 AI812374 1F12 Pine Lambda Zap Xylem library Pinus t 32 2.2
15	* 1 1 0 - 1 4 - 1 1 1 - 1 - 1 1 1 1 - 1 1 1 1 1
13	emb A1728744 A1728744 BNLGHill 1492 Six-day Cotton fiber Gossypium 32 2.2
	gb BE036189 BE036189 MO20F12 MO Mesembryanthemum crystallinum cD 32 3.1
	emb AW925749 AW925749 HVSMEg0005G16 Hordeum vulgare pre-anthesis 32 3.1
	emb AQ411951 AQ411951 CpG0926A CpIOWAgDNA1 Cryptosporidium parvu 32 3.1
	emb AQ935548 AQ935548 CpG2528A CpIOWAgDNA1 Cryptosporidium parvu 32 3.1
20	emb AQ411952 AQ411952 CpG0926B CpIOWAgDNA1 Cryptosporidium parvu 32 3.1
	gb B67221 B67221 CpG0036A CpIOWAgDNA1 Cryptosporidium parvum gen 32 3.1
	emb AW030301 AW030301 EST273556 tomato callus, TAMU Lycopersicon 31 4.2
	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom 31 4.2
	emb AL122012 LMFL8342 Leishmania major Friedlin chromosome 23 co 31 4.2
25	construction of the constr
23	emb X60772 GMOLEOA G.max mRNA for 24 kDa oleosin isoform (partia 31 4.2
	Query= AJ006960.4 s_at 17930_s_at /id_source genbank /description
	emb caa07352.1 (aj006960) peroxidase [arabidopsis thaliana]
30	/blast_score 1.00e-111 /ec_number /family /chip nova /gb_link /ncgi
	(592 letters)
	Database: plantfungal
35	661,018 sequences; 426,114,510 total letters
	00-3010 00400000, 1203211,010 101111011010
	Searchingdone
	5-44-44-45-45-45-45-45-45-45-45-45-45-45
	Score E
40	· · · · · · · · · · · · · · · · · · ·
10	Sequences producing significant alignments: (bits) Value
	1 DAGGOOD CODAL DAGGOOD COLOR DATA COLOR DAT
	emb[X90695]MSRNAPE02 M.sativa mRNA for peroxidase 2. 339 1e-92
	emb AJ011939 TRE011939 Trifolium repens mRNA for peroxidase. 335 2e-91
	emb Y10469 SOPRXR8 S.oleracea mRNA for peroxidase, clone PC55. 332 2e-90
45	emb AI487510 AI487510 EST245832 tomato ovary, TAMU Lycopersicon 327 5e-89
	emb AI486784 AI486784 EST245106 tomato ovary, TAMU Lycopersicon 327 5e-89
	emb AI895842 AI895842 EST265285 tomato callus, TAMU Lycopersicon 325 1e-88
	emb AW032442 AW032442 EST276001 tomato callus, TAMU Lycopersicon 325 2e-88
	gb L36158 ALFPXDD Medicago sativa peroxidase (pxdD) mRNA, 3' end. 320 6e-87
50	emb AW216351 AW216351 EST295095 tomato callus, TAMU Lycopersicon 319 1e-86
,0	cinica w 210331 E31293093 tomato canus, 1AMO Lycopersicon 319 1e-80
	emb AW691003 AW691003 NF040C11ST1F1000 Developing stem Medicago 319 2e-86
	emb AW625601 AW625601 EST319508 tomato radicle, 5 d post-imbibit 318 3e-86
	gb BE124281 BE124281 EST394406 DSIL Medicago truncatula cDNA clo 314 4e-85
	emb AI894487 AI894487 EST263930 tomato callus, TAMU Lycopersicon 307 4e-83
55 -	emb AW666274 AW666274 sk34e11.yl Gm-c1028 Glycine max cDNA clone 304 4e-82
	emb AI897419 AI897419 EST266862 tomato ovary, TAMU Lycopersicon 295 2e-79
	emb AW329042 AW329042 N200241e rootphos(-) Medicago truncatula c 292 2e-78
	emb AW666298 AW666298 sk34h04.y1 Gm-c1028 Glycine max cDNA clone 292 2e-78
	embla W0307881A W030788 ECT374042 to an analysis of the state of the s
50	emb AW030788 AW030788 EST274043 tomato callus, TAMU Lycopersicon 292 2e-78
,U	emb AW031625 AW031625 EST275079 tomato callus, TAMU Lycopersicon 291 3e-78
	embla W278800 A W278800 af08a02 v1 Cm at 0.10 Chroing may aDNA along 200 20 79

```
emb|AW221693|AW221693 EST298504 tomato fruit red ripe, TAMU Lyco... 290 7e-78
      emb|AW216725|AW216725 EST295439 tomato callus, TAMU Lycopersicon... 287 4e-77
      emb|AW035689|AW035689 EST281843 tomato callus, TAMU Lycopersicon... 286 1e-76
      emb|AW221724|AW221724 EST298535 tomato fruit red ripe, TAMU Lyco... 285 2e-76
      emb|AW030405|AW030405 EST273660 tomato callus, TAMU Lycopersicon... 285 2e-76
      emb|AW216626|AW216626 EST295340 tomato callus, TAMU Lycopersicon... 284 5e-76
      emb|AA661001|AA661001 00898 MtRHE Medicago truncatula cDNA 5' si... 284 5e-76
      emb|AW032463|AW032463 EST276022 tomato callus, TAMU Lycopersicon... 282 2e-75
      emb|AW596100|AW596100 si97h09.yl Gm-c1032 Glycine max cDNA clone... 281 2e-75
10
      emb|AW035606|AW035606 EST281344 tomato callus, TAMU Lycopersicon... 281 4e-75
      gb|BE020228|BE020228 sm42b11.yl Gm-c1028 Glycine max cDNA clone ... 279 1e-74
      emb|AW686501|AW686501 NF038G03NR1F1000 Nodulated root Medicago t... 279 2e-74
      emb|AW031359|AW031359 EST274813 tomato callus, TAMU Lycopersicon... 278 2e-74
      emb|AW650288|AW650288 EST328742 tomato germinating seedlings, TA... 277 4e-74
15
      emb|AW705765|AW705765 sk51f01.yl Gm-c1019 Glycine max cDNA clone... 184 6e-74
      emb|AI895322|AI895322 EST264765 tomato callus, TAMU Lycopersicon... 268 2e-71
      emb|AW649016|AW649016 EST327470 tomato germinating seedlings, TA... 265 2e-70
      emb|AW703879|AW703879 sk25c06.yl Gm-c1028 Glycine max cDNA clone... 264 5e-70
      emb|AW306953|AW306953 sf50h05.yl Gm-c1009 Glycine max cDNA clone... 263 1e-69
20
      emblAW306251|AW306251 se48c03.yl Gm-c1017 Glycine max cDNA clone... 261 4e-69
      emb|AW704671|AW704671-sk39a11.yl Gm-c1028 Glycine max cDNA clone... 259 1e-68
      emb|AI895156|AI895156 EST264599 tomato callus, TAMU Lycopersicon... 257 6e-68
      emb|AW686857|AW686857 NF003C01RT1F1000 Developing root Medicago ... 241 8e-68
      emb|AV421737|AV421737 AV421737 Lotus japonicus young plants (two... 256 9e-68
25
      emb|AW029767|AW029767 EST273022 tomato callus, TAMU Lycopersicon... 253 8e-67
      emb|AW687854|AW687854 NF014B12RT1F1096 Developing root Medicago ... 214 1e-66
      emb|AW704702|AW704702 sk39d10.yl Gm-c1028 Glycine max cDNA clone... 248 3e-65
      emb|AI899344|AI899344 EST268787 tomato ovary, TAMU Lycopersicon ... 248 3e-65
      emb|AV420440|AV420440 AV420440 Lotus japonicus young plants (two... 248 3e-65
      emblAI895840|AI895840 EST265283 tomato callus, TAMU Lycopersicon... 248 4e-65
.30
      emb|A1894658|A1894658 EST264101 tomato callus, TAMU Lycopersicon... 246 1e-64
      emb|AW030796|AW030796 EST274051 tomato callus, TAMU Lycopersicon... 243 6e-64
      emb|AI896743|AI896743 EST266186 tomato callus, TAMU Lycopersicon... 242 2e-63
      emb|AW687617|AW687617 NF011E10RT1F1082 Developing root Medicago ... 241 4e-63
      emb|AW029904|AW029904 EST273159 tomato callus, TAMU Lycopersicon... 239 1e-62
35
      emb|AW676864|AW676864 DG1_1_D12.b1_A002 Dark Grown 1 (DG1) Sorgh... 237 4e-62
      emb|AI896941|AI896941 EST266384 tomato callus, TAMU Lycopersicon... 236 1e-61
      emb|AW622528|AW622528 EST313328 tomato root during/after fruit s... 232 1e-60
      emblAW208032|AW208032 M111060e DSIR Medicago truncatula cDNA clo... 232 1e-60
40
      emb|AW830948|AW830948 sm30f07.yl Gm-c1028 Glycine max cDNA clone... 232 2e-60
      emb|AI055677|AI055677 coau0004L19 Cotton Boll Abscission Zone cD... 205 4e-58
      emb|AW034420|AW034420 EST277991 tomato callus, TAMU Lycopersicon... 149 6e-56
      emb|AW032120|AW032120 EST275574 tomato callus, TAMU Lycopersicon... 217 6e-56
      emb|AW039340|AW039340 EST281597 tomato mixed elicitor, BTI Lycop... 217 6e-56
45
      emb|AI896467|AI896467 EST265898 tomato callus, TAMU Lycopersicon... 216 9e-56
      emb|AV422712|AV422712 AV422712 Lotus japonicus young plants (two... 216 1e-55
      emb|AW651552|AW651552 EST330018 tomato germinating seedlings, TA... 131 1e-54
      emb|AW706479|AW706479 sj57a08.y1 Gm-c1033 Glycine max cDNA clone... 204 2e-54
      emb|AW234624|AW234624 sf17d08.y1 Gm-c1028 Glycine max cDNA clone... 212 2e-54
50
      emb|AW832025|AW832025 sm30b11.yl Gm-c1028 Glycine max cDNA clone... 210 1e-53
      emb|AV416661|AV416661 AV416661 Lotus japonicus young plants (two... 209 1e-53
      emb|AW033980|AW033980 EST277642 tomato callus, TAMU Lycopersicon... 208 3e-53
      emb|AW029821|AW029821 EST273076 tomato callus, TAMU Lycopersicon... 208 4e-53
55
      emb|AW428756|AW428756 Ljirnpest23-845-c9 Ljirnp Lambda HybriZap ... 207 5e-53
      emb|AV409794|AV409794 AV409794 Lotus japonicus young plants (two... 205 2e-52
      emb|AI895300|AI895300 EST264743 tomato callus, TAMU Lycopersicon... 204 3e-52
      emb|AV417685|AV417685 AV417685 Lotus japonicus young plants (two... 204 5e-52
      emb|AW033463|AW033463 EST277034 tomato callus, TAMU Lycopersicon... 202 2e-51
      emb|AW030999|AW030999 EST274306 tomato callus, TAMU Lycopersicon... 201 3e-51
60
      emb|AV412313|AV412313 AV412313 Lotus japonicus young plants (two... 201 4e-51
```

emb|AV424264|AV424264 AV424264 Lotus japonicus young plants (two... 200 6e-51 gb|BE021904|BE021904 sm63h11.yl Gm-c1028 Glycine max cDNA clone ... 198 3e-50 emb|AW725608|AW725608 GA_Ea0018P10 Gossypium arboreum 7-10 dpa ... 123 7e-50 emb|AW725586|AW725586 GA __Ea0018N10 Gossypium arboreum 7-10 dpa ... 123 7e-50 emb|AI896550|AI896550 EST265993 tomato callus, TAMU Lycopersicon... 193 7e-49 emb|AW559285|AW559285 EST306328 DSIR Medicago truncatula cDNA cl... 95 3e-48 emb|AW684576|AW684576 NF018E05NR1F1000 Nodulated root Medicago t... 93 1e-46 emb|AW428680|AW428680 Ljirnpest22-757-d2 Ljirnp Lambda HybriZap ... 158 1e-46 emb|AW216534|AW216534 EST295248 tomato callus, TAMU Lycopersicon... 186 2e-46 10 emb|AW620815|AW620815 sj09h04.yl Gm-c1032 Glycine max cDNA clone... 109 7e-46 emb|AI728054|AI728054 BNLGHi9697 Six-day Cotton fiber Gossypium ... 107 1e-45 emb|AI730473|AI730473 BNLGHi7273 Six-day Cotton fiber Gossypium ... 105 2e-44 emb|AI729618|AI729618 BNLGHi13779 Six-day Cotton fiber Gossypium... 105 3e-44 emb|AV422463|AV422463 AV422463 Lotus japonicus young plants (two... 177 9e-44 15 emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 106 1e-43 emb|AW621198|AW621198 EST311996 tomato root during/after fruit s... 106 1e-43 emb[AW031587]AW031587 EST275041 tomato callus, TAMU Lycopersicon... 176 1e-43 gb|U51193|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial ... 95 2e-43 gb|L13654|TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN... 105 2e-43 20

Query=X95573.2_at 18216_at/id_source genbank/description gb|aaf24959.1|ac012375_22 (ac012375) t22c5.18 [arabidopsis thaliana] /blast_score 1.00e-119/ec_number /family /chip nova/gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|x95573|/ncgi

post/entrez/query?db=n&form=6&dopt=g&uid=gb|x95573| /ncgi http://www.ncgr.org/cgi-bin/ff?x95573 (940 letters)

Database: plantfungal

30 661,018 sequences; 426,114,510 total letters

Searching......done

Score E

35 Sequences producing significant alignments:

(bits) Value

emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 73 1e-43 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 72 2e-39 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 69 4e-38

emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 125 7e-38 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 62 3e-36 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 133 3e-35 emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 70 8e-35 dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 70 2e-34

45 gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 70 2e-34 emb|AW781249|AW781249 sk67b08.yl Gm-c1016 Glycine max cDNA clone... 67 4e-32 emb|AI988290|AI988290 sc98f10.yl Gm-c1020 Glycine max cDNA clone... 69 1e-31 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 62 3e-30 emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 66 6e-30

gb]BE123920]BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 66 6e-30 dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 59 8e-29 emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 70 1e-28 emb|AI988657|AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone... 70 2e-28 emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 66 5e-27

55 emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-27 emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 62 2e-26 emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 62 3e-26 emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 62 3e-26 emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 119 3e-26

60 emb|AW153229|AW153229 se37f05.yl Gm-c1015 Glycine max cDNA clone... 62 4e-26 emb|AW616587|AW616587 EST322998 L. hirsutum trichome, Cornell Un... 63 6e-26

-- WO 02/22675 -- PCT/US01/28506

	gb BE059872 BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone 72 2e-25
	emb AW278572 AW278572 sf46c03.yl Gm-c1009 Glycine max cDNA clone 62 5e-25
	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon 62 9e-25
	emb AV426673 AV426673 AV426673 Lotus japonicus young plants (two 76 1e-24
5	emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon 62 2e-24
,	emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop 62 2e-24
	· · · · · · · · · · · · · · · · · · ·
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar 69 5e-23
10	emb AI938565 AI938565 sb55e03.y1 Gm-c1018 Glycine max cDNA clone 70 le-22
10	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA 63 4e-22
	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR 63 4e-22
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit 62 4e-22
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s 62 2e-21
	emb AW185023 AW185023 se85f12.yl Gm-c1023 Glycine max cDNA clone 58 5e-21
15	emb AW277333 AW277333 sf80a11.yl Gm-c1019 Glycine max cDNA clone 69 6e-21
	emb AI900061 AI900061 sb98d02.yl Gm-c1012 Glycine max cDNA clone 69 6e-21
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s 62 8e-21
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon 62 1e-20
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon 62 4e-20
20	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds. 62 7e-20
	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds. 62 7e-20
	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two 76 3e-19
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two 76 3e-19
	emb AV424707 AV424707 AV424707 Lotus japonicus young plants (two 76 3e-19
25	emb AV411009 AV411009 AV411009 Lotus japonicus young plants (two 76 3e-19
23	emb AV413230 AV413230 AV413230 Lotus japonicus young plants (two 76 3e-19
	emb AV418453 AV418453 AV418453 Lotus japonicus young plants (two 76 3e-19
	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two 76 3e-19 emb AV412443 AV412443 AV412443 Lotus japonicus young plants (two 76 3e-19
30	
J U	• i · · · · · · · · · · · · · · · · · ·
	• • • • • • • • • • • • • • • • • • •
35	* * · · · · · · · · · · · · · · · · · ·
<i>J J</i>	
	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two 73 le-18
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon 61 1e-18
	emb AW706014 AW706014 sk64g01.yl Gm-c1016 Glycine max cDNA clone 66 3e-18
40	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA 62 4e-18
40	emb AW622660 AW622660 EST313460 tomato root during/after fruit s 62 5e-18
	emb AV411226 AV411226 AV411226 Lotus japonicus young plants (two 71 6e-18
	emb[AV419929]AV419929 AV419929 Lotus japonicus young plants (two 71 6e-18
	gb BE058334 BE058334 sn14g01.yl Gm-c1016 Glycine max cDNA clone 72 8e-18
AE	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon 62 2e-17
45	emb AV423254 AV423254 AV423254 Lotus japonicus young plants (two 76 3e-17
	emb AW755973 AW755973 sl11h06.yl Gm-c1036 Glycine max cDNA clone 70 4e-17
	emb AI960244 AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone 70 5e-17
	emb AV411565 AV411565 AV411565 Lotus japonicus young plants (two 68 7e-17
	emb AV424084 AV424084 AV424084 Lotus japonicus young plants (two 68 7e-17
50	emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two 68 7e-17
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon 54 3e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t 70 3e-10
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two 70 3e-16
	gb BE021759 BE021759 sm62a09.yl Gm-c1028 Glycine max cDNA clone 66 3e-16
55	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two 70 5e-16
	emb AI736394 AI736394 sb28a06.yl Gm-c1009 Glycine max cDNA clone 64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD 57 9e-16
	emb AV411832 AV411832 AV411832 Lotus japonicus young plants (two 64 9e-16
	emb AV408053 AV408053 AV408053 Lotus japonicus young plants (two 48 1e-15
60	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon 54 2e-15
	embla VA 16264 IA VA 16264 A VA 16264 I othe impositive volume plants (type 62 40 15

```
emb|AV412367|AV412367 AV412367 Lotus japonicus young plants (two...
      emb|AV420478|AV420478 AV420478 Lotus japonicus young plants (two...
      emb|AV412447|AV412447 AV412447 Lotus japonicus young plants (two...
                                                                          62 4e-15
      emb|AV414463|AV414463 AV414463 Lotus japonicus young plants (two...
                                                                          62 4e-15
      emb|AV419425|AV419425 AV419425 Lotus japonicus young plants (two...
                                                                          62 4e-15
      emb|AV425774|AV425774 AV425774 Lotus japonicus young plants (two...
                                                                          46 6e-15
      emb|AW981180|AW981180 EST392374 DSIL Medicago truncatula cDNA cl...
                                                                             76 1e-14
      emb|AV428712|AV428712 AV428712 Lotus japonicus young plants (two... 42 2e-14
      emb|AV418073|AV418073 AV418073 Lotus japonicus young plants (two...
10
      emb|AV419180|AV419180 AV419180 Lotus japonicus young plants (two... 58 5e-14
      emb|AV423498|AV423498 AV423498 Lotus japonicus young plants (two... 58 5e-14
      emb|AV428398|AV428398 AV428398 Lotus japonicus young plants (two... 58 5e-14
      emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 62 5e-14
      emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 62 5e-14
15
      Query= X95573.2 g at 18217 g at /id source genbank /description
      gb|aaf24959.1|ac012375 22 (ac012375) t22c5.18 [arabidopsis thaliana]
      /blast score 1.00e-119/ec number /family /chip nova/gb link /ncgi
20
           (940 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
25
      Searching......done
                                          Score
      Sequences producing significant alignments:
                                                          (bits) Value
30
      emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 73 1e-43
      gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 72 2e-39
      dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 69 4e-38
      emb[Y18788]MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 125 7e-38
35
      dbj|D26086|PETZFP4 Petunia zinc-finger protein gene.
      emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 133 3e-35
      emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 70 8e-35
      dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 70 2e-34
      gb|BE095284|BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-... 70 2e-34
40
      emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 67 4e-32
      emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 69 1e-31
      emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 62 3e-30
      emb|AW775559|AW775559 EST334624 DSIL Medicago truncatula cDNA cl... 66 6e-30
      gb|BE123920|BE123920 EST394045 DSIL Medicago truncatula cDNA clo... 66 6e-30
45
      dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene.
      emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 70 1e-28
      emb|AI988657|AI988657 sd06b03.yl Gm-c1020 Glycine max cDNA clone... 70 2e-28
      emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 66 5e-27
      emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-27
50
      emb|AI778714|AI778714 EST259593 tomato susceptible, Cornell Lyco... 62 2e-26
      emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 62 3e-26
      emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 62 3e-26
      emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 119 3e-26
      emb|AW153229|AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone... 62 4e-26
55
      emb|AW616587|AW616587 EST322998 L. hirsutum trichome, Cornell Un... 63 6e-26
      gb|BE059872|BE059872 sn38c04.yl Gm-c1016 Glycine max cDNA clone ... 72 2e-25
      emb|AW278572|AW278572 sf46c03.yl Gm-c1009 Glycine max cDNA clone... 62 5e-25
      emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 62 9e-25
      emb|AV426673|AV426673 AV426673 Lotus japonicus young plants (two... 76 1e-24
60
      emb|AI488218|AI488218 EST246540 tomato ovary, TAMU Lycopersicon ... 62 2e-24
      emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 62 2e-24
```

__WO 02/22675 _____PCT/US01/28506

	emb AI966679 AI966679 sc55a11.yl Gm-c1015 Glycine max cDNA clone 68 1e-23
	emb AW720367 AW720367 LjNEST21g11r Lotus japonicus nodule librar 69 5e-23
	emb AI938565 AI938565 sb55e03.y1 Gm-c1018 Glycine max cDNA clone 70 1e-22
5	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA 63 4e-22
)	gb[U76554]BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR 63 4e-22
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit 62 4e-22
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s 62 2e-21
	emb AW185023 AW185023 se85f12.y1 Gm-c1023 Glycine max cDNA clone 58 5e-21
10	emb AW277333 AW277333 sf80a11.y1 Gm-c1019 Glycine max cDNA clone 69 6e-21
10.	emb AI900061 AI900061 sb98d02.yl Gm-c1012 Glycine max cDNA clone 69 6e-21
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s 62 8e-21
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon 62 1e-20 emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon 62 4e-20
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon 62 4e-20 dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds. 62 7e-20
15	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds. 62 7e-20
	emb AV422972 AV422972 AV422972 Lotus japonicus young plants (two 76 3e-19
	emb AV423707 AV423707 AV423707 Lotus japonicus young plants (two 76 3e-19
	emb AV424707 AV424707 AV424707 Lotus japonicus young plants (two 76 3e-19)
	emb AV411009 AV411009 AV411009 Lotus japonicus young plants (two 76 3e-19
20	emb AV413230 AV413230 AV413230 Lotus japonicus young plants (two 76 3e-19
	emb AV418453 AV418453-AV418453 Lotus japonicus young plants (two 76 3e-19
	emb AV411580 AV411580 AV411580 Lotus japonicus young plants (two 76 3e-19
	emb AV412443 AV412443 AV412443 Lotus japonicus young plants (two 76 3e-19
-	emb AV412455 AV412455 AV412455 Lotus japonicus young plants (two 76 3e-19
25	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon 61 9e-19
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon 61 1e-18
	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon 61 1e-18
	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon 61 1e-18
	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon 61 le-18
30	emb AV424248 AV424248 AV424248 Lotus japonicus young plants (two 73 1e-18
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon 61 1e-18
	emb AW706014 AW706014 sk64g01.yl Gm-c1016 Glycine max cDNA clone 66 3e-18
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA 62 4e-18
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s 62 5e-18
35	emb AV411226 AV411226 AV411226 Lotus japonicus young plants (two 71 6e-18
	emb AV419929 AV419929 AV419929 Lotus japonicus young plants (two 71 6e-18
	gbBE058334BE058334 sn14g01.yl Gm-c1016 Glycine max cDNA clone 72 8e-18
	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon 62 2e-17
40	emb AV423254 AV423254 AV423254 Lotus japonicus young plants (two 76 3e-17
40	emb AW755973 AW755973 sl11h06.yl Gm-c1036 Glycine max cDNA clone 70 4e-17
	emb AI960244 AI960244 sc80g07.yl Gm-c1018 Glycine max cDNA clone 70 5e-17
	emb AV411565 AV411565 AV411565 Lotus japonicus young plants (two 68 7e-17
	emb AV424084 AV424084 AV424084 Lotus japonicus young plants (two 68 7e-17 emb AV413163 AV413163 AV413163 Lotus japonicus young plants (two 68 7e-17
45	A LANGUAGA A MARAMATAN A MARAMATAN A MARAMATAN A MARAMATAN A MARAMATAN A MARAMATAN A MARAMATAN A MARAMATAN A M
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon 54 3e-16 emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t 70 3e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two 70 3e-16
	gb[BE021759]BE021759 sm62a09.yl Gm-c1028 Glycine max cDNA clone 66 3e-16
	emb AV423639 AV423639 AV423639 Lotus japonicus young plants (two 70 5e-16
50	emb AI736394 AI736394 sb28a06.yl Gm-c1009 Glycine max cDNA clone 64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD 57 9e-16
•	emb AV411832 AV411832 AV411832 Lotus japonicus young plants (two 64 9e-16
	emb AV408053 AV408053 AV408053 Lotus japonicus young plants (two 48 1e-15
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon 54 2e-15
55	emb AV416264 AV416264 AV416264 Lotus japonicus young plants (two 62 4e-15
	emb AV412367 AV412367 AV412367 Lotus japonicus young plants (two 62 4e-15
	emb AV420478 AV420478 AV420478 Lotus japonicus young plants (two 62 4e-15
	emb AV412447 AV412447 AV412447 Lotus japonicus young plants (two 62 4e-15
	emb AV414463 AV414463 AV414463 Lotus japonicus young plants (two 62 4e-15
50	emb AV419425 AV419425 AV419425 Lotus japonicus young plants (two 62 4e-15
	embla VA25774 AVA25774 AVA25774 I otus ignonique voung planta (type 46 60 15

```
emb|AW981180|AW981180 EST392374 DSIL Medicago truncatula cDNA cl... 76 1e-14
      emb|AV428712|AV428712 AV428712 Lotus japonicus young plants (two...
      emb|AV418073|AV418073 AV418073 Lotus japonicus young plants (two...
      emb|AV419180|AV419180 AV419180 Lotus japonicus young plants (two... 58 5e-14
  5
      emb|AV423498|AV423498 AV423498 Lotus japonicus young plants (two... 58 5e-14
      emb|AV428398|AV428398 AV428398 Lotus japonicus young plants (two... 58 5e-14
      emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 62 5e-14
      emb|AW738399|AW738399 EST339826 tomato flower buds, anthesis, Co... 62 5e-14
10
      Query= AL021890.57 s_at 18224 s at /id source genbank /description
      emb|caa17150.1| (al021890) putative protein [arabidopsis thaliana]
      /blast_score 4.00e-81 /ec_number /family /chip nova /gb link /ncgi
           (426 letters)
15
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
20
                                         Score
      Sequences producing significant alignments:
                                                        (bits) Value
      25
      emb|AW224013|AW224013 EST300824 tomato fruit red ripe, TAMU Lyco... 244 3e-64
      emb|AW223703|AW223703 EST300514 tomato fruit red ripe, TAMU Lyco... 244 3e-64
      emb|AW441269|AW441269 EST310665 tomato fruit red ripe, TAMU Lyco... 244 3e-64
      emb|AW034892|AW034892 EST279121 tomato callus, TAMU Lycopersicon... 244 3e-64
      gb|BE124622|BE124622 EST393657 GVN Medicago truncatula cDNA clon... 243 5e-64
30
      emblAW747419|AW747419 WS1 68 E10.b1_A002 Water-stressed 1 (WS1) ... 242 1e-63
      gb|BE033541|BE033541 MF02E10 MF Mesembryanthemum crystallinum cD... 242 1e-63
      emb|AI943438|AI943438 MF02E10 MF Mesembryanthemum crystallinum c... 242 1e-63
      emb|AW730496|AW730496 GA__Ea0026O23 Gossypium arboreum 7-10 dpa ... 242 1e-63
      emb|AI960575|AI960575 sc86c01.yl Gm-c1018 Glycine max cDNA clone... 240 4e-63
35
      emb|AW706639|AW706639 sj62h07.yl Gm-c1033 Glycine max cDNA clone... 240 4e-63
      emb|AW568285|AW568285 si69g11.yl Gm-r1030 Glycine max cDNA clone... 240 5e-63
      emb|AW186193|AW186193 se64g04.yl Gm-c1019 Glycine max cDNA clone... 240 5e-63
      gb|BE020351|BE020351 sm43b05.yl Gm-c1028 Glycine max cDNA clone ... 240 5e-63
      emb|AW981480|AW981480 EST392633 DSIL Medicago truncatula cDNA cl... 239 1e-62
40
      emb|AW747501|AW747501 WS1_68_E10.g1_A002 Water-stressed 1 (WS1) ... 238 1e-62
      emb|AI443884|AI443884 sa44f06.y1 Gm-c1004 Glycine max cDNA clone... 237 5e-62
      emb|AI855496|AI855496 sc16h05.yl Gm-c1013 Glycine max cDNA clone... 232 8e-61
      emb|AW132618|AW132618 se06f04.yl Gm-c1013 Glycine max cDNA clone... 222 9e-58
      emb|AW760599|AW760599 s152d09.y1 Gm-c1027 Glycine max cDNA clone... 217 3e-56
45
      emb|AI965929|AI965929 sc79h07.yl Gm-c1018 Glycine max cDNA clone... 199 1e-50
      emb|AV398027|AV398027 AV398027 Chlamydomonas reinhardtii C9 Chla... 127 9e-50
      emb|AW907232|AW907232 EST343355 potato stolon, Cornell Universit... 193 4e-49
      emb|AW738874|AW738874 gb03e09.yl Moss EST library PPN Physcomitr... 184 2e-46
      emb[AW685341]AW685341 NF026D08NR1F1000 Nodulated root Medicago t... 177 4e-44
50
      emb|AW739119|AW739119 gb26a12.yl Moss EST library PPN Physcomitr... 173 7e-43
      emb|AL049558|SPBC216 S.pombe chromosome II cosmid c216.
                                                                     84 1e-38
      emb|AV408412|AV408412 AV408412 Lotus japonicus young plants (two... 157 5e-38
      emb|AA948748|AA948748 LO-267M13R Ice plant Lambda Uni-Zap XR exp... 155 1e-37
      emb|AW597401|AW597401 si92d06.yl Gm-c1031 Glycine max cDNA clone... 154 3e-37
      emb|AI495735|AI495735 sb15f07.yl Gm-c1004 Glycine max cDNA clone... 154 4e-37
      emb|AW351206|AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA ... 154 4e-37
      emb|AI777814|AI777814 EST258693 tomato susceptible, Cornell Lyco... 143 8e-36
      emb|AI166395|AI166395 xylem.est.231 Poplar xylem Lambda ZAPII li... 148 3e-35
      emb|AW335287|AW335287 S45D10 AGS-1 Pneumocystis carinii f. sp. c... 76 5e-35
60
      emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 124 3e-31
      emb|AW156084|AW156084 ga24f11.y1 Moss EST library PPU Physcomitr... 130 5e-30
```

	emb AA740047 AA740047 812 PtIFG2 Pinus taeda cDNA clone 9275M 3' 126 1e-28 emb AI822525 AI822525 L0-1030T3 Ice plant Lambda Uni-Zap XR expr 92 8e-26
	emb AW933878 AW933878 EST359721 tomato fruit mature green, TAMU 89 7e-25
	emb AW222361 AW222361 EST299172 tomato fruit red ripe, TAMU Lyco 89 7e-25
5	emb X59720 SCCHRIII S.cerevisiae chromosome III complete DNA seq 80 8e-25
	emb AW617209 AW617209 EST323620 L. hirsutum trichome, Cornell Un 89 1e-24
	emb AW775277 AW775277 EST334342 DSIL Medicago truncatula cDNA cl 85 3e-24
	emb AI730110 AI730110 BNLGHi6160 Six-day Cotton fiber Gossypium 90 3e-23
	emb AW933218 AW933218 EST359061 tomato fruit mature green, TAMU 89 2e-22
10	emb AW222638 AW222638 EST299449 tomato fruit red ripe, TAMU Lyco 89 2e-22
	emb AW094164 AW094164 EST287344 tomato mixed elicitor, BTI Lycop 89 2e-22
	emb AW145744 AW145744 ga34c05.yl Moss EST library PPN Physcomitr 103 9e-22
	emb AV427426 AV427426 AV427426 Lotus japonicus young plants (two 101 3e-21
	gb BE060018 BE060018 sn39h09.yl Gm-c1027 Glycine max cDNA clone 82 6e-21
15	gb BE022658 BE022658 sm75g09.yl Gm-c1015 Glycine max cDNA clone 100 1e-20
	emb AI939238 AI939238 sc68h11.yl Gm-c1016 Glycine max cDNA clone 82 5e-20
	emb AL160493 LMFLCHR26 Leishmania major Friedlin assembled chrom 94 5e-19
	emb AW222387 AW222387 EST299198 tomato fruit red ripe, TAMU Lyco 91 3e-18
~~	emb AW476911 AW476911 ga38h10.yl Moss EST library PPU Physcomitr 91 3e-18
20	emb AW220746 AW220746 EST297215 tomato fruit mature green, TAMU 89 2e-17
	emb AW094112 AW094112 EST287292 tomato mixed elicitor, BTI Lycop 57 3e-16
	emb AW127596 AW127596 M110327 DSLC Medicago truncatula cDNA clon 78 5e-14
	gb[T36700]T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar 74 6e-13
25	emb AW650769 AW650769 EST329223 tomato germinating seedlings, TA 72 3e-12
25	emb AT000681 AT000681 AT000681 Brassica rapa guard cell Brassica 61 3e-12
	gb BE035973 BE035973 MO22G04 MO Mesembryanthemum crystallinum cD 68 4e-11
	gb BE036098 BE036098 MO22G05 MO Mesembryanthemum crystallinum cD 68 4e-11
	gb N81594 N81594 TgESTzy60e01.rl TgRH Tachyzoite cDNA Toxoplasma 48 8e-10
30	emb AW907238 AW907238 EST343361 potato stolon, Cornell Universit 63 9e-10 emb AZ215418 AZ215418 Sheared DNA-79B7.TF Sheared DNA Trypanosom 54 2e-09
30	11. 10.1000 (1) 10.1000 (2000 2000 2000 2000 2000 2000 2000
	emb AA842826 AA842826 CFB57 Floral bud cDNA library of Hot peppe 59 2e-08 gb T37143 T37143 EST102217 S. cerevisiae strain X2180-1A Sacchar 46 3e-07
	114774100001477410000 477440000 7
	gb U14566 SCU14566 Saccharomyces cerevisiae formylglycinamide ri 35 0.23
35	emb Z72847 SCYGR062C S.cerevisiae chromosome VII reading frame O 35 0.23
	emb AW156147 AW156147 se20b05.yl Gm-c1015 Glycine max cDNA clone 35 0.23
	gb[M83672]YSCSPT4A Saccharomyces cerevisiae zinc finger protein 35 0.23
	gb U59742 SCU59742 Saccharomyces cerevisiae Cox18p (COX18) gene, 35 0.23
	emb AI374413 AI374413 T6768 MVAT4 bloodstream form of serodeme W 26 1.7
40	emb AQ945483 AQ945483 Sheared DNA-44G3.TR Sheared DNA Trypanosom 32 2.1
	emb AI374297 AI374297 T6531 MVAT4 bloodstream form of serodeme W 26 2.3
	emb AW030467 AW030467 EST273722 tomato callus, TAMU Lycopersicon 31 4.0
	emb AW624450 AW624450 EST322395 tomato flower buds 3-8 mm, Corne 31 4.0
	emb AW979733 AW979733 EST341357 tomato root deficiency, Cornell 31 4.0
45	emb AW737565 AW737565 EST338992 tomato flower buds, anthesis, Co 31 4.0
	emb AW679327 AW679327 WS1_23_A02.g1_A002 Water-stressed 1 (WS1) 31 5.5
	emb AW282515 AW282515 LG1_312_G03.g1_A002 Light Grown 1 (LG1) So 31 5.5
	emb AF077352 AF077352 Chlamydomonas reinhardtii myosin heavy cha 30 7.6
	emb[X55012]PSUSP43 Pisum sativum mRNA for an unknown seed prote 30 7.6
50	gb U73817 CRU73817 Chlamydomonas reinhardtii LRG5 mRNA, complete 30 7.6
	gb U73818 CRU73818 Chlamydomonas reinhardtii LRG5 gene, complete 30, 7.6

1 1

Query= AC002391.163_at 18551_at /id_source genbank /description gb|aab87112.1| (ac002391) putative cytochrome p450 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-55 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002391| /ncgi http://www.ncgr.org/cgi-bin/ff?ac002391 60 (1632 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters 5 Score E Sequences producing significant alignments: (bits) Value emb|AB001379|AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto... 337 e-149 10 emb|AJ238439|CAR238439 Cicer arietinum mRNA for a cytochrome P45... 338 e-149 emb|AB022732|AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy... 334 e-148 emb|AJ012581|CAR012581 Cicer arietinum mRNA for cytochrome P450. 333 e-147 emb|AB025016|AB025016 Lotus japonicus mRNA for cytochrome P450, ... 309 e-145 emb|AJ000478|HTCYP81L Helianthus tuberosus mRNA for cytochrome P... 227 e-136 15 emb|AJ000477|HTCYP81C Helianthus tuberosus mRNA for cytochrome P... 227 e-135 emb|AJ239051|CAR239051 Cicer arietinum mRNA for cytochrome P450 ... 236 7e-85 emb|AJ249800|CAR249800 Cicer arietinum partial mRNA for cytochro... 299 3e-80 emb[AW185361]AW185361 se90e02.yl Gm-c1027 Glycine max cDNA clone... 272 4e-72 emb|AW234443|AW234443 sf25c03.yl Gm-c1028 Glycine max cDNA clone... 264 1e-69 20 emb|AW307234|AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone... 261 1e-68 emb|AF082028|AF082028 Hemerocallis hybrid cultivar senescence-as... 194 3e-67 emb|AW775904|AW775904 EST334969 DSIL Medicago truncatula cDNA cl... 223 9e-66 emb|AJ249801|CAR249801 Cicer arietinum partial mRNA for cytochro... 250 2e-65 emb|AW733691|AW733691 sk83g07.yl Gm-c1016 Glycine max cDNA clone... 247 2e-64 emb|AW171738|AW171738 N100632e rootphos(-) Medicago truncatula c... 245 6e-64 25 emb|AI495626|AI495626 sb11c08.yl Gm-c1004 Glycine max cDNA clone... 231 2e-59 emb|AI729126|AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium... 183 4e-58 emb|AI725744|AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium... 182 1e-57 emb|AW257188|AW257188 EST305325 KV2 Medicago truncatula cDNA clo... 189 1e-56 30 emb|AW329224|AW329224 N200436e rootphos(-) Medicago truncatula c... 220 2e-56 emb|AF029856|AF029856 Sorghum bicolor cytochrome P450 CYP98A1 (C... 152 9e-55 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycope... 152 4e-54 emb|X95342|NTHSR515 N.tabacum mRNA for HSR515 protein. 84 5e-54 emb|AW932147|AW932147 EST357990 tomato fruit mature green, TAMU ... 212 7e-54 35 emb|AW684707|AW684707 NF020A02NR1F1000 Nodulated root Medicago t... 189 7e-53 emb|AW171672|AW171672 N100566e rootphos(-) Medicago truncatula c... 207 2e-52 emb|AW688601|AW688601 NF009D12ST1F1000 Developing stem Medicago ... 185 2e-51 emb|AI731081|AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ... 203 3e-51 emb[AW100311]AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone... 202 6e-51 40 emb|AW299084|AW299084 EST305758 KV2 Medicago truncatula cDNA clo... 182 8e-51 emb|AW616170|AW616170 EST307209 L. hirsutum trichome, Cornell Un... 142 2e-50 emb|AW695923|AW695923 NF100G02ST1F1018 Developing stem Medicago ... 174 1e-49 emb|AI731481|AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ... 172 9e-49 emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 142 6e-48 45 emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 142 6e-48 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 142 8e-48 emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 142 1e-47 emb|AI728374|AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium... 167 3e-47 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 100 5e-47 50 emb|AF014802|AF014802 Eschscholzia californica (S)-N-methylcocla... 165 7e-47 emb|AW773754|AW773754 EST332740 KV3 Medicago truncatula cDNA clo... 169 1e-46 emb|AW686025|AW686025 NF037D11NR1F1000 Nodulated root Medicago t... 105 1e-46 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 140 2e-46 emb|AV412147|AV412147 AV412147 Lotus japonicus young plants (two... 184 1e-45 gb[U29333[PSU29333 Pisum sativum novel wound-inducible cytochrom... 161 6e-45 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycope... 106 3e-44 emb|AW687247|AW687247 NF007E11RT1F1086 Developing root Medicago ... 178 8e-44 emb|AW616086|AW616086 EST296847 L. hirsutum trichome, Cornell Un... 142 1e-43 emb|AW617900|AW617900 EST324311 L. hirsutum trichome, Cornell Un... 142 1e-43 60 emb|AW031264|AW031264 EST274639 tomato callus, TAMU Lycopersicon... 143 5e-43 emblAW309826|AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone... 175 8e-43

dbj[E13663|E13663 cDNA encoding cytochrome P450 which is induced... 103 8e-43 dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 103 8e-43 emb|AW617323|AW617323 EST323734 L. hirsutum trichome, Cornell Un... 138 1e-42 emb|AW617605|AW617605 EST324016 L. hirsutum trichome, Cornell Un... 138 1e-42 emb|Y10492|GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 105 2e-42 emb|AF195809|AF195809 Vigna radiata isoflavone synthase 4 (ifs4)... 100 3e-42 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 155 3e-42 emb|AF135484|AF135484 Glycine max cytochrome P450 monooxygenase ... 100 4e-42 emb|AF195807|AF195807 Vigna radiata isoflavone synthase 2 (ifs2)... 100 4e-42 10 emb|AW616809|AW616809 EST323220 L. hirsutum trichome, Cornell Un... 137 4e-42 emb|AF195811|AF195811 Trifolium pratense isoflavone synthase 2 (... 100 5e-42 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 100 5e-42 emb|AF195808|AF195808 Vigna radiata isoflavone synthase 3 (ifs3)... 100 5e-42 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 100 5e-42 15 emblAF195800|AF195800 Medicago sativa isoflavone synthase 1 (ifs... 100 5e-42 emb|AF195802|AF195802 Medicago sativa isoflavone synthase 3 (ifs... 100 5e-42 emb|AI973839|AI973839 sd11c06.y1 Gm-c1020 Glycine max cDNA clone... 103 5e-42 emb|AW734404|AW734404 sk19f09.yl Gm-c1028 Glycine max cDNA clone... 154 6e-42 emb|AB024931|AB024931 Lotus japonicus mRNA for cytochrome P450, ... 98 7e-42 20 emb|Y10491|GMC450CP4 G.max mRNA for putative cytochrome P450, cl... 144 8e-42 emb|AB015762|AB015762 Nicotiana tabacum mRNA for cytochrome P450... 155 8e-42 emb|AF124372|AF124372 Nicotiana tabacum NT7 mRNA, partial cds. 135 8e-42 emblAF195798|AF195798 Glycine max isoflavone synthase 1 (ifs1) m... 100 1e-41 emb|AF195799|AF195799 Glycine max isoflavone synthase 2 (ifs2) m... 99 1e-41 25 emb|AF022462|AF022462 Glycine max cytochrome P450 monooxygenase ... 99 1e-41 emb|AF195806|AF195806 Vigna radiata isoflavone synthase 1 (ifs1)... 99 1e-41 emb|AF195812|AF195812 Pisum sativum isoflavone synthase 1 (ifs1)... 100 2e-41 emblAW617833|AW617833 EST324232 L. hirsutum trichome, Cornell Un... 142 3e-41 30 emb|AW617284|AW617284 EST323695 L. hirsutum trichome, Cornell Un... 142 3e-41 emb|AW616181|AW616181 EST307220 L. hirsutum trichome, Cornell Un... 142 3e-41 emb|AF195813|AF195813 Lupinus albus isoflavone synthase 1 (ifs1)... 99 3e-41 emb|AF195815|AF195815 Trifolium repens isoflavone synthase 2 (if... 98 3e-41 emb|AW616381|AW616381 EST322792 L. hirsutum trichome, Cornell Un... 141 5e-41 35 emb|AF195801|AF195801 Medicago sativa isoflavone synthase 2 (ifs... 100 6e-41 emb|AW278589|AW278589 sf46e01.yl Gm-c1009 Glycine max cDNA clone... 98 6e-41 dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 103 9e-41 emb[AB023636]AB023636 Glycyrrhiza echinata CYP Ge-8 mRNA for cyt... 100 1e-40 emb|AF195814|AF195814 Trifolium repens isoflavone synthase 1 (if... 100 1e-40 40 emblAF195805|AF195805 Lens culinaris isoflavone synthase 2 (ifs2... 100 2e-40 emb|AW617099|AW617099 EST323510 L. hirsutum trichome, Cornell Un... 139 3e-40 emb|AF195803|AF195803 Vicia villosa isoflavone synthase 1 (ifs1)... 97 3e-40 emb[Y10982]GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 150 4e-40 emb|AW255096|AW255096 ML139 peppermint glandular trichome Mentha... 154 5e-40 45 emb|AF195804|AF195804 Lens culinaris isoflavone synthase 1 (ifs1... 96 6e-40 emb|AF195816|AF195816 Beta vulgaris isoflavone synthase 1 (ifs1)... 99 6e-40 emb|AJ243804|CAR243804 Cicer arietinum mRNA for cytochrome P450 ... 96 8e-40

Query= AC004411.25_at 18567_at /id_source genbank /description gb|aac34217.1| (ac004411) putative alcohol dehydrogenase [arabidopsis thaliana] /blast_score 1.00e-133 /ec_number /family dehydrogenase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004411| /ncgi http://www.ncgr.org/cgi-bin/ff?ac004411 (826 letters)

Database: plantfungal
60 661,018 sequences; 426,114,510 total letters

Searching......done Score E Sequences producing significant alignments: (bits) Value 5 emb|AJ277945|LES277945 Lycopersicon esculentum mRNA for putative... 125 3e-72 emblAW234215|AW234215 sf22f01.yl Gm-c1028 Glycine max cDNA clone... 256 1e-67 gb[U21801]LEU21801 Lycopersicon esculentum alcohol dehydrogenase... 111 1e-64 emb|AW729170|AW729170 GA Ea0024E17 Gossypium arboreum 7-10 dpa ... 126 3e-59 10 emb|AW625848|AW625848 EST319755 tomato radicle, 5 d post-imbibit... 125 2e-54 emb]AW096560]AW096560 EST289740 tomato mixed elicitor, BTI Lycop... 117 5e-52 emb|AI494929|AI494929 sa92g06.yl Gm-c1004 Glycine max cDNA clone... 203 le-51 emb|AB018559|AB018559 Citrullus lanatus mRNA for wts2L, complete... 74 1e-50 emb|AF053638|AF053638 Pisum sativum short-chain alcohol dehydrog... 103 3e-50 15 emb|AF097651|AF097651 Pisum sativum short-chain alcohol dehydrog... 103 8e-50 emb|AF053639|AF053639 Pisum sativum short-chain alcohol dehydrog... 103 2e-49 emb|AW092874|AW092874 EST286054 tomato mixed elicitor, BTI Lycop... 112 3e-49 emb[AJ223178]NTAJ3178 Nicotiana tabacum SCANT gene. 93 7e-49 emb|AJ223177|NTAJ3177 Nicotiana tabacum mRNA for short chain alc... 93 7e-49 20 emblAW350415|AW350415 GM210008B10E12R Gm-r1021 Glycine max cDNA ... 155 2e-47 gb[U53828|SLU53828 Silene latifolia ssp. alba STA1-12 (STA1-12) ... 140 8e-47 emb|AW682978|AW682978 NF005G04LF1F1035 Developing leaf Medicago ... 107 8e-47 emb|AW093147|AW093147 EST286327 tomato mixed elicitor, BTI Lycop... 118 8e-47 gb|U53827|SLU53827 Silene latifolia ssp. alba STA1-2 (STA1-2) mR... 140 2e-46 25 gb|U53829|SLU53829 Silene latifolia ssp. alba STA1-18 (STA1-18) ... 140 2e-46 emb|AI773378|AI773378 EST254478 tomato resistant, Cornell Lycope... 117 2e-45 emb|AF072447|AF072447 Ipomoea trifida short-chain alcohol dehydr... 97 5e-45 emb|AF072449|AF072449 Ipomoea trifida short-chain alcohol dehydr... 96 9e-45 emb|AF072450|AF072450 Ipomoea trifida short-chain alcohol dehydr... 94 4e-44 30 emb|AF072448|AF072448 Ipomoea trifida short-chain alcohol dehydr... 94 4e-44 emb|AW349377|AW349377 GM210007A20C11R Gm-r1021 Glycine max cDNA ... 78 2e-43 emb|AI778245|AI778245 EST259124 tomato susceptible, Cornell Lyco... 117 3e-41 emb|AW776982|AW776982 EST336047 DSIL Medicago truncatula cDNA cl... 105 5e-41 dbj|D88121|D88121 Vigna unguiculata mRNA for CPRD12 protein, com... 79 8e-41 35 emblAW945039|AW945039 EST337089 tomato flower buds 3-8 mm, Corne... 107 3e-38 emb|AI486382|AI486382 EST244703 tomato ovary, TAMU Lycopersicon ... 101 1e-35 emb|AW032711|AW032711 EST276270 tomato callus, TAMU Lycopersicon... 98 9e-35 emb|AI483613|AI483613 EST249463 tomato ovary, TAMU Lycopersicon ... 98 9e-35 emb|AW441202|AW441202 EST310598 tomato fruit red ripe, TAMU Lyco... 98 2e-34 40 emb|AI486640|AI486640 EST244961 tomato ovary, TAMU Lycopersicon ... 95 4e-34 emb|AW185846|AW185846 se60d03.yl Gm-c1019 Glycine max cDNA clone... 83 3e-33 emb|AW255499|AW255499 ML524 peppermint glandular trichome Mentha... 100 1e-32 emb|AW185845|AW185845 se60d02.yl Gm-c1019 Glycine max cDNA clone... 86 2e-32 emb|AW692543|AW692543 NF056F02ST1F1000 Developing stem Medicago ... 103 2e-31 45 emb|AW202061|AW202061 sf10f02.yl Gm-c1027 Glycine max cDNA clone... 98 5e-30 dbj|D29976|TOBTFHP1 Tobacco mRNA for TFHP-1 protein, complete cds. 87 9e-30 emb|AW254739|AW254739 ML1026 peppermint glandular trichome Menth... 92 1e-29 gb|U89270|TDU89270 Tripsacum dactyloides short-chain alcohol deh... 84 2e-29 gb U89271 TDU89271 Tripsacum dactyloides short-chain alcohol deh... 84 2e-29 50 emb|AI443505|AI443505 sa32f06.x1 Gm-c1004 Glycine max cDNA clone... 80 6e-28 emb|AW278238|AW278238 sf41e03.yl Gm-c1009 Glycine max cDNA clone... 98 7e-28 emblAW039180|AW039180 EST281415 tomato mixed elicitor, BTI Lycop... 75 1e-27 emb|AW031743|AW031743 EST275197 tomato callus, TAMU Lycopersicon... 71 9e-27 emb|AW203395|AW203395 sf29g01.yl Gm-c1028 Glycine max cDNA clone... 50 8e-25 55 emb|AW031891|AW031891 EST275345 tomato callus, TAMU Lycopersicon... 60 2e-24 emb|AL115211|CNS01C8J Botrytis cinerea strain T4 cDNA library un... 111 1e-23 emb|AW221824|AW221824 EST298635 tomato fruit red ripe, TAMU Lyco... 60 1e-23 emb[AW093827]AW093827 EST287007 tomato mixed elicitor, BTI Lycop... 60 1e-23 emb|AI488267|AI488267 EST246589 tomato ovary, TAMU Lycopersicon ... 60 3e-23 60 emb|AW679848|AW679848 WS1_32 F10.g1_A002 Water-stressed 1 (WS1) ... 78 5e-23 emb|AW040207|AW040207 EST282706 tomato mixed elicitor, BTI Lycop... 58 5e-23

	emb AW040198 AW040198 EST282697 tomato mixed elicitor, BTI Lycop 58 5e-23
	emb AI897246 AI897246 EST266605 tomato ovary, TAMU Lycopersicon 57 9e-23
	emb AW757208 AW757208 sl30e10.yl Gm-c1027 Glycine max cDNA clone 94 2e-22
	11177740045011777400450 440 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
5	1 14 332 CO CO AO LA 337 CO CO AO 3 77 CO CO TO A 77 LO CO A 7 LO C
,	emb A W 080040 A W 080040 NF03/F0/NK1F1000 Nodulated root Medicago t 104 1e-21
	emb AW689744 AW689744 NF023H04ST1F1000 Developing stem Medicago 104 1e-21
	emb AW559784 AW559784 EST314832 DSIR Medicago truncatula cDNA cl 101 6e-21
	emb AW862634 AW862634 00093 leafy spurge Lambda HybriZAP 2.1 two 75 1e-20
10	emb AW821919 AW821919 00010 leafy spurge Lambda HybriZAP 2.1 two 75 1e-20
10	emb AW277819 AW277819 sf87a01.y1 Gm-c1019 Glycine max cDNA clone 65 2e-20
	emb AW032875 AW032875 EST276434 tomato callus, TAMU Lycopersicon 53 2e-20
	gb BE020693 BE020693 sm45g06.yl Gm-c1028 Glycine max cDNA clone 82 3e-20
	emb AW094463 AW094463 EST287643 tomato mixed elicitor, BTI Lycop 98 7e-20
	emb AI442526 AI442526 sa32f06.yl Gm-c1004 Glycine max cDNA clone 98 7e-20
15	emb AI900071 AI900071 sb98e02.yl Gm-c1012 Glycine max cDNA clone 98 7e-20
	emb AW931981 AW931981 EST357824 tomato fruit mature green, TAMU 98 7e-20
	emb AW759370 AW759370 sl41e03.y1 Gm-c1027 Glycine max cDNA clone 98 1e-19
	emb AI813131 AI813131 23C8 Pine Lambda Zap Xylem library Pinus t 49 2e-19
	emb AW222302 AW222302 EST299113 tomato fruit red ripe, TAMU Lyco 55 2e-19
20	* 1 1 771000 0001 1 77700 0000 0000 0000
	emb AI495898 AI495898 sb17e12.yl Gm-c1004 Glycine max cDNA clone 95 7e-19
	emb AW034003 AW034003 EST277665 tomato callus, TAMU Lycopersicon 55 1e-18
	emb AI486457 AI486457 EST244778 tomato ovary, TAMU Lycopersicon 55 1e-18
25	emb AI441861 AI441861 sa53c11.y1 Gm-c1004 Glycine max cDNA clone 91 8e-18
.25	emb AW932087 AW932087 EST357930 tomato fruit mature green, TAMU 55 4e-17
	emb AW277586 AW277586 sf84a04.yl Gm-c1019 Glycine max cDNA clone 61 6e-17
	emb AW290533 AW290533 NXNV025G01F Nsf Xylem Normal wood Vertical 60 1e-16
	emb AW928544 AW928544 EST337332 tomato flower buds 8 mm to pre-a 85 5e-16
	emb AI494694 AI494694 sb14a12.yl Gm-c1004 Glycine max cDNA clone 84 1e-15
30	emb AW923985 AW923985 WS1_32_F10.b1_A002 Water-stressed 1 (WS1) 57 le-15
	emb AW432507 AW432507 sh75b08.yl Gm-c1015 Glycine max cDNA clone 64 1e-15
	emb AW030102 AW030102 EST273357 tomato callus, TAMU Lycopersicon 55 2e-15
	emb AA825003 AA825003 CT286.SK Tomato Leaf cDNA from cv. VFNT ch 55 3e-15
	emb AW309265 AW309265 sf29f03.x1 Gm-c1028 Glycine max cDNA clone 60 9e-15
35	emb AW728352 AW728352 GA_Ea0016G23 Gossypium arboreum 7-10 dpa 81 9e-15
	emb AW676767 AW676767 DG1_14_E09.g1_A002 Dark Grown 1 (DG1) Sorg 61 6e-14
	emb AW648661 AW648661 EST327031 tomato germinating seedlings, TA 53 6e-14
	emb AW309650 AW309650 sf22f01.x1 Gm-c1028 Glycine max cDNA clone 56 1e-13
	emb AQ162057 AQ162057 mgxb0010H24r CUGI Rice Blast BAC Library P 66 9e-13
40	emb AV408902 AV408902 AV408902 Lotus japonicus young plants (two 52 9e-12
	emb AW727400 AW727400 GA_Ea0011017 Gossypium arboreum 7-10 dpa 69 3e-11
	emb AW442057 AW442057 EST311453 tomato fruit red ripe, TAMU Lyco 49 3e-11
	emb AW037838 AW037838 EST279467 tomato mixed elicitor, BTI Lycop 68 7e-11
45	emb[X72730]LEERT10 L.esculentum (ERT 10) ripening-related mRNA. 47 1e-10
75	
	Openie A 1222713 A at 18500 at lid assess combants libraries
	Query= AJ222713.4 at 18590 at /id_source genbank /description
	emb caa10955.1 (aj222713) unnamed protein product [arabidopsis
50	thaliana] /blast_score 1.00e-151 /ec_number /family /chip nova
50	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb aj222713 /ncgi
	http://www.ncgr.org/cgi-bin/ff?aj222713
	(1056 letters)
C F	

55 Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching......done

60 Score E Sequences producing significant alignments:

(bits) Value

```
emb|AI488099|AI488099 EST246421 tomato ovary, TAMU Lycopersicon ... 341 5e-93
      emb|AI487552|AI487552 EST245874 tomato ovary, TAMU Lycopersicon ... 337 9e-92
      emb|AI487693|AI487693 EST246015 tomato ovary, TAMU Lycopersicon ... 336 1e-91
      emb|AI898890|AI898890 EST268333 tomato ovary, TAMU Lycopersicon ... 336 2e-91
      emb|AI490551|AI490551 EST249105 tomato ovary, TAMU Lycopersicon ... 336 2e-91
      emb|AI898058|AI898058 EST267501 tomato ovary, TAMU Lycopersicon ... 336 2e-91
      emb|AI488773|AI488773 EST247112 tomato ovary, TAMU Lycopersicon ... 336 2e-91
      emb|AW032532|AW032532 EST276091 tomato callus, TAMU Lycopersicon... 334 6e-91
10
      emb|AI488959|AI488959 EST247298 tomato ovary, TAMU Lycopersicon ... 334 6e-91
      emb|AW035679|AW035679 EST281698 tomato callus, TAMU Lycopersicon... 331 4e-90
      emb|AI488673|AI488673 EST247012 tomato ovary, TAMU Lycopersicon ... 330 2e-89
      emb|AW220879|AW220879 EST297348 tomato fruit mature green, TAMU ... 329 3e-89
      emb|AW650556|AW650556 EST329010 tomato germinating seedlings, TA... 328 5e-89
15
      emb|AI484813|AI484813 EST243074 tomato ovary, TAMU Lycopersicon ... 325 5e-88
      gb|BE020071|BE020071 sm38f07.yl Gm-c1028 Glycine max cDNA clone ... 314 5e-85
      emblAI488758|AI488758 EST247097 tomato ovary, TAMU Lycopersicon ... 308 5e-83
      emb|AI898567|AI898567 EST268010 tomato ovary, TAMU Lycopersicon ... 287 3e-82
      emb|AI897442|AI897442 EST266885 tomato ovary, TAMU Lycopersicon ... 304 8e-82
20
      emb|AI486892|AI486892 EST245214 tomato ovary, TAMU Lycopersicon ... 284 3e-81
      emb|AW032194|AW032194 EST275648 tomato callus, TAMU Lycopersicon... 302 4e-81
      emb|AI489402|AI489402 EST247741 tomato ovary, TAMU Lycopersicon ... 282 6e-81
      emb|AW035194|AW035194 EST280456 tomato callus, TAMU Lycopersicon... 299 2e-80
      emb|AI485389|AI485389 EST243710 tomato ovary, TAMU Lycopersicon ... 297 1e-79
25
      emb|AI487373|AI487373 EST245695 tomato ovary, TAMU Lycopersicon ... 284 4e-79
      emb|AI897257|AI897257 EST266616 tomato ovary, TAMU Lycopersicon ... 292 4e-78
      emb|AI771859|AI771859 EST252959 tomato ovary, TAMU Lycopersicon ... 292 4e-78
      emb|AI487093|AI487093 EST245415 tomato ovary, TAMU Lycopersicon ... 292 4e-78
      emb|AI898263|AI898263 EST267706 tomato ovary, TAMU Lycopersicon ... 291 8e-78
30
      emb|AI899016|AI899016 EST268459 tomato ovary, TAMU Lycopersicon ... 288 5e-77
      emb|AI490061|AI490061 EST248400 tomato ovary, TAMU Lycopersicon ... 286 2e-76
      emb|AW650475|AW650475 EST328929 tomato germinating seedlings, TA... 281 5e-75
      emb|AW036798|AW036798 EST252187 tomato ovary, TAMU Lycopersicon ... 185 2e-72
      emb|AI894523|AI894523 EST263966 tomato callus, TAMU Lycopersicon... 185 2e-72
35
      emb|AI897596|AI897596 EST267039 tomato ovary, TAMU Lycopersicon ... 270 1e-71
      emb|AW034429|AW034429 EST278000 tomato callus, TAMU Lycopersicon... 193 6e-70
      emb|AW442290|AW442290 EST311686 tomato fruit red ripe, TAMU Lyco... 186 3e-68
      emb|AF011555|AF011555 Lycopersicon esculentum jasmonic acid 2 (L... 233 5e-68
      emb|AW931430|AW931430 EST357273 tomato fruit mature green, TAMU ... 233 5e-68
40
      emblAW934046|AW934046 EST359889 tomato fruit mature green, TAMU ... 233 5e-68
      emb|AW032396|AW032396 EST275935 tomato callus, TAMU Lycopersicon... 233 5e-68
      emb|AJ010829|TSP010829 Triticum sp. mRNA for GRAB1 protein.
                                                                       258 7e-68
      emb|A82384|A82384 Sequence 9 from Patent WO9856811.
                                                                   258 7e-68
      emb|A82380|A82380 Sequence 5 from Patent WO9856811.
                                                                   255 5e-67
45
      emb|AI896316|AI896316 EST265759 tomato callus, TAMU Lycopersicon... 185 2e-66
      emb|AI895235|AI895235 EST264678 tomato callus, TAMU Lycopersicon... 169 2e-66
      emb|AW932278|AW932278 EST358121 tomato fruit mature green, TAMU ... 169 2e-66
      emblAI489104|AI489104 EST247443 tomato ovary, TAMU Lycopersicon ... 215 5e-66
      emb|AI771112|AI771112 EST252212 tomato ovary, TAMU Lycopersicon ... 215 5e-66
50
      emb|AW035978|AW035978 EST282837 tomato callus, TAMU Lycopersicon... 193 9e-66
      emb|AW560823|AW560823 EST315871 DSIR Medicago truncatula cDNA cl... 193 1e-65
      emb|AW775926|AW775926 EST334991 DSIL Medicago truncatula cDNA cl... 229 1e-65
      emb|AW442348|AW442348 EST311744 tomato fruit red ripe, TAMU Lyco... 169 1e-65
      emb|AW775866|AW775866 EST334931 DSIL Medicago truncatula cDNA cl... 166 5e-65
55
      emb|AI896441|AI896441 EST265872 tomato callus, TAMU Lycopersicon... 233 5e-65
      emb|AI487186|AI487186 EST245508 tomato ovary, TAMU Lycopersicon ... 229 7e-65
      emb|AW625882|AW625882 EST319789 tomato radicle, 5 d post-imbibit... 169 2e-64
      emb|AI485002|AI485002 EST243265 tomato ovary, TAMU Lycopersicon ... 143 2e-64
      emb|AW932996|AW932996 EST358839 tomato fruit mature green, TAMU ... 193 3e-64
60
      gb|BE034140|BE034140 MG05E02 MG Mesembryanthemum crystallinum cD... 224 5e-64
      emb|AW443857|AW443857 EST308787 tomato mixed elicitor, BTI Lycop... 224 6e-64
```

	emb AI487893 AI487893 EST246215 tomato ovary, TAMU Lycopersicon 229 9e-64 emb AI488078 AI488078 EST246400 tomato ovary, TAMU Lycopersicon 241 6e-63 emb AW164307 AW164307 se70g05.y1 Gm-c1023 Glycine max cDNA clone 190 1e-62
5	emb AW216517 AW216517 EST295231 tomato callus, TAMU Lycopersicon 213 1e-62 emb AW668121 AW668121 GA
	emb AI773092 AI773092 EST254192 tomato resistant, Cornell Lycope 160 7e-62 emb AI488314 AI488314 EST246636 tomato ovary, TAMU Lycopersicon 160 1e-61 emb AI489361 AI489361 EST247700 tomato ovary, TAMU Lycopersicon 160 1e-61
10	emb AW680754 AW680754 WS1_7_A09.b1_A002 Water-stressed 1 (WS1) S 170 3e-61 emb AI856667 AI856667 sb42d09.y1 Gm-c1014 Glycine max cDNA clone 169 3e-61 emb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 144 5e-61
15	emb AW100389 AW100389 sd27a08.y2 Gm-c1012 Glycine max cDNA clone 180 6e-61 emb AW737167 AW737167 EST338594 tomato flower buds, anthesis, Co 160 9e-61
15	emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 193 2e-60 emb AW223963 AW223963 EST300774 tomato fruit red ripe, TAMU Lyco 186 4e-60 emb AW033350 AW033350 EST276921 tomato callus, TAMU Lycopersicon 230 1e-59 emb AI896351 AI896351 EST265794 tomato callus, TAMU Lycopersicon 230 2e-59
20	emb AI897423 AI897423 EST266866 tomato ovary, TAMU Lycopersicon 230 2e-59 emb AI484784 AI484784 EST243045 tomato ovary, TAMU Lycopersicon 230 2e-59 emb AI771893 AI771893 EST252993 tomato ovary, TAMU Lycopersicon 229 2e-59
25	emb AW560904 AW560904 EST315952 DSIR Medicago truncatula cDNA cl 168 3e-59 emb AW040320 AW040320 EST283184 tomato mixed elicitor, BTI Lycop 229 3e-59 emb AW736371 AW736371 EST332290 KV3 Medicago truncatula cDNA clo 160 5e-59
23	emb AI484577 AI484577 EST242807 tomato ovary, TAMU Lycopersicon 228 5e-59 emb AI488159 AI488159 EST246481 tomato ovary, TAMU Lycopersicon 228 6e-59 gb BE124309 BE124309 EST394434 DSIL Medicago truncatula cDNA clo 161 1e-58 emb AW775409 AW775409 EST334474 DSIL Medicago truncatula cDNA cl 161 1e-58
30	emb AW092910 AW092910 EST286090 tomato mixed elicitor, BTI Lycop 160 1e-58 emb AW559397 AW559397 EST314445 DSIR Medicago truncatula cDNA cl 159 4e-58 emb AI487779 AI487779 EST246101 tomato ovary, TAMU Lycopersicon 160 7e-58 emb AV410710 AV410710 AV410710 Lotus japonicus young plants (two 224 1e-57 emb AI773440 AI773440 EST254540 tomato resistant, Cornell Lycope 169 3e-57
35	emb AW041100 AW041100 EST283964 tomato mixed elicitor, BTI Lycop 222 4e-57 emb AW930743 AW930743 EST356586 tomato fruit mature green, TAMU 221 5e-57 emb AW775964 AW775964 EST335029 DSIL Medicago truncatula cDNA cl 161 1e-56 emb AI490656 AI490656 EST249210 tomato ovary, TAMU Lycopersicon 220 1e-56 emb AI490318 AI490318 EST248644 tomato ovary, TAMU Lycopersicon 220 2e-56
40	emb AI490458 AI490458 EST248784 tomato ovary, TAMU Lycopersicon 199 4e-56 emb AI486445 AI486445 EST244766 tomato ovary, TAMU Lycopersicon 199 4e-56
	Query= X74756.2_at 18591_at /id_source genbank /description emb caa52772.1 (x74756) ataf2 [arabidopsis thaliana] /blast_score
45	2.00e-99 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb x74756 /ncgi http://www.ncgr.org/cgi-bin/ff?x74756
50	(1216 letters)
÷	Database: plantfungal 661,018 sequences; 426,114,510 total letters
55	Searchingdone
	Score E
2	Sequences producing significant alignments: (bits) Value
60	emb AW775866 AW775866 EST334931 DSIL Medicago truncatula cDNA cl 317 1e-97 emb AW668121 AW668121 GA_Ea0012N05 Gossypium arboreum 7-10 dpa 304 6e-94 gb BE124309 BE124309 EST394434 DSIL Medicago truncatula cDNA clo 304 9e-94

emb|AW775409|AW775409 EST334474 DSIL Medicago truncatula cDNA cl... 304 9e-94 emb|AW559397|AW559397 EST314445 DSIR Medicago truncatula cDNA cl... 301 6e-93 emb|AI856667|AI856667 sb42d09.yl Gm-c1014 Glycine max cDNA clone... 293 2e-92 emb|AW442068|AW442068 EST311464 tomato fruit red ripe, TAMU Lyco... 300 5e-92 emb|AI773092|AI773092 EST254192 tomato resistant, Cornell Lycope... 300 5e-92 emb|AW442348|AW442348 EST311744 tomato fruit red ripe, TAMU Lyco... 306 7e-91 emb|AW737167|AW737167 EST338594 tomato flower buds, anthesis, Co... 297 7e-91 emb|AI489361|AI489361 EST247700 tomato ovary, TAMU Lycopersicon ... 296 9e-91 emb|AW696936|AW696936 NF110E07ST1F1054 Developing stem Medicago ... 301 2e-90 10 emb|AI895235|AI895235 EST264678 tomato callus, TAMU Lycopersicon... 302 2e-90 emb|AW932278|AW932278 EST358121 tomato fruit mature green, TAMU ... 302 2e-90 emb|AI488314|AI488314 EST246636 tomato ovary, TAMU Lycopersicon ... 300 1e-89 emb|AW775964|AW775964 EST335029 DSIL Medicago truncatula cDNA cl... 304 6e-89 emb|AW690801|AW690801 NF035B09ST1F1000 Developing stem Medicago ... 304 2e-88 15 emblAW687506|AW687506 NF010C12RT1F1097 Developing root Medicago ... 302 3e-88 emb|AW680754|AW680754 WS1_7_A09.b1_A002 Water-stressed 1 (WS1) S... 292_5e-88 emb|AW625882|AW625882 EST319789 tomato radicle, 5 d post-imbibit... 306 7e-88 emb|AW560904|AW560904 EST315952 DSIR Medicago truncatula cDNA cl... 282 1e-87 emb|AW686733|AW686733 NF041H04NR1F1000 Nodulated root Medicago t... 304 2e-87 20 emb|AW736371|AW736371 EST332290 KV3 Medicago truncatula cDNA clo... 280 5e-87 emb|AW203537|AW203537 sf35d02.y1 Gm=c1028 Glycine max cDNA clone... 287 5e-87 emblAW092910|AW092910 EST286090 tomato mixed elicitor, BTI Lycop... 300 3e-85 emb|AW278088|AW278088 sf39e10.y1 Gm-c1009 Glycine max cDNA clone... 314 6e-85 emb|AI487779|AI487779 EST246101 tomato ovary, TAMU Lycopersicon ... 300 1e-84 25 emb|AI896058|AI896058 EST265501 tomato callus, TAMU Lycopersicon... 306 3e-82 emb|AI773440|AI773440 EST254540 tomato resistant, Cornell Lycope... 305 5e-82 emb|AI486492|AI486492 EST244813 tomato ovary, TAMU Lycopersicon ... 297 8e-80 emb|AW220707|AW220707 EST297176 tomato fruit mature green, TAMU ... 297 2e-79 emb|AI486833|AI486833 EST245155 tomato ovary, TAMU Lycopersicon ... 295 5e-79 30 emb|AW030038|AW030038 EST273293 tomato callus, TAMU Lycopersicon... 293 2e-78 emb|AW931009|AW931009 EST356852 tomato fruit mature green, TAMU ... 291 7e-78 emb|AW306698|AW306698 sf47c01.yl Gm-c1009 Glycine max cDNA clone... 275 4e-77 gb|BE126167|BE126167 DG1_66_F07.b1_A002 Dark Grown 1 (DG1) Sorgh... 281 8e-75 emb|AJ010829|TSP010829 Triticum sp. mRNA for GRAB1 protein. 195 2e-69 35 emblA82384|A82384 Sequence 9 from Patent WO9856811. 195 2e-69 emb|AW776648|AW776648 EST335713 DSIL Medicago truncatula cDNA cl... 262 5e-69 emb|AI488057|AI488057 EST246379 tomato ovary, TAMU Lycopersicon ... 261 6e-69 emb|AI900247|AI900247 sc03a01.yl Gm-c1012 Glycine max cDNA clone... 251 1e-65 emb|AW617735|AW617735 EST324146 L. hirsutum trichome, Cornell Un... 250 1e-65 40 emb|AI777446|AI777446 EST258325 tomato susceptible, Cornell Lyco... 248 6e-65 emb|AW775926|AW775926 EST334991 DSIL Medicago truncatula cDNA cl... 179 3e-64 emb|AW442290|AW442290 EST311686 tomato fruit red ripe, TAMU Lyco... 175 3e-64 emb|AW034429|AW034429 EST278000 tomato callus, TAMU Lycopersicon... 176 4e-64 gb|BE034140|BE034140 MG05E02 MG Mesembryanthemum crystallinum cD... 182 5e-64 45 emb|AI487038|AI487038 EST245360 tomato ovary, TAMU Lycopersicon ... 206 7e-64 emb|A82380|A82380 Sequence 5 from Patent WO9856811. 183 9e-64 emb|AI352742|AI352742 MB56-5B PZ204.BNlib Brassica napus cDNA cl... 211 1e-63 emb|AW560823|AW560823 EST315871 DSIR Medicago truncatula cDNA cl... 179 1e-63 emb|AW443857|AW443857 EST308787 tomato mixed elicitor, BTI Lycop... 182 8e-63 50 emb|AW727788|AW727788 GA_Ea0028C07 Gossypium arboreum 7-10 dpa ... 200 2e-62 emb|AI896316|AI896316 EST265759 tomato callus, TAMU Lycopersicon... 171 2e-61 emb|AW035978|AW035978 EST282837 tomato callus, TAMU Lycopersicon... 176 9e-61 emb|AI484102|AI484102 EST249973 tomato ovary, TAMU Lycopersicon ... 234 1e-60 emb|AI488099|AI488099 EST246421 tomato ovary, TAMU Lycopersicon ... 167 6e-60 emb|AV410710|AV410710 AV410710 Lotus japonicus young plants (two... 185 2e-59 emb|AI487693|AI487693 EST246015 tomato ovary, TAMU Lycopersicon ... 167 4e-59 emb|AW755370|AW755370 sl03b07.yl Gm-c1036 Glycine max cDNA clone... 159 3e-58 emb|AW932996|AW932996 EST358839 tomato fruit mature green, TAMU ... 176 4e-58 emb|AI487552|AI487552 EST245874 tomato ovary, TAMU Lycopersicon ... 160 5e-58 60 emb|AI488773|AI488773 EST247112 tomato ovary, TAMU Lycopersicon ... 160 5e-58 emb|AI490551|AI490551 EST249105 tomato ovary, TAMU Lycopersicon ... 160 5e-58

emb A1898058 A1898058 EST267501 tomato ovary, TAMU Lycopersicon 160 5e-58 emb A189890 A189890 ST268333 tomato ovary, TAMU Lycopersicon 160 5e-58 emb AW022532 AW032532 EST276091 tomato callus, TAMU Lycopersicon 160 2e-57 emb AW041100 AW041100 EST280396 tomato mixed elicitor, BTILycop 182 3e-57 emb AW031430 AW3934046 EST359889 tomato ovary, TAMU Lycopersicon 160 2e-57 emb AW031430 AW391430 EST373737 tomato fruit mature green, TAMU 174 4e-57 emb AW031430 AW391430 EST273735 tomato fruit mature green, TAMU 174 4e-57 emb AW032396 AW032396 EST273735 tomato fruit mature green, TAMU 174 4e-57 emb AW032396 AW032396 EST273735 tomato fruit mature green, TAMU 174 4e-57 emb AW3340 AW32396 AW032396 EST273735 tomato fruit mature green, TAMU 174 4e-57 emb AW33464 AW032396 EST273735 tomato fruit mature green, TAMU 174 4e-57 emb AW3640 AW040220 EST283184 tomato callus, TAMU Lycopersicon 160 1e-56 emb AW040220 AW040220 EST283184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW035679 AW023596 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW220879 AW220879 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW7680556 AW680556 EST259010 tomato germianting seedlings, T 160 3e-55 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW703374 AW733637 sk83505.yl Gme-1016 Glycine max cDNA clone 167 3e-54 emb AW703374 AW733637 sk83505.yl Gme-1016 Glycine max cDNA clone 167 3e-54 emb AW703394 AW03017 EST27327 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW030317 AW030017 EST27327 tomato callus, TAMU Lycopersicon 167 4e-52 emb AW33990 A AW89399 AW28999		
cmb A1488599 A1488959 EST247298 tomato ovary, TAMU Lycopersiscon 160 2e-57 cmb AF011555 AF011555 Lycopersiscon esculentum jasmouia acid 2 (L 174 4e-57 cmb AW931430 AW931430 EST357273 tomato fruit mature green, TAMU 174 4e-57 cmb AW931430 AW931430 EST357273 tomato fault mature green, TAMU 174 4e-57 cmb AW931430 AW931440 EST357273 tomato callus, TAMU Lycopersiscon 174 4e-57 cmb AW934046 AW932496 EST275935 tomato callus, TAMU Lycopersiscon 174 4e-57 cmb AW934046 AW9320 EST275935 tomato callus, TAMU Lycopersiscon 160 1e-56 cmb AW164307 AW164307 sc70g05.y1 Gm-c1023 Glycine max cDNA clone 174 1e-56 cmb AW040320 AW040320 EST28184 tomato orany, TAMU Lycopersiscon 160 1e-56 cmb AW040320 AW040320 EST28184 tomato mixed elicitor, BTI Lycop 174 1e-56 cmb AW0220879 AW035679 EST281698 tomato callus, TAMU Lycopersiscon 160 2e-56 cmb AW0220879 AW735679 EST281698 tomato callus, TAMU Lycopersiscon 160 2e-56 cmb AW0220879 AW73679 EST281698 tomato callus, TAMU Lycopersiscon 160 2e-56 cmb AW73679 AW73679 EST3813844 DESIL Medicage funcatula cDNA cl 219 4e-56 cmb AW73679 AW73679 EST3813844 DESIL Medicage funcatula cDNA cl 219 4e-56 cmb AW73679 AW73679 EST3813844 DESIL Medicage funcatula cDNA cl 219 4e-56 cmb AW73637 AW73679 EST3813844 DESIL Medicage funcatula cDNA cl 219 4e-56 cmb AW73637 AW73679 EST38470 tomato resistant, Cornell Lycope 215 4e-55 cmb AW73637 AW73679 EST37674 tomato resistant, Cornell Lycopersion 160 2e-58 cmb AW73637 AW73679 EST37677 tomato vary, TAMU Lycopersion 167 2e-54 cmb AW73637 AW73677 Set377677 tomato vary, TAMU Lycopersion 167 3e-54 cmb AW73679 AW73677 Set377677 tomato vary, TAMU Lycopersion 167 3e-54 cmb AW736742 AST876145767767 tomato vary, TAMU Lycopersion 160 4e-52 cmb AW736742 AST876742 EST266885 tomato callus, TAMU Lycopersion 160 4e-52 cmb AW738594AW678664 AW678664 WS1 Hotol Lycopersion 160 4e-52 cmb AW70895 AW678664 AW678664 WS1 Hotol Lycopersion 160 4e-52 cmb AW708986 AW678664 WS1 Hotol Lycopersion 160 4e-52 cmb		emb AI898890 AI898890 EST268333 tomato ovary, TAMU Lycopersicon 160 5e-58
 emb AW041100 AW041100 EST283964 tomato mixed elicitor, BTI Lycop 182 3e-57 emb AF011555 Ay011555 Lycopresicon esculentum gismonic acid 2 (L 174 4e-57 emb AW931430 AW931430 EST3578273 tomato fruit mature green, TAMU 174 4e-57 emb AW931406 AW931406 EST359889 tomato fruit mature green, TAMU 174 4e-57 emb AW932396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb A188673 A1848673 1848738 A18488738 A1848738 A1848738 A1848738 A18488738 A18488738 A1848		
emb AF0 1555 AF0 1555 Lycopersicon esculentum jazmomic acid 2 (L 174 4e-57 emb AW93 1430 AW93 1430 EST357273 tomato fruit mature green, TAMU 174 4e-57 emb AW93 4046 AW93 4046 EST359889 tomato fruit mature green, TAMU 174 4e-57 emb AW93 4046 AW93 4046 EST359889 tomato callus, TAMU Lycopersicon 174 4e-57 emb AW93 403 64 AW03 20 65872 tomato callus, TAMU Lycopersicon 174 4e-57 emb AH88673 AJ488673 EST2470 12 tomato ovary, TAMU Lycopersicon 160 1e-56 emb AW040320 AW040320 EST283 84 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW040320 AW040320 EST283 84 tomato callus, TAMU Lycopersicon 160 2e-56 emb AW020879 BST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW020879 BST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW0220879 AW720879 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW0220879 AW720879 BST33844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW023053 AW223963 BST300774 tomato fruit rad ripe, TAMU Lycopersicon 160 2e-56 emb AW733963 AW223963 BST3300744 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW84813 AI448413 EST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW84813 AI448413 BST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW733637 AW733637 sk33b05.y1 Gm-e1016 Glycine max cDNA clone 213 3e-54 emb AW103039 AW100339 AW100389 sd2708.y2 Gm-e1012 Glycine max cDNA clone 167 3e-54 emb AW930017 BST273272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW930017 BST273272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW930017 BST273272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW930017 BST3742 EST286456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW930016 AW930017 EST273272 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW930016 AW903017 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW930016 AW903017 EST2959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW930016 AW903017 EST2959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW930016 AW903016 AW903016 AW903016 AW903016 AW903016 A	5	
emb AW934463 AW93446 EST359889 tomato fruit mature green, TAMU 174 4e-57 emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb AW8673 AH88673 AH88673 EST27012 tomato vary, TAMU Lycopersicon 160 1e-56 emb AW040320 AW040320 EST28184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW040320 AW040320 EST28184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW035679 AW035679 EST281698 tomato callus, TAMU Lycopersicon 160 2e-56 emb AW0228963 AW022986]EST297348 tomato fruit red ripe, TAMU Lycop 177 3e-56 emb AW0228963 AW022986]EST297348 tomato fruit red ripe, TAMU Lycop 177 3e-56 emb AW0228963 AW022986]EST297348 tomato fruit red ripe, TAMU Lycop 177 3e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW776779 AW773679 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW776779 AW773679 EST335844 DSIL Medicago truncatula cDNA cl 213 3e-54 emb AW73637 AW733637 A	3	
emb AW93306 AW93306 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb AI896441 AI896441 EST255872 tomato callus, TAMU Lycopersicon 174 4e-57 emb AI89643 AI488673 EST247012 tomato ovary, TAMU Lycopersicon 160 1e-56 emb AW164307 AW040320 SST283184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW0320 AW040320 SST283184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW023067 AW040320 EST283184 tomato fruit red ripe, TAMU Lycopersicon 160 2e-56 emb AW0220879 AW0220879 EST281698 tomato callus, TAMU Lycopersicon 167 2e-56 emb AW223963 AW0223963 EST300774 tomato fruit red ripe, TAMU Lycopersicon 167 2e-56 emb AW723963 AW0223963 EST300774 tomato fruit red ripe, TAMU Lycopersicon 167 2e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 129 4e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 129 2e-56 emb AW773941 AU773941 EST255041 tomato resistant, Cornell Lycopersicon 150 2e-54 emb AW8758134484813 EST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW87303637 AW733637 sk33105_y1 Gm-c1016 Glycine max cDNA clone 213 3e-54 emb AW87303637 AW733637 sk33105_y1 Gm-c1016 Glycine max cDNA clone 167 3e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW930017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW930017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW93194 AW03194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW93194 AW03194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW93194 AW03194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW93194 AW03194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW938194 AW0399384 sd3903.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW99384 AW099384 sd3903.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW999384 W099388 est 26005278 formato vary, TAMU Lycopersicon		
emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57 emb A1488673 A1488673 EST247012 tomato ovary, TAMU Lycopersicon 160 1e-56 emb AW164307 AW164307 sc70g05.y1 Gm-e1023 Glycine max cDNA clone 174 1e-56 emb AW040320 AW040320 EST283184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW040320 AW020879 EST283184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW223876 AW022879 EST297348 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW223963 AW222963 EST300774 tomato fruit mature green, TAMU 167 2e-56 emb AW223963 AW223963 EST300774 tomato fruit mature green, TAMU 167 2e-56 emb AW223963 AW223963 EST300774 tomato fruit mature green, TAMU 167 2e-56 emb AW776779 AW776779 EST333844 DSIL Medicago truncatula cDNA cl 219 4e-55 emb AW7736779 AW73637 EST325844 DSIL Medicago truncatula cDNA cl 219 4e-55 emb AW733637 AW733637 sk83b05.y1 Gm-e1016 Glycine max cDNA clone 150 2e-54 emb AW733637 AW733637 sk83b05.y1 Gm-e1016 Glycine max cDNA clone 150 2e-54 emb AW733637 AW733637 sk83b05.y1 Gm-e1016 Glycine max cDNA clone 163 1e-52 emb AW8030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 167 7e-54 gb BE02007 BE02007 BE02007 SE02007	,	emb AW931430 AW931430 EST357273 tomato fruit mature green, TAMU 174 4e-57
embjAl1896441 Al1896441 EST265872 tomato callus, TAMU Lycopersicon 174 4e-57 embjAl488673 Al488673 EST247012 tomato ovary, TAMU Lycopersicon 160 1e-56 embjAW164307AW164307 s670g05.yl Gm-c1023 Glycine max cDNA clone 174 1e-56 embjAW040320JAW040320 EST281384 tomato mixed elicitor, BTI Lycop 174 1e-56 embjAW036679 AW036679 EST281698 tomato callus, TAMU Lycopersicon 160 2e-56 embjAW220879 AW220879 EST297348 tomato fruit mature green, TAMU 167 2e-56 embjAW220879 AW220879 EST297348 tomato fruit red ripe, TAMU Lyco 177 3e-56 embjAW76779/AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-55 embjAW76779/AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-55 embjAW767059 AW75056 EST329010 tomato germinating seedlings, TA 160 3e-55 embjAW7303173941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 embjAW733637/AW733637 sk33065.yl Gm-c1016 Glycine max cDNA clone 213 3e-54 embjAW8630374 AW733637 sk33065.yl Gm-c1016 Glycine max cDNA clone 167 3e-54 embjAW8030017848758 AH88758 LST247097 tomato ovary, TAMU Lycopersicon 167 3e-54 embjAW03001784875273272 tomato covary, TAMU Lycopersicon 167 3e-54 embjAW930017849030017 EST273272 tomato callus, TAMU Lycopersicon 167 3e-54 embjAB87940 AB87980 AB9742 EST266818 tomato ovary, TAMU Lycopersicon 168 4e-52 embjAW93194 AW03194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW032194 AW033194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW03194 AW03194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW03194 AW03194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW03194 AW03194 EST284056 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW03194 AW03194 EST2845659 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW03194 AW03194 EST2845656 tomato callus, TAMU Lycopersicon 160 4e-52 embjAW03194 AW030984 sd3903.yl Cm-c1016 Glycine max cDNA clone 170 4e-51 embjAW03001 AB99061 EST248400 tomato ovary, TAMU Lycopersicon 160 4e-52 embjAW03001 AB99061 EST248400 tomato o		
emb A1488673 A1488673 EST247012 tomato ovary, TAMU Lycopersicon 160 1e-56 emb AW0164307 AW164307 sc70g05.y1 Gm-e1023 Glycine max cDNA clone 174 1e-56 emb AW040320 AW040320 EST2813184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW020379 AW023679 EST281698 tomato callus, TAMU Lycopersicon 160 2e-56 emb AW22039963 AW223963 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW22039963 AW223963 EST300774 tomato fruit red ripe, TAMU Lyco 177 3e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW7373637 AW736779 EST3259010 tomato germinating seedlings, TA 160 3e-55 emb AH733941 A1773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AH733941 A1773941 EST255041 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW733637 AW733637 sk83005.y1 Gm-e1016 Glycine max cDNA clone 121 3e-54 emb AW733637 AW733637 sk83005.y1 Gm-e1016 Glycine max cDNA clone 167 3e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW100389 AW100389 g42708,92 Gm-e1012 Glycine max cDNA clone 167 4e-54 emb AW03019 AW03019 EST278489 fornato ovary, TAMU Lycopersicon 160 4e-52 emb AH89916 A1899016 EST268459 fornato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW7933 A187093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW79384 A8793 EST252599 fornato ovary, TAMU Lycopersicon 160 4e-52 emb AW79384 A8793 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW7039384 A87093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW7039384 A87093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW703963 A187093 EST24501 Comato ovary, TAMU Lycopersicon 160 4e-52 emb AW703963 A87664 WS1 _1 H04.b1 A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW703963 AW703985 sk2		emb AW032396 AW032396 EST275935 tomato callus, TAMU Lycopersicon 174 4e-57
emb AW16307 AW164307 se70g05.y1 Gm-e1023 Glycine max cDNA clone 174 1e-56 emb AW040320 AW040320 EST28184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW0303679 AW035679 EST281698 tomato callus, TAMU Lycopersicon 160 2e-56 emb AW0220879 AW0220879 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW0220879 AW0220879 EST300774 tomato fruit mature green, TAMU 167 2e-56 emb AW0223963 AW0229863 EST3200710 tomato fruit mature green, TAMU 167 2e-56 emb AW736779 AW776779 EST35844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW767579 AW776779 EST35844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW73637144773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AH783941 AH773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AW360319 AW736373 483800.5y Gm-c1016 Glycine max cDNA clone 133 8-54 emb AW3363714W7363071 8ET2732727 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW030017 BW736371,848758 EST247097 tomato ovary, TAMU Lycopersicon 167 4e-54 emb AW030017 BW736371,848758 EST273648 tomato callus, TAMU Lycopersicon 167 6e-54 emb AW03019 AW030017 EST278459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW39016 AH899016 EST28459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW03019 AW031914 EST286459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW03194 AW031914 EST286459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH9035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AH87035194 AW035194 EST286456 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH870351448703 EST25959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH870351448703 EST25959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH870351448703 EST2545415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH703644144678664 WS1 1, H04-b1, A002 Water-stressed I (WS1) S 120 3e-51 emb AH870354144678664 WS1 1, H04-b1, A002 Water-stressed I (WS1) S 120 3e-51 emb AH70304144678664 WS1 1, H04-b1, A002 Water-stressed I (WS1) S 120 3e-51 emb AH8703541447	10	emb AI896441 AI896441 EST265872 tomato callus, TAMU Lycopersicon 174 4e-57
emb AW16307 AW164307 se70g05.y1 Gm-e1023 Glycine max cDNA clone 174 1e-56 emb AW040320 AW040320 EST28184 tomato mixed elicitor, BTI Lycop 174 1e-56 emb AW0303679 AW035679 EST281698 tomato callus, TAMU Lycopersicon 160 2e-56 emb AW0220879 AW0220879 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW0220879 AW0220879 EST300774 tomato fruit mature green, TAMU 167 2e-56 emb AW0223963 AW0229863 EST3200710 tomato fruit mature green, TAMU 167 2e-56 emb AW736779 AW776779 EST35844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW767579 AW776779 EST35844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW73637144773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AH783941 AH773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AW360319 AW736373 483800.5y Gm-c1016 Glycine max cDNA clone 133 8-54 emb AW3363714W7363071 8ET2732727 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW030017 BW736371,848758 EST247097 tomato ovary, TAMU Lycopersicon 167 4e-54 emb AW030017 BW736371,848758 EST273648 tomato callus, TAMU Lycopersicon 167 6e-54 emb AW03019 AW030017 EST278459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW39016 AH899016 EST28459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW03019 AW031914 EST286459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW03194 AW031914 EST286459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH9035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AH87035194 AW035194 EST286456 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH870351448703 EST25959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH870351448703 EST25959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH870351448703 EST2545415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH703644144678664 WS1 1, H04-b1, A002 Water-stressed I (WS1) S 120 3e-51 emb AH870354144678664 WS1 1, H04-b1, A002 Water-stressed I (WS1) S 120 3e-51 emb AH70304144678664 WS1 1, H04-b1, A002 Water-stressed I (WS1) S 120 3e-51 emb AH8703541447		emb AI488673 AI488673 EST247012 tomato ovary, TAMU Lycopersicon 160 1e-56
emb AW04320 AW040320 EST283188 tomato mixed elicitor, BTI Lycop		
emb AW035679 AW035679 EST281698 tomato callus, TAMU Lycopersicon 160 2e-56 emb AW220879 AW220879 EST297348 tomato fruit mature green, TAMU 167 2e-56 emb AW720879 AW223963 EST300774 tomato fruit red ripe, TAMU Lyco 177 3e-56 emb AW776779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW730673 AW6505556 EST239010 tomato germinating seedlings, TA 160 3e-55 emb AI773941 AI773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AI773941 AI773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb AI488413 AI488413 EST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW33037 AW733037 sk83005,y1 Gm-c1016 Glycine max cDNA clone 213 3e-54 emb AW33031/AW0330017 EST2737272 tomato callus, TAMU Lycopersicon 167 3e-54 emb AW030017 AW0300017 EST2737272 tomato callus, TAMU Lycopersicon 167 4e-54 emb AW030017 AW0300017 EST2737272 tomato callus, TAMU Lycopersicon 167 4e-54 emb AW03019 AW030017 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI899016 AI899016 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW03019 AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW030194 AW0303194 EST228059 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW030194 AW030194 EST2845415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI89709384 AW099384 S4590 SST2645415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW678664 AWG78664 WS1H04.bl_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW09384 AW099384 AW09385] tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW09384 AW099384 AW039385] tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb c5511, gb d2324 and gb c20569 come from this g		emblAW040320IAW040320 EST283184 tomato mixed elicitor, BTI Lycop 174 1e-56
15 emb AW220879 AW220879 EST297348 tomato fruit mature green, TAMU		
emb AW223963 AW223963 EST300774 tomato fruit red ripe, TAMU Lyco 177 3e-56 emb AW716779 AW776779 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW650556 AW650556 EST329010 tomato germinating seedlings, TA 160 3e-55 emb A1773941 A1773941 EST255041 tomato resistant, Cornell Lycopersicon 150 3e-54 emb AW733637 AW733637 sk83b05.y1 Gm-c1016 Glycine max cDNA clone 213 3e-54 emb AW733637 AW733637 sk83b05.y1 Gm-c1016 Glycine max cDNA clone 167 3e-54 emb AW6303017 AW030017 EST273272 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 163 1e-52 emb A1899016 EST268459 tomato callus, TAMU Lycopersicon 163 1e-52 emb AW032194 AW032194 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03194 AW032194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03194 AW032194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03194 AW033194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03194 AW033194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03194 AW033194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03391A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW678664 AW678664 WS1 1 H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39703.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW099384 AW099384 sd39703.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW09385 AW03985 sk26b05.yl Gm-c1028 Glycine max cDNA clone 137 4e-51 emb AW0826380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW0626380 AW626380 EST320287 tomato radicle, 6 d post-imbibit 122 5e-43 emb AW089503 AW	15	
emb AW776779 AW77679 EST335844 DSIL Medicago truncatula cDNA cl 219 4e-56 emb AW650556 AW650556 EST329010 tomato germinating seedlings, TA 160 3e-55 emb A1773941 A1773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb A17484813 A1484813 EST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb A1488758 A1488758 EST247097 tomato ovary, TAMU Lycopersicon 167 3e-54 emb A1488758 A1488758 EST247097 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW100389 AW100389 sd27a08, y2 Gm-c1012 Glycine max cDNA clone 116 7e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 167 4e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 168 4e-52 emb A1899016 A1899016 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A189742 A1897442 EST266885 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb A197257 A1897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A171859 B1771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A14870031 A1487093 EST284400 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1490061 B1490061 EST284400 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW039384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW099384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb a36966, gb c55511, gb 42324 and gb 20569 come from this gene. (arabidopsis thaliana)" /blast_score 0 // re_number /family /cbip nova /gb_link http://www.negr.org/egi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
emb AW650556 AW650556 EST329010 tomato germinating seedlings, TA 160 3e-55 emb A1773941 A1773941 EST255041 tomato resistant, Cornell Lycope 215 4e-55 emb A1484813 A1484813 EST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW33637 AW733637 sk83b05.yl Gm-c1016 Glycine max cDNA clone 213 3e-54 emb AW130389 AW100389 sd27a08.y2 Gm-c1012 Glycine max cDNA clone 167 3e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 emb AW39016 A1899016 EST268459 tomato ovary, TAMU Lycopersicon 161 3e-52 emb A1899016 A1899016 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST266885 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb A1897257 A1897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1897257 A1897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW678664 AW678664 WS1 1, H04.b1, A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW678664 AW678664 WS1 1, H04.b1, A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW678664 AW678664 WS1 1, H04.b1, A002 Water-stressed 1 (WS1) S 120 3e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb p65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
emb A1773941 A1773941 EST255041 tomato resistant, Cornell Lycopes		
emb Al484813 Al484813 EST243074 tomato ovary, TAMU Lycopersicon 150 2e-54 emb AW733637 AW733637 sk83b05.yl Gm-c1016 Glycine max cDNA clone 213 3e-54 emb AW873814488758 EST247097 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW100389 AW100389 sd27a08.y2 Gm-c1012 Glycine max cDNA clone 169 4e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 gb BE02007 BE020071 sm3807.yl Gm-c1028 Glycine max cDNA clone 171 2e-53 emb A1899016 A1899016 EST268459 tomato ovary, TAMU Lycopersicon 163 1e-52 emb A1899442 A1897442 EST2566485 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW03194 AW03194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW03194 AW03194 EST256648 tomato callus, TAMU Lycopersicon 160 4e-52 emb A1971859 A1771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1971859 A1771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A149061 A1490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1 _1 H04.bl _A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id source genbank /description 40 "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb r42324 and gb r20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /cc_number /family /cbip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query/db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
emb AW733637 AW733637 sk83b05.yl Gm-c1016 Glycine max cDNA clone 213 3e-54 emb AH88758 A1488758 EST247097 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW100389 AW100389 sd27a68.y2 Gm-c1012 Glycine max cDNA clone 169 4e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 gb BE020071 BE020071 sm38f07.yl Gm-c1028 Glycine max cDNA clone 171 2e-53 emb A1899016 EST2764859 tomato ovary, TAMU Lycopersicon 163 1e-52 emb A189916 A1899016 EST275648 tomato callus, TAMU Lycopersicon 163 1e-52 emb AW033194 AW035194 EST275648 tomato callus, TAMU Lycopersicon 163 0e-52 emb AW033194 AW035194 EST275648 tomato callus, TAMU Lycopersicon 160 0e-52 emb AW033194 AW035194 EST275648 tomato callus, TAMU Lycopersicon 160 0e-52 emb AW037194 AW035194 EST275648 tomato callus, TAMU Lycopersicon 160 0e-52 emb AW037194 AW035194 EST275648 tomato ovary, TAMU Lycopersicon 160 0e-52 emb AH87035 A1487093 EST252959 tomato ovary, TAMU Lycopersicon 160 0e-52 emb A1487093 A1487093 EST2545415 tomato ovary, TAMU Lycopersicon 160 0e-52 emb A1490061 A1490061 EST248400 tomato ovary, TAMU Lycopersicon 160 0e-52 emb AW678664 AW678664 WS1_1 H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW99384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW99384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW626380 AW626380 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description "gb aco72125.1 (ac005278) ests gb h36966, gb r65511, gb r42324 and gb r20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching	20	
emb Al488758 Al488758 EST247097 tomato ovary, TAMU Lycopersicon 167 3e-54 emb AW100389 AW100389 sd27a08.y2 Gm-c1012 Glycine max cDNA clone 169 4e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 gb BE020071 BE020071 sm38f07.y1 Gm-c1028 Glycine max cDNA clone 167 1e-53 emb Al899016 Al899016 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST266845 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW035194 AW035194 EST256456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW035194 AW035194 EST256456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW78759 AI771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH897257 Al897257 EST256959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AH87093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW678664 AW678664 WSI_1 H04.b1 A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW09384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW09384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW09384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb h65511, gb d2324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /cc_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbim- post/entrez/query/db-n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching	20	
emb AW100389 AW100389 sd27a08.y2 Gm-c1012 Glycine max cDNA clone 169 4e-54 emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 gb BE020071 BE020071 sm3807.y1 Gm-c1028 Glycine max cDNA clone 171 2e-53 emb AI899016 AI899016 EST268459 tomato ovary, TAMU Lycopersicon 163 1e-52 emb AI897442 AI897442 EST2766885 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI490061 AI490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW099384AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 emb AW099384AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 emb AW099384AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 160 5e-50 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 emb AI898263 AI898263 EST26706 tomato ovary, TAMU Lycopersicon 160 5e-50 emb AI898263 AI898263 EST26705 emb AI898263 AI898263 AI898263 EST26718 emb AI898263 AI89826		
emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 176 7e-54 gb BE020071 BE020071 sm38f07.y1 Gm-c1028 Glycine max cDNA clone 171 2e-53 emb A1899016 [A1899016 EST268459 tomato ovary, TAMU Lycopersicon 163 1e-52 emb A1897442 A1897442 EST266885 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb A1897257 A1897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1877359 A1771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1490061 A1490061 EST248400 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1490061 A1490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WSI_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22_at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb r42324 and gb r20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www.ncgir.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
gb BE020071 BE020071 sm38f07.yl Gm-c1028 Glycine max cDNA clone 171 2e-53 emb A1899016 A1899016 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1897442 A1897442 EST266885 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb A1897257 A1897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1791859 A1771859 EST252595 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW09364 AW678664 WS1 _1 H04.bl _A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description		
emb A1899016 A1899016 EST268459 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1897442 A1897442 EST266885 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW032194 AW033194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW71859 A1771859 EST2525959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1731859 A1771859 EST2525959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1490061 A1490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03_y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AW099384 AW099384 sd39f03_y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22_at 18625_at/id_source genbank/description Query= AC005278.22_at 18625_at/id_source genbank/description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching	0.5	
emb Al897442 Al897442 EST266885 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW032194 AW033194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb Al897257 Al897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb Al7971859 A1771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb Al487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb Al487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AW678664 AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03,yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb Al898263 Al898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625_at /id_source genbank /description Query= AC005278.22 at 18625_at /id_source genbank /description Query= AC005278.22 at 18625_at /id_source genbank /description gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb 20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /cc_number /family /chip nova /gb_link http://www.ncbr.org/cgb-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching	25	
emb AW032194 AW032194 EST275648 tomato callus, TAMU Lycopersicon 160 4e-52 emb AW035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI771859 AI771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI490061 AI490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39703.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		emb AI899016 AI899016 EST268459 tomato ovary, TAMU Lycopersicon 163 1e-52
emb AW035194 AW035194 EST280456 tomato callus, TAMU Lycopersicon 160 4e-52 emb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI771859 AI771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI490061 AI490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1 1 H04.b1 A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova/gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching	-	
amb AI897257 AI897257 EST266616 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI771859 AI771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW699384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22_at 18625_at /id_source genbank /description Query= AC005278.22_at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb z20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
emb A1771859 A1771859 EST252959 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1490061 A14909384 A149093384		
emb A1487093 A1487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52 emb A1490061 A1490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1 _ HO4.bl _ A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39ft3.yl Gm-c1016 Glycine max cDNA clone 137 4e-51 emb A1898263 A1898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22_ at 18625_ at /id_ source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb r42324 and gb r20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching	30	
emb AI490061 AI490061 EST248400 tomato ovary, TAMU Lycopersicon 160 8e-52 emb AW678664 AW678664 WS1 1 H04.b1 A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ecc_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/ntbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
emb AW678664 AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51 emb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22_at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /cc_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal		emb AI487093 AI487093 EST245415 tomato ovary, TAMU Lycopersicon 160 4e-52
### cmb AW099384 AW099384 sd39f03.y1 Gm-c1016 Glycine max cDNA clone 137 4e-51 emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22 at 18625 at /id_source genbank /description		
emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50 Query= AC005278.22_at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /cc_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searchingdone Score E Sequences producing significant alignments: (bits) Value emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.y1 Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		emb AW678664 AW678664 WS1_1_H04.b1_A002 Water-stressed 1 (WS1) S 120 3e-51
Query= AC005278.22_at 18625_at /id_source genbank /description "gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278	35	emb AW099384 AW099384 sd39f03.yl Gm-c1016 Glycine max cDNA clone 137 4e-51
"gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		emb AI898263 AI898263 EST267706 tomato ovary, TAMU Lycopersicon 160 5e-50
"gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
"gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and gb t20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278 (1716 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching		
gb 20569 come from this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278		Query= AC005278.22_at 18625_at /id_source genbank /description
/ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278	40	"gb aac72125.1 (ac005278) ests gb h36966, gb r65511, gb t42324 and
/ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278		gb t20569 come from this gene. [arabidopsis thaliana]" /blast score 0
http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278		
post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005278 /ncgi http://www.ncgr.org/cgi-bin/ff?ac005278		
45 http://www.ncgr.org/cgi-bin/ff?ac005278	•	
Database: plantfungal 661,018 sequences; 426,114,510 total letters	45	
Database: plantfungal 661,018 sequences; 426,114,510 total letters 50 Searchingdone Score E Sequences producing significant alignments: (bits) Value 55 emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.yl Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		
661,018 sequences; 426,114,510 total letters Searching		(1.10 101010)
661,018 sequences; 426,114,510 total letters Searching		Database: plantfilmoal
Score E Sequences producing significant alignments: (bits) Value 55 emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.y1 Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		
Score E	50	001,010 30quencos, 420,114,310 total fottols
Score E Sequences producing significant alignments: (bits) Value 55 emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.y1 Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16	50	Searching done
Sequences producing significant alignments: (bits) Value 55 emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.y1 Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16	•	bomoningdone
Sequences producing significant alignments: (bits) Value 55 emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.y1 Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		Coom F
60 emb AV605003 AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		=
emb AI780241 AI780241 EST261120 tomato susceptible, Cornell Lyco 156 2e-49 emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.y1 Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16	55	Sequences producing significant angiments. (bits) value
emb AW626380 AW626380 EST320287 tomato radicle, 5 d post-imbibit 122 5e-43 emb AW703985 AW703985 sk26b05.yl Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16	55	amble 179004114 1790041 E0T361100 sameta massarilla Camall I ann 156 0-40
emb AW703985 AW703985 sk26b05.yl Gm-c1028 Glycine max cDNA clone 132 6e-30 emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		embla Wich Carolina Discourse of the formation of the state of the sta
emb AW289599 AW289599 NXNV002D08F Nsf Xylem Normal wood Vertical 115 1e-24 60 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		
60 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago 88 2e-16		
i i i i i i i i i i i i i i i i i i i	60	
children of 3013 fa w 063013 in rus 2012 in Rifficult Nothlated root Medicago t 88 2e-16	UU	
		emupa w oood 15 pa w oood 15 parus 2C12 pak 1 r 1000 podulated root Medicago t 88 2e-16

	emb AW736154 AW736154 EST332140 KV3 Medicago truncatula cDNA clo 88 2e-16 emb AW736412 AW736412 EST332426 KV3 Medicago truncatula cDNA clo 88 2e-16 emb AW929060 AW929060 EST337764 tomato flower buds 8 mm to pre-a 76 9e-13
5	gb C95256 C95256 C95256 Citrus unshiu Miyagawa-wase maturation s 59 1e-07 emb AW981624 AW981624 PC14G07 Pine TriplEx pollen cone library P 58 2e-07
	emb Z72807 SCYGR022C S.cerevisiae chromosome VII reading frame O 29 1.3
	emb AW726115 AW726115 GA_Ea0020L02 Gossypium arboreum 7-10 dpa 35 1.7
	emb AW690315 AW690315 NF029D02ST1F1000 Developing stem Medicago 34 3.1
10	emb AQ852328 AQ852328 LMAJFV1 lm68c02.yl Leishmania major FV1 ra 34 3.1
10	emb AW695266 AW695266 NF092H10ST1F1091 Developing stem Medicago 34 3.1 emb AW691641 AW691641 NF047D12ST1F1000 Developing stem Medicago 34 3.1
	emb AE001413 AE001413 Plasmodium falciparum chromosome 2, sectio 34 3.1
	emb AL136326 LMFL377 Leishmania major Friedlin chromosome 23 cos 34 3.1
1.5	emb AW683188 AW683188 NF008F07LF1F1062 Developing leaf Medicago 34 3.1
15	emb AJ001925 PAAJ1925 Picea abies cad7 gene. 33 4.3
	emb AV395482 AV395482 AV395482 Chlamydomonas reinhardtii C9 Chla 33 4.3 emb AW981387 AW981387 EST392540 DSIL Medicago truncatula cDNA cl 33 5.6
	emb AW759380 AW759380 sl41f02.yl Gm-c1027 Glycine max cDNA clone 33 5.9
	emb AQ641451 AQ641451 RPCI93-EcoRI-4117.TV RPCI93-EcoRI Trypanos 33 5.9
20	emb AC006281 AC006281 Plasmodium falciparum chromosome 12 clone 33 7.7
•	gb C96380 C96380 C96380 Marchantia polymorpha immature sex organ 33 7.7 emb AW735863 AW735863 EST336631 tomato flower buds 0-3 mm, Corne 32 8.1
	emb AW184933 AW184933 se83h06.y1 Gm-c1023 Glycine max cDNA clone 32 8.1
	emb AW030335 AW030335 EST273590 tomato callus, TAMU Lycopersicon 32 8.1
25	emb AW221805 AW221805 EST298616 tomato fruit red ripe, TAMU Lyco 32 8.1
	gb U33007 SCD9461 Saccharomyces cerevisiae chromosome IV lambda 32 8.1 emb AW311676 AW311676 NXNV055A06F Nsf Xylem Normal wood Vertical 32 8.1
	emb Al895127 Al895127 EST264570 tomato callus, TAMU Lycopersicon 32 8.1
	gb S69101 S69101 HKR1=Hansenula mrakii killer toxin-resistant ge 32 8.1
30	
	Query= AF055848.2 i at 18908 i at /id source genbank /description
	gb aac62611.1 (af055848) subtilisin-like protease [arabidopsis
	thaliana] /blast_score 0 /ec_number /family protease /chip nova
35	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb af055848 /ncgi http://www.ncgr.org/cgi-bin/ff?af055848
	(2403 letters)
40	Detahana alamtimasi
70	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
45	Score E
	Sequences producing significant alignments: (bits) Value
	114 TOO COPOLY TO COPO Y
	emb AJ006378 LES6378 Lycopersicon esculentum sbt1 gene. 240 e-157 emb X98929 LESBT1 L.esculentum mRNA for serine protease, SBT1. 240 e-157
50	emb X98929 LESBT1 L.esculentum mRNA for serine protease, SBT1. 240 e-157 emb Y18932 LES18932 Lycopersicon esculentum p69F gene. 142 e-152
	emb Y17278 LES17278 Lycopersicon esculentum p69d gene, complete 141 e-146
	emb AJ005173 LEAJ5173 Lycopersicon esculentum p69f gene, complet 141 e-146
	emb AJ005172 LEAJ5172 Lycopersicon esculentum p69e gene, complet 142 e-146
55	emb Y18931 LES18931 Lycopersicon esculentum p69E gene. 144 e-144 emb AJ006379 LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
,,,	emb AJ006379 LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142 emb X98930 LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
	emb AJ006786 LES6786 Lycopersicon esculentum p69d gene. 141 e-136
	emb AJ005171 LEAJ517 Lycopersicon esculentum p69c gene, complete 142 e-136
50	emb Y17276 LES17276 Lycopersicon esculentum p69b gene, complete 138 e-130
50	emb Y10149 LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130 emb Y17275 LES17275 Lycopersicon esculentum p69a gene complete 138 e-126

WO 02/22675 ____ PCT/US01/28506

emb|X95270|LESUBENDO L.esculentum mRNA for subtilisin-like endop... 138 e-126 dbi|D32206|CUSSP Melon mRNA for cucumisin (serine protease), com... 92 e-120 emb|Y17277|LES17277 Lycopersicon esculentum p69c gene, complete ... 148 2e-97 emb|AI960990|AI960990 sc93f09.yl Gm-c1019 Glycine max cDNA clone... 338 9e-92 5 emb|AW218382|AW218382 EST303565 tomato radicle, 5 d post-imbibit... 322 6e-87 dbilD86598|D86598 Norway spruce mRNA for antifreeze-like protein... 135 6e-77 emb|X85975|AGAG12 A.glutinosa mRNA for subtilisin-like protein. gb|BE124129|BE124129 EST394254 DSIL Medicago truncatula cDNA clo... 263 5e-69 emb|AJ006380|LES6380 Lycopersicon esculentum sbt3 gene. 102 3e-68 10 emb|AJ006376|LES6376 Lycopersicon esculentum mRNA for serine pro... 102 3e-68 emb|AJ006480|LES6480 Lycopersicon esculentum sbt4b gene. 146 2e-66 emb|AJ006481|LES6481 Lycopersicon esculentum sbt4c gene. 138 2e-66 emb|AW267784|AW267784 EST305912 DSIR Medicago truncatula cDNA cl... 128 3e-65 emb|AJ006483|LES6483 Lycopersicon esculentum sbt4e gene. 140 5e-65 15 emb|AJ006377|LES6377 Lycopersicon esculentum mRNA for serine pro... 138 5e-65 emb|AW459354|AW459354 sh41a03.y1 Gm-c1017 Glycine max cDNA clone... 192 6e-64 emb|AW349252|AW349252 GM210004B21G12R Gm-r1021 Glycine max cDNA ... 144 1e-63 emb|AJ276710|GMA276710 Glycine max mRNA for putative subtilisin ... 124 8e-63 20 emb|AJ012164|CGL012164 Casuarina glauca mRNA for cg12 gene fragm... 114 4e-62 emb|AI730592|AI730592 BNLGHi7352 Six-day Cotton fiber Gossypium ... 216 2e-61 emb|AW728806|AW728806 GA_Ea0028122 Gossypium arboreum 7-10 dpa ... 125 5e-60 emb|AI794673|AI794673 sb67d01.y1 Gm-c1019 Glycine max cDNA clone... 171 1e-59 emb|AW773858|AW773858 EST332844 KV3 Medicago truncatula cDNA clo... 87 2e-58 25 emb|AW695319|AW695319 NF093H12ST1F1103 Developing stem Medicago ... 105 2e-57 emb|AW299160|AW299160 EST305970 KV2 Medicago truncatula cDNA clo... 135 3e-57 emb|AF201883|AF201883 Gossypioides kirkii subtilisin-like protea... 108 7e-57 emb|AW720622|AW720622 LjNEST22e12rc Lotus japonicus nodule libra... 137 2e-56 emb|AW925917|AW925917 HVSMEg0005N16 Hordeum vulgare pre-anthesis... 157 4e-56 30 emb|AW668484|AW668484 GA_Ea0014C06 Gossypium arboreum 7-10 dpa ... 188 4e-56 emb|AF139438|AF139438 Gossypium hirsutum (A-subgenome) locus A17... 106 5e-55 emb|AF139437|AF139437 Gossypium herbaceum locus A1751, sequence ... 106 5e-55 emb|AF139441|AF139441 Gossypium robinsonii locus A1751, sequence... 106 7e-55 emb|AF139440|AF139440 Gossypium hirsutum (D-subgenome) locus A17... 106 7e-55 35 emb|AF139439|AF139439 Gossypium raimondii locus A1751, sequence ... 106 7e-55 emb|AW687885|AW687885 NF014E10RT1F1082 Developing root Medicago ... 91 5e-54 emb|AW563397|AW563397 LG1 214 C02.b1 A002 Light Grown 1 (LG1) So... 210 4e-53 emb|AW257362|AW257362 EST305499 KV2 Medicago truncatula cDNA clo... 138 4e-52 40 emb|AW221342|AW221342 EST297811 tomato fruit mature green, TAMU ... 154 7e-52 emb|AW221343|AW221343 EST297812 tomato fruit mature green, TAMU ... 154 7e-52 emb|AI441432|AI441432 sa59h01.y1 Gm-c1004 Glycine max cDNA clone... 189 1e-51 emb|AW279412|AW279412 sf79c02.y1 Gm-c1019 Glycine max cDNA clone... 204 3e-51 emblAI730369|AI730369 BNLGHi6751 Six-day Cotton fiber Gossypium ... 166 3e-51 45 emb|AW221789|AW221789 EST298600 tomato fruit red ripe, TAMU Lyco... 95 3e-51 emb|AW030462|AW030462 EST273717 tomato callus, TAMU Lycopersicon... 173 4e-51 emb|AQ917453|AQ917453 T233488b Medicago truncatula BAC library M... 134 5e-51 emb|AW559414|AW559414 EST314462 DSIR Medicago truncatula cDNA cl... 152 1e-50 emb|AW697284|AW697284 NF117B12ST1F1096 Developing stem Medicago ... 128 2e-50 50 emb|AQ917126|AQ917126 T233155b Medicago truncatula BAC library M... 148 3e-50 emb|AW780798|AW780798 s176c06.v1 Gm-c1027 Glycine max cDNA clone... 161 1e-49 emb|AW221341|AW221341 EST297810 tomato fruit mature green, TAMU ... 154 2e-49 emb|AI727340|AI727340 BNLGHi7810 Six-day Cotton fiber Gossypium ... 194 2e-48 55 emb[AW704701]AW704701 sk39d09.yl Gm-c1028 Glycine max cDNA clone... 124 2e-47 emb|AW101793|AW101793 sd70e04.yl Gm-c1008 Glycine max cDNA clone... 190 3e-47 emb|AW219463|AW219463 EST301861 tomato root during/after fruit s... 141 8e-47 emb|AW688392|AW688392 NF006H03ST1F1000 Developing stem Medicago ... 78 1e-46 60 gb|BE053648|BE053648 GA_Ea0001B22f Gossypium arboreum 7-10 dpa ... 81 9e-46

emb|AW108783|AW108783 gate0001B22f Gossypium arboreum 7-10 dpa f... 81 5e-45

	emb AI727162 AI727162 BNLGHi7467 Six-day Cotton fiber Gossypium 167 2e-44
	emb AW725183 AW725183 GA_Ea0015F02 Gossypium arboreum 7-10 dpa 158 2e-44
	emb AJ006482 LES6482 Lycopersicon esculentum sbt4d gene. 101 4e-44
_	emb AA660563 AA660563 00449 MtRHE Medicago truncatula cDNA 5' si 138 4e-44
5	emb AW597797 AW597797 sj86c05.yl Gm-c1034 Glycine max cDNA clone 157 2e-43
	emb AW220186 AW220186 EST302669 tomato root during/after fruit s 104 2e-43
	emb AW720560 AW720560 LjNEST10e10rc Lotus japonicus nodule libra 84 4e-43
	emb AI729604 AI729604 BNLGHi13761 Six-day Cotton fiber Gossypium 84 8e-43 emb AF036960 AF036960 Glycine max subtilisin-like protease mRNA, 145 2e-42
10	4 1 1 VT *** 4 4 4 1 1 VT *** 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
10	emb AW774365 AW774365 EST333516 KV3 Medicago truncatula cDNA clo 94 3e-42 emb AW278983 AW278983 sg04b02.yl Gm-c1019 Glycine max cDNA clone 174 3e-42
	emb AW775672 AW775672 EST334737 DSIL Medicago truncatula cDNA cl 135 7e-42
	emb AW441244 AW441244 EST310640 tomato fruit red ripe, TAMU Lyco 95 3e-41
•	emb AW220925 AW220925 EST297394 tomato fruit mature green, TAMU 138 5e-41
15	emb AW278806 AW278806 sf98f09.y1 Gm-c1019 Glycine max cDNA clone 74 8e-41
	emb AI728612 AI728612 BNLGHi11202 Six-day Cotton fiber Gossypium 123 1e-40
-	emb AW234933 AW234933 sf20h03.y1 Gm-c1028 Glycine max cDNA clone 134 2e-40
	gb BE021322 BE021322 sm57b06.yl Gm-c1028 Glycine max cDNA clone 134 2e-40
*	emb AW032762 AW032762 EST276321 tomato callus, TAMU Lycopersicon 167 4e-40
20	emb AW691170 AW691170 NF041H07ST1F1000 Developing stem Medicago 122 5e-40
	emb AW186434 AW186434 se67g06.yl Gm-c1019 Glycine max cDNA clone 122 5e-39
	emb AI778546 AI778546 EST259425 tomato susceptible, Cornell Lyco 133 5e-39
•	emb AI900421 AI900421 sc05e05.yl Gm-c1012 Glycine max cDNA clone 98 5e-39
0.5	emb AW287918 AW287918 N100762e rootphos(-) Medicago truncatula c 93 1e-38
25	emb AW692289 AW692289 NF054B05ST1F1000 Developing stem Medicago 128 2e-38
	emb AW185724 AW185724 se58g11.y1 Gm-c1019 Glycine max cDNA clone 122 2e-38
	Onome AE055949.2 a at 19000 a at //d account of the control of the
30	Query= AF055848.2_s_at 18909_s_at /id_source genbank /description gb aac62611.1 (af055848) subtilisin-like protease [arabidopsis
50	thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
	/ncgi
	(2403 letters)
35	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
40	
40	Score E
	Sequences producing significant alignments: (bits) Value
	emb AJ006378 LES6378 Lycopersicon esculentum sbt1 gene. 240 e-157
	emb[X98929]LESBT1 L.esculentum mRNA for serine protease, SBT1. 240 e-157
45	emb[Y18932]LES18932 Lycopersicon esculentum p69F gene. 142 e-152
-	emb Y17278 LES17278 Lycopersicon esculentum p69d gene, complete 141 e-146
	emb AJ005173 LEAJ5173 Lycopersicon esculentum p69f gene, complet 141 e-146
	emb AJ005172 LEAJ5172 Lycopersicon esculentum p69e gene, complet 142 e-146
	emb Y18931 LES18931 Lycopersicon esculentum p69E gene. 144 e-144
50	emb AJ006379 LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
	emb[X98930]LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
	emb AJ006786 LES6786 Lycopersicon esculentum p69d gene. 141 e-136
	emb AJ005171 LEAJ517 Lycopersicon esculentum p69c gene, complete 142 e-136
	emb[Y17276]LES17276 Lycopersicon esculentum p69b gene, complete 138 e-130
55	emb[Y10149]LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130
	emb[Y17275]LES17275 Lycopersicon esculentum p69a gene, complete 138 e-126
	emb X95270 LESUBENDO L.esculentum mRNA for subtilisin-like endop 138 e-126
	dbj D32206 CUSSP Melon mRNA for cucumisin (serine protease), com 92 e-120
60	emb Y17277 LES17277 Lycopersicon esculentum p69c gene, complete 148 2e-97
60	emb AI960990 AI960990 sc93f09.yl Gm-c1019 Glycine max cDNA clone 338 9e-92
	emb AW218382 AW218382 EST303565 tomato radicle, 5 d post-imbibit 322 6e-87

dbi|D86598|D86598 Norway spruce mRNA for antifreeze-like protein... 135 6e-77 emb[X85975]AGAG12 A.glutinosa mRNA for subtilisin-like protein. 139 1e-73 gb|BE124129|BE124129 EST394254 DSIL Medicago truncatula cDNA clo... 263 5e-69 emb|AJ006380|LES6380 Lycopersicon esculentum sbt3 gene. 102 3e-68 emb|AJ006376|LES6376 Lycopersicon esculentum mRNA for serine pro... 102 3e-68 emb|AJ006480|LES6480 Lycopersicon esculentum sbt4b gene. 146 2e-66 emb|AJ006481|LES6481 Lycopersicon esculentum sbt4c gene. 138 2e-66 emb|AW267784|AW267784 EST305912 DSIR Medicago truncatula cDNA cl... 128 3e-65 emb|AJ006483|LES6483 Lycopersicon esculentum sbt4e gene. 140 5e-65 emblAJ006377|LES6377 Lycopersicon esculentum mRNA for serine pro... 138 5e-65 10 emb|AW459354|AW459354 sh41a03.yl Gm-c1017 Glycine max cDNA clone... 192 6e-64 emb[AW349252]AW349252 GM210004B21G12R Gm-r1021 Glycine max cDNA ... 144 1eemb|AJ276710|GMA276710 Glycine max mRNA for putative subtilisin ... 124 8e-63 15 emb|AJ012164|CGL012164 Casuarina glauca mRNA for cg12 gene fragm... 114 4e-62 emb|AI730592|AI730592 BNLGHi7352 Six-day Cotton fiber Gossypium ... 216 2e-61 emb|AI794673|AI794673 sb67d01.yl Gm-c1019 Glycine max cDNA clone... 171 1e-59 emb|AW773858|AW773858 EST332844 KV3 Medicago truncatula cDNA clo... 87 2e-58 20 emb|AW695319|AW695319 NF093H12ST1F1103 Developing stem Medicago ... 105 2e-57 emb|AW299160|AW299160 EST305970 KV2 Medicago truncatula cDNA clo... 135 3e-57 emb|AF201883|AF201883 Gossypioides kirkii subtilisin-like protea... 108 7e-57 emb|AW720622|AW720622 LjNEST22e12rc Lotus japonicus nodule libra... 137 2e-56 emb|AW925917|AW925917 HVSMEg0005N16 Hordeum vulgare pre-anthesis... 157 4e-56 25 emb|AW668484|AW668484 GA__Ea0014C06 Gossypium arboreum 7-10 dpa ... 188 4e-56 emb|AF139438|AF139438 Gossypium hirsutum (A-subgenome) locus A17... 106 5e-55 emb|AF139437|AF139437 Gossypium herbaceum locus A1751, sequence ... 106 5e-55 emb|AF139441|AF139441 Gossypium robinsonii locus A1751, sequence... 106 7e-55 emb|AF139440|AF139440 Gossypium hirsutum (D-subgenome) locus A17... 106 7e-55 30 emb|AF139439|AF139439 Gossypium raimondii locus A1751, sequence ... 106 7e-55 emb|AW687885|AW687885 NF014E10RT1F1082 Developing root Medicago ... 91 5e-54 emb|AW563397|AW563397 LG1_214 C02.b1_A002 Light Grown 1 (LG1) So... 210 4e-53 emb|AW257362|AW257362 EST305499 KV2 Medicago truncatula cDNA clo... 138 4e-52 35 emb|AW221342|AW221342 EST297811 tomato fruit mature green, TAMU ... 154 7e-52 emb|AW221343|AW221343 EST297812 tomato fruit mature green, TAMU ... 154 7e-52 emb|AI441432|AI441432 sa59h01.y1 Gm-c1004 Glycine max cDNA clone... 189 1e-51 emb[AW279412]AW279412 sf79c02.yl Gm-c1019 Glycine max cDNA clone... 204 3e-51 emb|AI730369|AI730369 BNLGHi6751 Six-day Cotton fiber Gossypium ... 166 3e-51 40 emb|AW221789|AW221789 EST298600 tomato fruit red ripe, TAMU Lyco... 95 3e-51 emb|AW030462|AW030462 EST273717 tomato callus, TAMU Lycopersicon... 173 4e-51 emb|AQ917453|AQ917453 T233488b Medicago truncatula BAC library M... 134 5e-51 emb|AW559414|AW559414 EST314462 DSIR Medicago truncatula cDNA cl... 152 1e-50 emb|AW697284|AW697284 NF117B12ST1F1096 Developing stem Medicago ... 128 2e-50 45 emb|AW666485|AW666485 GA_ Ea0005E24 Gossypium arboreum 7-10 dpa ... 137 3e-50 emb|AQ917126|AQ917126 T233155b Medicago truncatula BAC library M... 148 3e-50 emb|AW780798|AW780798 s176c06.y1 Gm-c1027 Glycine max cDNA clone... 161 1e-49 emb|AW221341|AW221341 EST297810 tomato fruit mature green, TAMU ... 154 2e-49 emblAI727340|AI727340 BNLGHi7810 Six-day Cotton fiber Gossypium ... 194 2e-48 50 emb|AW704701|AW704701 sk39d09.y1 Gm-c1028 Glycine max cDNA clone... 124 2e-47 emb|AW101793|AW101793 sd70e04.y1 Gm-c1008 Glycine max cDNA clone... 190 3e-47 emb|AW730930|AW730930 GA_Ea0029M05 Gossypium arboreum 7-10 dpa ... 122 6e-47 emb|AW219463|AW219463 EST301861 tomato root during/after fruit s... 141 8e-47 emb|AW688392|AW688392 NF006H03ST1F1000 Developing stem Medicago ... 78 1e-46 gb|BE053648|BE053648 GA_Ea0001B22f Gossypium arboreum 7-10 dpa ... 81 9e-46 55 emblAW108783|AW108783 gate0001B22f Gossypium arboreum 7-10 dpa f... 81 5e-45 emb|AI727162|AI727162 BNLGHi7467 Six-day Cotton fiber Gossypium ... 167 2e-44 emb|AW725183|AW725183 GA_ Ea0015F02 Gossypium arboreum 7-10 dpa ... 158 2e-44 emb|AJ006482|LES6482 Lycopersicon esculentum sbt4d gene. 60 emb|AA660563|AA660563 00449 MtRHE Medicago truncatula cDNA 5' si... 138 4e-44 emb|AW597797|AW597797 sj86c05.yl Gm-c1034 Glycine max cDNA clone... 157 2e-43

.....WO 02/22675 PCT/US01/28506

emb|AW220186|AW220186 EST302669 tomato root during/after fruit s... 104 2e-43 emb|AW720560|AW720560 LjNEST10e10rc Lotus japonicus nodule libra... 84 4e-43 emblAI729604|AI729604 BNLGHi13761 Six-day Cotton fiber Gossypium... 84 8e-43 emblAF036960|AF036960 Glycine max subtilisin-like protease mRNA,... 145 2e-42 emb|AW774365|AW774365 EST333516 KV3 Medicago truncatula cDNA clo... 94 3e-42 emb|AW278983|AW278983 sg04b02.y1 Gm-c1019 Glycine max cDNA clone... 174 3e-42 emb|AW775672|AW775672 EST334737 DSIL Medicago truncatula cDNA cl... 135 7e-42 emb|AW441244|AW441244 EST310640 tomato fruit red ripe, TAMU Lyco... 95 3e-41 emb|AW220925|AW220925 EST297394 tomato fruit mature green, TAMU ... 138 5e-41 10 emb|AW278806|AW278806 sf98f09.yl Gm-c1019 Glycine max cDNA clone... 74 8e-41 emb|AI728612|AI728612 BNLGHi11202 Six-day Cotton fiber Gossypium... 123 1e-40 emb|AW234933|AW234933 sf20h03.yl Gm-c1028 Glycine max cDNA clone... 134 2e-40 gb|BE021322|BE021322 sm57b06.y1 Gm-c1028 Glycine max cDNA clone ... 134 2e-40 emb|AW032762|AW032762 EST276321 tomato callus, TAMU Lycopersicon... 167 4e-40 15 emb|AW691170|AW691170 NF041H07ST1F1000 Developing stem Medicago ... 122 5e-40 emb|AW186434|AW186434 se67g06.y1 Gm-c1019 Glycine max cDNA clone... 122 5e-39 emb|AI778546|AI778546 EST259425 tomato susceptible, Cornell Lyco... 133 5e-39 emb|AI900421|AI900421 sc05e05.y1 Gm-c1012 Glycine max cDNA clone... 98 5e-39 emb|AW287918|AW287918 N100762e rootphos(-) Medicago truncatula c... 93 1e-38 20 emb|AW692289|AW692289 NF054B05ST1F1000 Developing stem Medicago ... 128 2e-38 emb|AW185724|AW185724 se58g11.yl Gm-c1019 Glycine max cDNA clone... 122 2e-38

Query= AC002338.11_at 18920_at /id_source genbank /description gb|aac16927.1| (ac002338) putative laccase [arabidopsis thaliana] /blast_score 0 /ec_number /family oxidase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002338| /ncgi http://www.ncgr.org/cgi-bin/ff?ac002338

(2002 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

35 Searching.....done

Score E

Sequences producing significant alignments:

(bits) Value

40 emb|Y13772|PTY13772 Populus trichocarpa mRNA for laccase, lac90 ... 314 0.0 gb U73106 LTU73106 Liriodendron tulipifera high-pl laccase (LAC2... 356 e-179 gb|U73105|LTU73105 Liriodendron tulipifera high-pI laccase (LAC2... 355 e-178 gb|U45243|NTU45243 Nicotiana tabacum diphenol oxidase mRNA, part... 232 e-124 emb[Y13769]PTY13769 Populus trichocarpa mRNA for laccase, lacl g... 237 e-121 45 emb|AW774748|AW774748 EST333899 KV3 Medicago truncatula cDNA clo... 419 e-116 gb|BE033690|BE033690 MF07A08 MF Mesembryanthemum crystallinum cD... 408 e-113 gb|U43542|NTU43542 Nicotiana tabacum diphenol oxidase mRNA, comp... 379 e-104 gb|U73103|LTU73103 Liriodendron tulipifera high-pI laccase (LAC2... 363 e-103 gb|U12757|APU12757 Acer pseudoplatanus laccase mRNA, complete cds. 368 e-100 50 gb|U73104|LTU73104 Liriodendron tulipifera high-pI laccase (LAC2... 353 3e-99 emb[Y13773]PTY13773 Populus trichocarpa mRNA for laccase, lac110... 355 4e-99 emb|AW688902|AW688902 NF013A07ST1F1000 Developing stem Medicago ... 360 2e-98 gb|BE033689|BE033689 MF07A07 MF Mesembryanthemum crystallinum cD... 349 4e-95 emb|AW559612|AW559612 EST314660 DSIR Medicago truncatula cDNA cl... 328 2e-93 emb[Y13771]PTY13771 Populus trichocarpa mRNA for laccase, lac3 g... 257 1e-88 emb|AW696424|AW696424 NF103G08ST1F1067 Developing stem Medicago ... 323 3e-87 emb|AW649943|AW649943 EST328397 tomato germinating seedlings, TA... 268 9e-84 emb|AW706547|AW706547 sj57h07.yl Gm-c1033 Glycine max cDNA clone... 297 1e-79 emb|AW693679|AW693679 NF067A06ST1F1040 Developing stem Medicago ... 279 1e-75

emb|AW696234|AW696234 NF104B07ST1F1060 Developing stem Medicago ... 258 4e-75 emb|AV406815|AV406815 AV406815 Lotus japonicus young plants (two... 270 3e-71

```
emb[Y13770]PTY13770 Populus trichocarpa mRNA for laccase, lac2 g... 256 3e-70
       emb|AI896093|AI896093 EST265536 tomato callus, TAMU Lycopersicon... 238 9e-70
       emblAW056468|AW056468 ST52C01 Pine TriplEx shoot tip library Pin... 261 2e-68
       emb|AW689490|AW689490 NF019H02ST1F1000 Developing stem Medicago ... 248 1e-64
       emb|AW625159|AW625159 EST319066 tomato radicle, 5 d post-imbibit... 247 3e-64
       emb|AW625489|AW625489 EST319396 tomato radicle, 5 d post-imbibit... 245 1e-63
       emb|AW691876|AW691876 NF045B04ST1F1000 Developing stem Medicago ... 243 4e-63
      emb|AW693746|AW693746 NF068F07ST1F1062 Developing stem Medicago ... 243 4e-63
      emb|AW869960|AW869960 NXNV_120_D07_F Nsf Xylem Normal wood Verti... 158 1e-62
10
      emb|AI166538|AI166538 xylem.est.360 Poplar xylem Lambda ZAPII li... 240 2e-62
      emb|AW688017|AW688017 NF003D03ST1F1000 Developing stem Medicago ... 231 1e-59
      emb|AI166411|AI166411 xylem.est.246 Poplar xylem Lambda ZAPII li... 227 2e-58
      emb|AW290117|AW290117 NXNV010D09F Nsf Xylem Normal wood Vertical... 226 5e-58
      emb|AW693528|AW693528 NF067B10ST1F1080 Developing stem Medicago ... 223 4e-57
15
      emb|AW869847|AW869847 NXNV_122_B11_F Nsf Xylem Normal wood Verti... 223 4e-57 emb|AW698095|AW698095 NXNV_066_B07_F Nsf Xylem Normal wood Verti... 160 2e-56
      emb|AW306602|AW306602 se52h11.y1 Gm-c1017 Glycine max cDNA clone... 202 1e-54
      emb|AW694378|AW694378 NF075F01ST1F1013 Developing stem Medicago ... 138 3e-54
      emb|AW688967|AW688967 NF013G11ST1F1000 Developing stem Medicago ... 197 3e-53
20
      emb|AW692427|AW692427 NF055E11ST1F1000 Developing stem Medicago ... 209 6e-53
      emb|AI166601|AI166601 xylem.est.417 Poplar xylem Lambda ZAPII li... 207 3e-52
      emb|AI167062|AI167062 xylem.est.832 Poplar xylem Lambda ZAPII li... 207 3e-52
      emb|AI166632|AI166632 xylem.est.445 Poplar xylem Lambda ZAPII li... 207 3e-52
      emb|AI166389|AI166389 xylem.est.226 Poplar xylem Lambda ZAPII li... 207 3e-52
25
      emb|AI166520|AI166520 xylem.est.344 Poplar xylem Lambda ZAPII li... 207 3e-52
      emb|AI166460|AI166460 xylem.est.290 Poplar xylem Lambda ZAPII li... 207 3e-52
      emb|AI166300|AI166300 xylem.est.146 Poplar xylem Lambda ZAPII li... 207 3e-52
      emb|AI166804|AI166804 xylem.est.60 Poplar xylem Lambda ZAPII lib... 207 3e-52
      emb|AI167056|AI167056 xylem.est.827 Poplar xylem Lambda ZAPII li... 207 3e-52
30
      emb|AW694997|AW694997 NF082C04ST1F1033 Developing stem Medicago ... 180 2e-51
      emb|AI895135|AI895135 EST264578 tomato callus, TAMU Lycopersicon... 203 2e-51
      emb|AW032528|AW032528 EST276087 tomato callus, TAMU Lycopersicon... 196 2e-51
      emb|AW126324|AW126324 N100431e rootphos(-) Medicago truncatula c... 204 3e-51
      emb|AB029124|AB029124 AB029124 Cucumis sativus library (Chono M)... 204 3e-51
      emb|AI167003|AI167003 xylem.est.78 Poplar xylem Lambda ZAPII lib... 204 3e-51
35
      emb|AW035109|AW035109 EST280371 tomato callus, TAMU Lycopersicon... 196 1e-50
      emb|AW289657|AW289657 NXNV003D03F Nsf Xylem Normal wood Vertical... 198 1e-49
      emb|AW455342|AW455342 EST311880 tomato root during/after fruit s... 196 6e-49
      emb|AW432566|AW432566 sh76a01.y1 Gm-c1015 Glycine max cDNA clone... 195 8e-49
40
      emb|AW695232|AW695232 NF092F05ST1F1046 Developing stem Medicago ... 195 1e-48
      emb|AW694631|AW694631 NF078E04ST1F1034 Developing stem Medicago ... 190 3e-48
      emb|AW691613|AW691613 NF047A09ST1F1000 Developing stem Medicago ... 193 5e-48
      emb|AW736716|AW736716 EST333208 KV3 Medicago truncatula cDNA clo... 187 2e-46
      emb|AW736717|AW736717 EST333209 KV3 Medicago truncatula cDNA clo... 187 2e-46
45
      emb|AA556518|AA556518 373 Loblolly pine C Pinus taeda cDNA clone... 164 1e-45
      emb|AW985001|AW985001 NXNV_118_H12_F Nsf Xylem Normal wood Verti... 122 2e-45
      emb|AI812943|AI812943 22G11 Pine Lambda Zap Xylem library Pinus ... 173 4e-45
      emb|AI812863|AI812863 20H3 Pine Lambda Zap Xylem library Pinus t... 183 4e-45
      emb|AW307139|AW307139 sf53c04.yl Gm-c1009 Glycine max cDNA clone... 157 9e-44
      emb|AW985217|AW985217 NXNV_132_E12_F Nsf Xylem Normal wood Verti... 178 1e-43
      emb|AW689013|AW689013 NF014D06ST1F1000 Developing stem Medicago ... 177 3e-43
      gb|BE022993|BE022993 sm69b10.yl Gm-c1028 Glycine max cDNA clone ... 177 3e-43
      emb|AA556786|AA556786 628 Loblolly pine NA Pinus taeda cDNA clon... 133 3e-43
      emb|AW350964|AW350964 GM210010A10B4R Gm-r1021 Glycine max cDNA 3... 177 4e-
55
      emb[AW887962]AW887962 NXNV 127 D08 F Nsf Xylem Normal wood Verti... 176 7e-43
      emb|AW690520|AW690520 NF035E02ST1F1000 Developing stem Medicago ... 174 2e-42
      emb|AW626092|AW626092 EST319999 tomato radicle, 5 d post-imbibit... 119 5e-42
      emb|AW698220|AW698220 NXNV_070_B05_F Nsf Xylem Normal wood Verti... 172 9e-42
60
      emb|AW289555|AW289555 NXNV002H11F Nsf Xylem Normal wood Vertical... 170 3e-41
      emb|AW698218|AW698218 NXNV_070_B03_F Nsf Xylem Normal wood Verti... 107 4e-41
```

emb|AW693471|AW693471 NF065C09ST1F1000 Developing stem Medicago ... 169 8e-41 emb|AJ234679|HVU234679 Hordeum vulgare genomic DNA fragment; clo... 88 9e-41 emb|AI166348|AI166348 xylem.est.19 Poplar xylem Lambda ZAPII lib... 168 1e-40 emb|AW032099|AW032099 EST275553 tomato callus, TAMU Lycopersicon... 163 3e-40 emb|AW691027|AW691027 NF036H01ST1F1000 Developing stem Medicago ... 115 Se-40 emb|AW290667|AW290667 NXNV044G05F Nsf Xylem Normal wood Vertical... 166 8e-40 gb|BE123599|BE123599 NXNV_146_A10_F Nsf Xylem Normal wood Vertic... 163 5e-39 gblU43543|NTU43543 Nicotiana tabacum diphenol oxidase mRNA, part... 163 5e-39 emb|AW979587|AW979587 EST341186 tomato root deficiency, Cornell ... 159 9e-38 10 emb|AW695246|AW695246 NF092G11ST1F1087 Developing stem Medicago ... 92 5e-37 gb|BE020582|BE020582 sm51a03.yl Gm-c1028 Glycine max cDNA clone ... 133 7e-37 emb|AI794703|AI794703 sb67h06.yl Gm-c1019 Glycine max cDNA clone... 136 6e-36 emb|AW597115|AW597115 sj71g06.y1 Gm-c1034 Glycine max cDNA clone... 150 4e-35 emb|AI920039|AI920039 1569 Pine Lambda Zap Xylem library Pinus t... 85 7e-35 15 emb|AW626664|AW626664 NXNV068B04 Nsf Xylem Normal wood Vertical ... 146 6e-34 emb|AV412458|AV412458 AV412458 Lotus japonicus young plants (two... 124 1e-33 emb|AI726707|AI726707 BNLGHi6374 Six-day Cotton fiber Gossypium ... 145 1e-33 emb|AW626589|AW626589 NXNV067B05 Nsf Xylem Normal wood Vertical ... 84 2e-33 20 Query= Y11788.1 at 18946 at /id source genbank /description emb|caa72484.1| (y11788) peroxidase atp24a [arabidopsis thaliana] /blast_score 1.00e-148/ec number /family peroxidase /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbin-25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|y11788|/ncgi http://www.ncgr.org/cgi-bin/ff?y11788 (965 letters) Database: plantfungal 30 661,018 sequences; 426,114,510 total letters 35 Sequences producing significant alignments: (bits) Value gblM37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 230 e-105 emb|X94943|LECEVI16G L.esculentum mRNA for peroxidase. emb|AB027753|AB027753 Nicotiana tabacum mRNA for peroxidase, com... 191 1e-94 40 emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 220 2e-94 gb|L36112|SSNPEROXIC Stylosanthes humilis peroxidase mRNA. 157 2e-86 emb|AW033820|AW033820 EST277391 tomato callus, TAMU Lycopersicon... 170 2e-79 emb|Y10468|SOPRXR7 S.oleracea mRNA for peroxidase, clone PC36. 196 6e-78 emb|AW759829|AW759829 sl54f01.yl Gm-c1027 Glycine max cDNA clone... 213 1e-77 45 emb|AW216873|AW216873 EST295587 tomato callus, TAMU Lycopersicon... 212 3e-73 emb|AW224632|AW224632 EST303075 tomato root, plants pre-anthesis... 193 2e-66 emb|AF145349|AF145349 Glycine max peroxidase (Prx3) mRNA, partia... 131 4e-66 emb|AW219312|AW219312 EST301794 tomato root during/after fruit s... 193 2e-65 emb|AW219112|AW219112 EST301594 tomato root during/after fruit s... 193 2e-65 50 emb|AW032353|AW032353 EST275807 tomato callus, TAMU Lycopersicon... 137 1e-61 emb|AW031362|AW031362 EST274816 tomato callus, TAMU Lycopersicon... 180 9e-60 emb|AW035239|AW035239 EST280501 tomato callus, TAMU Lycopersicon... 212 1e-58 emb|AW035958|AW035958 EST282817 tomato callus, TAMU Lycopersicon... 212 1e-58 emb|AW035446|AW035446 EST281184 tomato callus, TAMU Lycopersicon... 212 1e-58 emb|AW029850|AW029850 EST273105 tomato callus, TAMU Lycopersicon... 170 5e-58 emb|AW030052|AW030052 EST273307 tomato callus, TAMU Lycopersicon... 165 7e-58 emb|AW569733|AW569733 si79g02.yl Gm-c1031 Glycine max cDNA clone... 153 1e-57 emb|AW224631|AW224631 EST303074 tomato root, plants pre-anthesis... 193 3e-57 emb|AW348753|AW348753 GM210003A22D6R Gm-r1021 Glycine max cDNA 3... 144 6e-60

emb|AW033082|AW033082 EST276641 tomato callus, TAMU Lycopersicon... 129 4e-56

	emb AV414872 AV414872 AV414872 Lotus japonicus young plants (two 182 2e-55
	dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part 94 3e-55
	emb AV414074 AV414074 AV414074 Lotus japonicus young plants (two 215 4e-55
	emb AW032485 AW032485 EST276044 tomato callus, TAMU Lycopersicon 212 3e-54
5	emb AW216562 AW216562 EST295276 tomato callus, TAMU Lycopersicon 210 2e-53
	emb X57564 ARNEUPERO A.rusticana mRNA for neutral peroxidase. 118 2e-53
	emb AI777064 AI777064 EST252031 tomato callus, TAMU Lycopersicon 206 2e-52
	emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox 93 6e-52
	emb]AW219314 AW219314 EST301796 tomato root during/after fruit s 193 4e-51
10	emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per 84 5e-51
	emb AW219926 AW219926 EST302409 tomato root during/after fruit s 193 8e-51
	embly W224620) A W224620 EST202072 tomato root along man and see 102 0 51
	emb AW224630 AW224630 EST303073 tomato root, plants pre-anthesis 193 8e-51
	emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor 81 8e-51
15	gb L13654 TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN 104 3e-50
15	emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod 82 5e-50
	emb Y10470 SOPRXR9 S.oleracea mRNA for peroxidase, clone PC56. 132 3e-49
	emb AV422753 AV422753 AV422753 Lotus japonicus young plants (two 195 4e-49
	emb AI773788 AI773788 EST254888 tomato resistant, Cornell Lycope 194 7e-49
	emb X90692 MSRNAPE1A M.sativa mRNA for peroxidase 1A. 76 1e-48
20	emb[X56011]TAPERO Wheat mRNA for peroxidase. 102 2e-48
	emb X97351 PTPXP4PER P.trichocarpa mRNA for anionic peroxidase P 90 8e-48
	emb AW666030 AW666030 sk31c04.yl Gm-c1028 Glycine max cDNA clone 191 9e-48
•	gb[M37636]ARCPNC1 Arachis hypogaea cationic peroxidase (PNC1) mR 89 1e-47
	emb AB024437 AB024437 Scutellaria baicalensis mRNA for peroxidas 122 1e-47
25	gb M74103 TOBANPER Nicotiana sylvestris anionic peroxidase mRNA, 100 2e-47
	gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge 78 3e-47
	emb AW621675 AW621675 EST312473 tomato root during/after fruit s 189 3e-47
	emb Y17192 CPY17192 Cucurbita pepo mRNA for peroxidase. 109 5e-47
	emb AI895427 AI895427 EST264870 tomato callus, TAMU Lycopersicon 121 7e-47
30	emb AW035207 AW035207 EST280469 tomato callus, TAMU Lycopersicon 188 8e-47
-	gb L13653 TOMTPX2A Lycopersicon esculentum peroxidase (TPX2) mRN 101 1e-46
	1 1774 A 4 COLO DE TOURS DE LA COLO DEL COLO DE LA COLO DE LA COLO DE LA COLO DE LA COLO DE LA COLO DEL LA COLO DE LA COLO DE LA COLO DE LA COLO DE LA COLO DE LA COL
	emb Y10463 SOPRXR2 S.oleracea mRNA for peroxidase, clone PB22. 140 4e-46 emb AW224633 AW224633 EST303076 tomato root, plants pre-anthesis 185 4e-46
	1 17 4 24 2 2 1 2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
35	1 h colonalarrana anno anno anno anno anno anno ann
55	1 brotocob compression
	emb X91232 MARNAPRX M.annua mRNA for peroxidase. 90 2e-45
	emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs 92 2e-45
	emb Z22920 SPPEROXDS S.polyrrhiza mRNA for peroxidase. 96 2e-45
40	emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C. 75 3e-45
70	gb M91374 CUSPREPERA Cucumis sativus peroxidase mRNA, complete cds. 109 4e-45
	emb AW035872 AW035872 EST282181 tomato callus, TAMU Lycopersicon 182 5e-45
	emb Y16776 SOY16776 Spinacia oleracea mRNA for peroxidase, prx10 95 5e-45
*	dbj D42065 TOBCPI40KB Tobacco mRNA for cationic peroxidase isozy 77 7e-45
10	dbj D42064 TOBCPI38KA Tobacco mRNA for cationic peroxidase isozy 77 1e-44
45	emb AI772237 AI772237 EST253337 tomato resistant, Cornell Lycope 180 2e-44
	emb AF149278 AF149278 Phaseolus vulgaris peroxidase 3 precursor 84 2e-44
	emb AW035660 AW035660 EST281492 tomato callus, TAMU Lycopersicon 178 5e-44
	emb AF244922 AF244922 Spinacia oleracea peroxidase prx13 precurs 83 1e-43
	emb X97350 PTPXP3PER P.trichocarpa mRNA for anionic peroxidase P 83 2e-43
50	gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 77 3e-43
	emb X58396 HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 90 3e-43
	emb X97348 PTPXP1PER P.trichocarpa mRNA for anionic peroxidase P 85 4e-43
	gb L36093 BLYPRX Barley peroxidase mRNA, complete cds. 89 4e-43
	emb AF043234 AF043234 Striga asiatica ferriprotein porphyrin-con 83 7e-43
55	emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B. 74 7e-43
	emb X97349 PTPXP2PER P.trichocarpa mRNA for anionic peroxidase P 83 2e-42
	gb L24120 LINFLXP Linum usitatissimum peroxidase precursor (FLXP 88 2e-42
	emb AW705192 AW705192 sk42h02.y1 Gm-c1019 Glycine max cDNA clone 111 2e-42
	emb AW705312 AW705312 sk59d04.y1 Gm-c1019 Glycine max cDNA clone 128 2e-42
60	
J-J	gb L0/354 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA 92 3e-42 gb L77080 SSNCAPEA Stylosanthes humilis cationic peroxidase gene 122 1e-41
	golden vooloon can be belots and the serious canonic peroxidase gene 122 1e-41

emb|AI778513|AI778513 EST259392 tomato susceptible, Cornell Lyco... 170 1e-41 emb|AB027752|AB027752 Nicotiana tabacum mRNA for peroxidase, com... 87 2e-41 emb|AF007211|AF007211 Glycine max peroxidase precursor (GMIPER1)... 72 2e-41 emb|A00741|A00741 A.rusticana synthetic gene (reverse complement... 76 2e-41 emb|A00740|A00740 A.rusticana synthetic gene for peroxidase. dbj E01651 E01651 cDNA encoding horseradish peroxidase. 76 2e-41 emb|AF244923|AF244923 Spinacia oleracea peroxidase prx14 precurs... 84 3e-41 emb|AF149277|AF149277 Phaseolus vulgaris peroxidase 1 precursor ... 71 3e-41 dbj|D30652|POPPA Populus kitakamiensis mRNA for peroxidase, part... 80 4e-41 10 emb|Y10469|SOPRXR8 S.oleracea mRNA for peroxidase, clone PC55. 111 4e-41 emb|AJ011939|TRE011939 Trifolium repens mRNA for peroxidase. 105 6e-41 emb|Y10465|SOPRXR4 S.oleracea mRNA for peroxidase, clone PC44. 86 6e-41 gb|U12315|CCU12315 Cenchrus ciliaris clone PX18 peroxidase mRNA,... 106 9e-41 dbj|D11337|VIRPRX Vigna angularis mRNA for peroxidase basic isoz... 77 1e-40 15 gb|M91373|CUSPREPER Cucumis sativus peroxidase mRNA, complete cds. 107 1e-40 Query= AF163823.4_at 18968_at /id source genbank /description gb|aad45127.1|af163823_1 (af163823) endoxyloglucan transferase [arabidopsis thaliana] /blast_score 1.00e-161 /ec_number /family 20 /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|af163823| /ncgi http://www.ncgr.org/cgi-bin/ff?af163823 (1025 letters) 25 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 30 Score, E Sequences producing significant alignments: (bits) Value emb|AJ130885|FSY130885 Fagus sylvatica mRNA for xyloglucan endot... 424 e-134 35 emb|X93174|HVXETXEA H.vulgare mRNA for xyloglucan endotransglyco... 418 e-130 gb|L22162|SOYMER5HOM Glycine max brassinosteroid-regulated prote... 384 e-118 emblAW220372|AW220372 EST302855 tomato root during/after fruit s... 416 e-115 emb|AW030111|AW030111 EST273366 tomato callus, TAMU Lycopersicon... 416 e-115 emb|AW032346|AW032346 EST275800 tomato callus, TAMU Lycopersicon... 415 e-115 40 emb|AW218856|AW218856 EST301338 tomato root during/after fruit s... 413 e-115 emb|AW031139|AW031139 EST274446 tomato callus, TAMU Lycopersicon... 380 e-115 emb|AI725820|AI725820 BNLGHi13219 Six-day Cotton fiber Gossypium... 413 e-114 emb|AI938507|AI938507 sb46e06.y1 Gm-c1015 Glycine max cDNA clone... 407 e-112 emb|AW776635|AW776635 EST335700 DSIL Medicago truncatula cDNA cl... 407 e-112 45 emb|AI488729|AI488729 EST247068 tomato ovary, TAMU Lycopersicon ... 406 e-112 emb|AI485531|AI485531 EST243852 tomato ovary, TAMU Lycopersicon ... 402 e-111 emb|AW033905|AW033905 EST277476 tomato callus, TAMU Lycopersicon... 401 e-111 emb|AW216717|AW216717 EST295431 tomato callus, TAMU Lycopersicon... 397 e-110 gb|BE035552|BE035552 MO09A12 MO Mesembryanthemum crystallinum cD... 353 e-109 50 emb[X93175]HVXETXEB H.vulgare mRNA for xyloglucan endotransglyco... 387 e-109 emb|AW651314|AW651314 EST329768 tomato germinating seedlings, TA... 390 e-108 emb|AW218734|AW218734 EST301214 tomato root during/after fruit s... 388 e-107 emb|AI460643|AI460643 sa71e04.yl Gm-c1004 Glycine max cDNA clone... 387 e-107 55 emb|AI898515|AI898515 EST267958 tomato ovary, TAMU Lycopersicon ... 386 e-106 emb|AI488903|AI488903 EST247242 tomato ovary, TAMU Lycopersicon ... 386 e-106 emb|AW218894|AW218894 EST301376 tomato root during/after fruit s... 386 e-106 emb|AI487536|AI487536 EST245858 tomato ovary, TAMU Lycopersicon ... 379 e-104 emb|AW981262|AW981262 EST392415 DSIL Medicago truncatula cDNA cl... 315 e-104 60 emb[AW033629[AW033629 EST277200 tomato callus, TAMU Lycopersicon... 378 e-104 emb|AW033699|AW033699 EST277270 tomato callus, TAMU Lycopersicon... 376 e-103

gb|BE036915|BE036915 MP09A12 MP Mesembryanthemum crystallinum cD... 368 e-101 emb|AI495154|AI495154 sa88f09.yl Gm-c1004 Glycine max cDNA clone... 367 e-101 emb|AW096328|AW096328 EST289508 tomato mixed elicitor, BTI Lycop... 366 e-100 emb|AI487279|AI487279 EST245601 tomato ovary, TAMU Lycopersicon ... 365 e-100 5 emb|AI485293|AI485293 EST243597 tomato ovary, TAMU Lycopersicon ... 364 e-100 emb|AW649744|AW649744 EST328198 tomato germinating seedlings, TA... 293 8e-99 emb|AW031478|AW031478 EST274932 tomato callus, TAMU Lycopersicon... 360 1e-98 emb|X82684|LETXETB2 L.esculentum tXET-B2 mRNA for xyloglucan end... 355 3e-97 emb|AW093001|AW093001 EST286181 tomato mixed elicitor, BTI Lycop... 354 5e-97 10 emb|AW218862|AW218862 EST301344 tomato root during/after fruit s... 354 5e-97 emblAI725839|AI725839 BNLGHi13291 Six-day Cotton fiber Gossypium... 354 7e-97 emb|AW033371|AW033371 EST276942 tomato callus, TAMU Lycopersicon... 354 7e-97 emb|X82685|LETXETB1 L.esculentum tXET-B1 mRNA for xyloglucan end... 354 7e-97 emb|AI490390|AI490390 EST248728 tomato ovary, TAMU Lycopersicon ... 352 2e-96 15 emb|AI773291|AI773291 EST254391 tomato resistant, Cornell Lycope... 293 1e-95 emb|AI486834|AI486834 EST245156 tomato ovary, TAMU Lycopersicon ... 350 1e-95 emb|AW930090|AW930090 EST340547 tomato fruit mature green, TAMU ... 348 4e-95 emblAI485404|AI485404 EST243725 tomato ovary, TAMU Lycopersicon ... 348 4e-95 emb[AW691431]AW691431 NF041B05ST1F1000 Developing stem Medicago ... 334 8e-95 20 emb|AW685669|AW685669 NF030A11NR1F1000 Nodulated root Medicago t... 276 1e-94 gb|BE124065|BE124065 EST394190 DSIL Medicago truncatula cDNA clo... 346 2e-94 emb|AW307509|AW307509 sf57h02.y1 Gm-c1009 Glycine max cDNA clone... 346 2e-94 emb|AI487162|AI487162 EST245484 tomato ovary, TAMU Lycopersicon ... 344 6e-94 emb|AI489159|AI489159 EST247498 tomato ovary, TAMU Lycopersicon ... 291 1e-93 25 emb|AI485855|AI485855 EST244176 tomato ovary, TAMU Lycopersicon ... 343 1e-93 emb|AW432541|AW432541 sh75f05.yl Gm-c1015 Glycine max cDNA clone... 342 3e-93 dbj|D16455|SOYEXT2 Soybean mRNA for endo-xyloglucan transferase,... 310 4e-93 dbj E06969 E06969 DNA encoding xyloglucan endotransferase. 310 4e-93 dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93 emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93 emb|AW394832|AW394832 sh35h09.y1 Gm-c1017 Glycine max cDNA clone... 341 7e-93 dbj|E06959|E06959 Anti-sense DNA of xyloglucan endotransferase g... 306 6e-92 gb|L46792|ACTXET Actinidia deliciosa clone AdXET-5 xyloglucan en... 320 8e-92 35 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90 gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90 dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 le-90 dbj|E06963|E06963 Anti-sense RNA of xyloglucan endotransferase g... 314 1e-90 dbj|E06958|E06958 Anti-sense DNA of xyloglucan endotransferase g... 314 1e-90 40 emb|AJ004917|CAAJ4917 Cicer arietinum mRNA for endoxyloglucan tr... 310 1e-89 emb[X91659]HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89 dbj|D16457|WHTEXT4 Wheat mRNA for endo-xyloglucan transferase, c... 319 2e-89 dbj|E06972|E06972 DNA encoding xyloglucan endotransferase. 319 6e-89 dbj E06967 E06967 Anti-sense RNA of xyloglucan endotransferase g... 319 6e-89 45 dbj|E06962|E06962 Anti-sense DNA of xyloglucan endotransferase g... 319 6e-89 emb[AW687253]AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88 emb|AI488724|AI488724 EST247063 tomato ovary, TAMU Lycopersicon ... 273 2e-88 dbj|D86730|D86730 Nicotiana tabacum mRNA for endoxyloglucan tran... 303 3e-88 emb|AB017025|AB017025 Nicotiana tabacum mRNA for endo-xyloglucan... 303 3e-88 50 emblAB015428|AB015428 Pisum sativum mRNA for EXGT1, complete cds. 309 3e-88 emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88 emb[AW184781]AW184781 se82c12.y1 Gm-c1023 Glycine max cDNA clone... 274 8e-88 emb|AI487551|AI487551 EST245873 tomato ovary, TAMU Lycopersicon ... 268 1e-87 emb|AW980364|AW980364 EST391517 GVN Medicago truncatula cDNA clo... 322 2e-87 55 emb|AI487338|AI487338 EST245660 tomato ovary, TAMU Lycopersicon ... 265 3e-87 emb|AI496348|AI496348 sb05e11.yl Gm-c1004 Glycine max cDNA clone... 320 8e-87 emblAF052194|AF052194 Actinidia deliciosa xyloglucan endotransgl... 320 1e-86 emb|AW598083|AW598083 sj88g10.yl Gm-c1034 Glycine max cDNA clone... 319 2e-86 emb|AI898560|AI898560 EST268003 tomato ovary, TAMU Lycopersicon ... 319 2e-86 60 emb|AW184871|AW184871 se69f08.y1 Gm-c1019 Glycine max cDNA clone... 300 7e-86 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85

emb|AI726805|AI726805 BNLGHi6594 Six-day Cotton fiber Gossypium ... 315 3e-85 emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton fiber Gossypium ... 315 4e-85 dbj|D16456|TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ... 295 4e-85 dbj|E06971|E06971 DNA encoding xyloglucan endotransferase ... 295 4e-85 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85 dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85 emb|AW934469|AW934469 EST353373 tomato flower buds 0-3 mm, Corne... 314 7e-85 emb|AW185234|AW185234 se88f12.yl Gm-c1023 Glycine max cDNA clone... 314 1e-84 emb|AI487776|AI487776 EST246098 tomato ovary, TAMU Lycopersicon ... 266 2e-84 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84 emb|AI895031|AI895031 EST264474 tomato callus, TAMU Lycopersicon... 312 4e-84

Query= AF163823.4_g_at 18969_g_at /id_source genbank /description gb|aad45127.1|af163823_1 (af163823) endoxyloglucan transferase [arabidopsis thaliana] /blast_score 1.00e-161 /ec_number /family /chip nova /gb_link /ncgi (1025 letters)

20 Database: plantfungal

60

661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score

Sequences producing significant alignments: (bits) Value

E

emb|AJ130885|FSY130885 Fagus sylvatica mRNA for xyloglucan endot... 424 e-134 emb|X93174|HVXETXEA H.vulgare mRNA for xyloglucan endotransglyco... 418 e-130 30 gb|L22162|SOYMER5HOM Glycine max brassinosteroid-regulated prote... 384 e-118 emb|AW220372|AW220372 EST302855 tomato root during/after fruit s... 416 e-115 emb|AW030111|AW030111 EST273366 tomato callus, TAMU Lycopersicon... 416 e-115 emb|AW032346|AW032346 EST275800 tomato callus, TAMU Lycopersicon... 415 e-115 emb|AW218856|AW218856 EST301338 tomato root during/after fruit s... 413 e-115 35 emb|AW031139|AW031139 EST274446 tomato callus, TAMU Lycopersicon... 380 e-115 emb|AI725820|AI725820 BNLGHi13219 Six-day Cotton fiber Gossypium... 413 e-114 emb|AI938507|AI938507 sb46e06.y1 Gm-c1015 Glycine max cDNA clone... 407 e-112 emb|AW776635|AW776635 EST335700 DSIL Medicago truncatula cDNA cl... 407 e-112 emb|AI488729|AI488729 EST247068 tomato ovary, TAMU Lycopersicon ... 406 e-112 40 emb|AI485531|AI485531 EST243852 tomato ovary, TAMU Lycopersicon ... 402 e-111 emb|AW033905|AW033905 EST277476 tomato callus, TAMU Lycopersicon... 401 e-111 emb|AW216717|AW216717 EST295431 tomato callus, TAMU Lycopersicon... 397 e-110 gb|BE035552|BE035552 MO09A12 MO Mesembryanthemum crystallinum cD... 353 e-109 emb|AW729695|AW729695 GA_Ea0025M09 Gossypium arboreum 7-10 dpa ... 394 e-109 45 emb|X93175|HVXETXEB H.vulgare mRNA for xyloglucan endotransglyco... 387 e-109 emb|AW651314|AW651314 EST329768 tomato germinating seedlings, TA... 390 e-108 emb|AW218734|AW218734 EST301214 tomato root during/after fruit s... 388 e-107 emb|AI460643|AI460643 sa71e04.y1 Gm-c1004 Glycine max cDNA clone... 387 e-107 emb|AI898515|AI898515 EST267958 tomato ovary, TAMU Lycopersicon ... 386 e-106 50 emb|AI488903|AI488903 EST247242 tomato ovary, TAMU Lycopersicon ... 386 e-106 emb|AW218894|AW218894 EST301376 tomato root during/after fruit s... 386 e-106 emb|AI487536|AI487536 EST245858 tomato ovary, TAMU Lycopersicon ... 379 e-104 emb|AW981262|AW981262 EST392415 DSIL Medicago truncatula cDNA cl... 315 e-104 emblAW033629|AW033629 EST277200 tomato callus, TAMU Lycopersicon... 378 e-104 emb|AW033699|AW033699 EST277270 tomato callus, TAMU Lycopersicon... 376 e-103 gb|BE036915|BE036915 MP09A12 MP Mesembryanthemum crystallinum cD... 368 e-101 emb|AI495154|AI495154 sa88f09.y1 Gm-c1004 Glycine max cDNA clone... 367 e-101 emb|AW096328|AW096328 EST289508 tomato mixed elicitor, BTI Lycop... 366 e-100

emb|AI487279|AI487279 EST245601 tomato ovary, TAMU Lycopersicon ... 365 e-100

emb|AI485293|AI485293 EST243597 tomato ovary, TAMU Lycopersicon ... 364 e-100 emb|AW649744|AW649744 EST328198 tomato germinating seedlings, TA... 293 8e-99

emb|AW031478|AW031478 EST274932 tomato callus, TAMU Lycopersicon... 360 1e-98 emb|X82684|LETXETB2 L.esculentum tXET-B2 mRNA for xyloglucan end... 355 3e-97 emb|AW093001|AW093001 EST286181 tomato mixed elicitor, BTI Lycop... 354 5e-97 emb|AW218862|AW218862 EST301344 tomato root during/after fruit s... 354 5e-97 5 emb|AI725839|AI725839 BNLGHi13291 Six-day Cotton fiber Gossypium... 354 7e-97 emb|AW033371|AW033371 EST276942 tomato callus, TAMU Lycopersicon... 354 7e-97 emb|X82685|LETXETB1 L.esculentum tXET-B1 mRNA for xyloglucan end... 354 7e-97 emb|AI490390|AI490390 EST248728 tomato ovary, TAMU Lycopersicon ... 352 2e-96 emb|AI773291|AI773291 EST254391 tomato resistant, Cornell Lycope... 293 1e-95 10 emb|AI486834|AI486834 EST245156 tomato ovary, TAMU Lycopersicon ... 350 1e-95 emb|AW930090|AW930090 EST340547 tomato fruit mature green, TAMU ... 348 4e-95 emb|AI485404|AI485404 EST243725 tomato ovary, TAMU Lycopersicon ... 348 4e-95 emb|AW691431|AW691431 NF041B05ST1F1000 Developing stem Medicago ... 334 8e-95 emb|AW685669|AW685669 NF030A11NR1F1000 Nodulated root Medicago t... 276 1e-94 15 gb|BE124065|BE124065 EST394190 DSIL Medicago truncatula cDNA clo... 346 2e-94 emb|AW307509|AW307509 sf57h02.y1 Gm-c1009 Glycine max cDNA clone... 346 2e-94 emb|AI487162|AI487162 EST245484 tomato ovary, TAMU Lycopersicon ... 344 6e-94 emb|AI489159|AI489159 EST247498 tomato ovary, TAMU Lycopersicon ... 291 1e-93 emb|AI485855|AI485855 EST244176 tomato ovary, TAMU Lycopersicon ... 343 1e-93 20 emb|AW432541|AW432541 sh75f05.yl Gm-c1015 Glycine max cDNA clone... 342 3e-93 dbj|D16455|SOYEXT2 Soybean mRNA for endo-xyloglucan transferase,... 310 4e-93 dbj|E06969|E06969 DNA encoding xyloglucan endotransferase. dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93 25 emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93 emb|AW394832|AW394832 sh35h09.y1 Gm-c1017 Glycine max cDNA clone... 341 7e-93 dbj|E06959|E06959 Anti-sense DNA of xyloglucan endotransferase g... 306 6e-92 gb|L46792|ACTXET Actinidia deliciosa clone AdXET-5 xyloglucan en... 320 8e-92 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90 30 gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 le-90 dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 le-90 dbj|E06963|E06963 Anti-sense RNA of xyloglucan endotransferase g... 314 1e-90 dbj|E06958|E06958 Anti-sense DNA of xyloglucan endotransferase g... 314 1e-90 emb|AJ004917|CAAJ4917 Cicer arietinum mRNA for endoxyloglucan tr... 310 1e-89 35 emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89 dbi[D16457[WHTEXT4 Wheat mRNA for endo-xyloglucan transferase, c... 319 2e-89 dbj|E06972|E06972 DNA encoding xyloglucan endotransferase. 319 6e-89 dbj|E06967|E06967 Anti-sense RNA of xyloglucan endotransferase g... 319 6e-89 dbj|E06962|E06962 Anti-sense DNA of xyloglucan endotransferase g... 319 6e-89 40 emb|AW687253|AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88 emb|AI488724|AI488724 EST247063 tomato ovary, TAMU Lycopersicon ... 273 2e-88 dbj|D86730|D86730 Nicotiana tabacum mRNA for endoxyloglucan tran... 303 3e-88 emb|AB017025|AB017025 Nicotiana tabacum mRNA for endo-xyloglucan... 303 3e-88 emb|AB015428|AB015428 Pisum sativum mRNA for EXGT1, complete cds. 45 emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88 emb|AW184781|AW184781 se82c12.yl Gm-c1023 Glycine max cDNA clone... 274 8e-88 emb|AI487551|AI487551 EST245873 tomato ovary, TAMU Lycopersicon ... 268 1e-87 emb|AW980364|AW980364 EST391517 GVN Medicago truncatula cDNA clo... 322 2e-87 emb|AI487338|AI487338 EST245660 tomato ovary, TAMU Lycopersicon ... 265 3e-87 50 emb|AI496348|AI496348 sb05e11.yl Gm-c1004 Glycine max cDNA clone... 320 8e-87 emb|AF052194|AF052194 Actinidia deliciosa xyloglucan endotransgl... 320 1e-86 emb|AW598083|AW598083 sj88g10.y1 Gm-c1034 Glycine max cDNA clone... 319 2e-86 emb|AI898560|AI898560 EST268003 tomato ovary, TAMU Lycopersicon ... 319 2e-86 emb[AW184871]AW184871 se69f08.y1 Gm-c1019 Glycine max cDNA clone... 300 7e-86 55 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85 emb|AI726805|AI726805 BNLGHi6594 Six-day Cotton fiber Gossypium ... 315 3e-85 emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton fiber Gossypium... 315 4e-85 dbi|D16456|TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ... 295 4e-85 dbj|E06971|E06971 DNA encoding xyloglucan endotransferase. 60 dbi|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85 dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85

emb|AW934469|AW934469 EST353373 tomato flower buds 0-3 mm, Corne... 314 7e-85 emb|AW185234|AW185234 se88f12.y1 Gm-c1023 Glycine max cDNA clone... 314 1e-84 emb|AI487776|AI487776 EST246098 tomato ovary, TAMU Lycopersicon ... 266 2e-84 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84 emb|AI895031|AI895031 EST264474 tomato callus, TAMU Lycopersicon... 312 4e-84

Query= AL049730.104_s_at 18983_s_at /id_source genbank /description emb|cab41722.1| (al049730) pearli 1-like protein [arabidopsis thaliana] /blast score 4.00e-25 /ec number /family /chip nova /gb link /ncgi (390 letters)

Database: plantfungal

10

20

661,018 sequences; 426,114,510 total letters

15 Searching......done

> Score E

emb[AW980687]AW980687 EST391840 GVN Medicago truncatula cDNA clo... 95 2e-22

Sequences producing significant alignments: (bits) Value

emb|AW980826|AW980826 EST391979 GVN Medicago truncatula cDNA clo... 95 2e-22 emb|AW980547|AW980547 EST391700 GVN Medicago truncatula cDNA clo... 95 2e-22 emb|AW685869|AW685869 NF031B09NR1F1000 Nodulated root Medicago t... 95 2e-22 25 gb|BE124445|BE124445 EST393480 GVN Medicago truncatula cDNA clon... 95 2e-22 gb|BE124752|BE124752 EST393787 GVN Medicago truncatula cDNA clon... 95 2e-22 emb|AW684629|AW684629 NF019B05NR1F1000 Nodulated root Medicago t... 95 2e-22 emb|AW329233|AW329233 N200445e rootphos(-) Medicago truncatula c... 95 2e-22 gb|BE124520|BE124520 EST393555 GVN Medicago truncatula cDNA clon... 95 4e-22 30 emb|AW125962|AW125962 N100157e rootphos(-) Medicago truncatula c... 92 2e-21 emb|AW622601|AW622601 EST313401 tomato root during/after fruit s... 101 2e-21

emb|AW624937|AW624937 EST313766 tomato radicle, 5 d post-imbibit... 101 2e-21 emb|AW560894|AW560894 EST315942 DSIR Medicago truncatula cDNA cl... 95 3e-21 emb|AW621250|AW621250 EST312048 tomato root during/after fruit s... 98 9e-21 35 emb|AW626221|AW626221 EST320128 tomato radicle, 5 d post-imbibit... 98 9e-21

emb|AW035571|AW035571 EST281309 tomato callus, TAMU Lycopersicon... 98 1e-20 emb|AW217082|AW217082 EST295796 tomato callus, TAMU Lycopersicon... 98 1e-20 emb|AW032764|AW032764 EST276323 tomato callus, TAMU Lycopersicon... 98 1e-20 emb|AW443140|AW443140 EST308070 tomato mixed elicitor, BTI Lycop... 98 1e-20

emb|AW622645|AW622645 EST313445 tomato root during/after fruit s... 96 1e-20 emb|AW907202|AW907202 EST343325 potato stolon, Cornell Universit... 99 2e-20 emb|AI776056|AI776056 EST257156 tomato resistant, Cornell Lycope... 98 3e-20 emb|AI779211|AI779211 EST260090 tomato susceptible, Cornell Lyco... 98 3e-20 emb|AW034083|AW034083 EST277578 tomato callus, TAMU Lycopersicon... 98 3e-20

45 emb|AW094444|AW094444 EST287624 tomato mixed elicitor, BTI Lycop... 98 3e-20 emb|AW685279|AW685279 NF025G02NR1F1000 Nodulated root Medicago t... 90 4e-20 emb|AF109654|AF109654 AF109654 Capsicum annuum root susceptible ... 97 5e-20 emb|AW625740|AW625740 EST319647 tomato radicle, 5 d post-imbibit... 96 9e-20 dbj|D83227|POPELPG Populus nigra gene for extensin like protein,... 92 2e-19

50 dbj|D83226|POPELP Populus nigra mRNA for extensin like protein, ... 92 2e-19 emb|AW287846|AW287846 N100689e rootphos(-) Medicago truncatula c... 95 2e-19 gb|BE124789|BE124789 EST393824 GVN Medicago truncatula cDNA clon... 95 2e-19 gb|BE124744|BE124744 EST393779 GVN Medicago truncatula cDNA clon... 95 2e-19 emb|AW217088|AW217088 EST295802 tomato callus, TAMU Lycopersicon... 95 3e-19

55 emb|AW725519|AW725519 GA_Ea0018G20 Gossypium arboreum 7-10 dpa ... 94 4e-19 gb|S68113|S68113 proline-rich SAC51 [Brassica napus=oilseed rape... 94 4e-19 emb|X71618|BNPRPPDA B.napus proline-rich mRNA accumulating durin... 94 4e-19 emb|AF026382|AF026382 Fragaria x ananassa HyPRP mRNA, complete cds. 94 4e-19 emb|AI779212|AI779212 EST260091 tomato susceptible, Cornell Lyco... 94 6e-19

60 emb|AV413531|AV413531 AV413531 Lotus japonicus young plants (two... 93 1e-18 emb|AW685624|AW685624 NF032E01NR1F1000 Nodulated root Medicago t... 81 2e-18

```
emb|AW287985|AW287985 N100829e rootphos(-) Medicago truncatula c... 89 1e-17
      emb|AW257148|AW257148 EST305285 KV2 Medicago truncatula cDNA clo... 89 1e-17
      emb|AW349572|AW349572 GM210005A21F12R Gm-r1021 Glycine max cDNA ... 88 3e-17
      emb[X85206]CRRNAHPRP C.roseus mRNA for hybrid proline-rich protein. 86 1e-16
 5
      emb|Z26880|CR14KDPP C.roseus mRNA for 14 kDa polypeptide.
      emb|AW278328|AW278328 sf42f09.yl Gm-c1009 Glycine max cDNA clone... 78 1e-16
      emb|AW703723|AW703723 sk23f03.yl Gm-c1028 Glycine max cDNA clone... 78 1e-16
      emb|AI352845|AI352845 MB69-3F PZ204.BNlib Brassica napus cDNA cl... 68 1e-16
      gb|BE021488|BE021488 sm59b04.y1 Gm-c1028 Glycine max cDNA clone ... 85 3e-16
10
      emb|AW234182|AW234182 sf22b12.y1 Gm-c1028 Glycine max cDNA clone... 65 3e-16
      gb|BE022318|BE022318 sm73d03.yl Gm-c1028 Glycine max cDNA clone ... 65 5e-16
      emb|AW625137|AW625137 EST313954 tomato radicle, 5 d post-imbibit... 83 9e-16
      emb|AV422321|AV422321 AV422321 Lotus japonicus young plants (two... 70 2e-15
      emb|AW597680|AW597680 sj49e04.yl Gm-c1033 Glycine max cDNA clone... 62 2e-15
15
      emblAW306872|AW306872 sf49g05.yl Gm-c1009 Glycine max cDNA clone... 62 3e-15
      emb|AW163963|AW163963 Ljirnpest17-382-g10 Ljirnp Lambda HybriZap... 78 3e-15
      dbj|D86629|D86629 Nicotiana tabacum mRNA for NT16 polypeptide, c... 81 3e-15
      emb|AW666281|AW666281 sk34f10.yl Gm-c1028 Glycine max cDNA clone... 62 4e-15
      emb|AV413898|AV413898 AV413898 Lotus japonicus young plants (two... 70 4e-15
20
      gb|BE022257|BE022257 sm72g11.yl Gm-c1028 Glycine max cDNA clone ... 62 5e-15
      dbj|D86721|D86721 Nicotiana tabacum DNA for glycine-rich polypep... 80 8e-15
      emb|AI166167|AI166167 A013P67U Hybrid aspen plasmid library Pop... 72 9e-15
      emb|AJ389048|AJ389048 AJ389048 Medicago truncatula R108 Medicago... 65 1e-14
      emb|AW719418|AW719418 LjNEST4c12r Lotus japonicus nodule library... 68 1e-14
25
      emb|AW031617|AW031617 EST275071 tomato callus, TAMU Lycopersicon... 79 2e-14
      emb|AV424931|AV424931 AV424931 Lotus japonicus young plants (two... 71 2e-14
      emb|AW625399|AW625399 EST319222 tomato radicle, 5 d post-imbibit... 78 2e-14
      emb|AW621368|AW621368 EST312166 tomato root during/after fruit s... 78 2e-14
      emb|AV423170|AV423170 AV423170 Lotus japonicus young plants (two... 71 2e-14
30
      emb|AI736342|AI736342 sb27c03.y1 Gm-c1009 Glycine max cDNA clone... 64 3e-14
      emb|AB035125|AB035125 Nicotiana tabacum mRNA for glycine-rich pr... 78 3e-14
      dbi|D26454|TOBTID23 Nicotiana glauca X Nicotiana langsdorffii mR... 78 3e-14
      emb|AV415427|AV415427 AV415427 Lotus japonicus young plants (two... 70 4e-14
      emb|AV416097|AV416097 AV416097 Lotus japonicus young plants (two...
                                                                         70 4e-14
35
      emb|AV415022|AV415022 AV415022 Lotus japonicus young plants (two...
                                                                         78 4e-14
      emb|AV413103|AV413103 AV413103 Lotus japonicus young plants (two...
                                                                          78 4e-14
      emb|AV411456|AV411456 AV411456 Lotus japonicus young plants (two...
                                                                          78 4e-14
      emb|AV411686|AV411686 AV411686 Lotus japonicus young plants (two...
                                                                          78 4e-14
      emb|AV425640|AV425640 AV425640 Lotus japonicus young plants (two...
                                                                          78 4e-14
40
      emb|AV411414|AV411414 AV411414 Lotus japonicus young plants (two...
      emb|AW163953|AW163953 Ljirnpest17-369-f9 Ljirnp Lambda HybriZap ...
      emb|AV424226|AV424226 AV424226 Lotus japonicus young plants (two...
                                                                          78.4e-14
      emb|AV423183|AV423183 AV423183 Lotus japonicus young plants (two...
                                                                          78 4e-14
      emb|AV411071|AV411071 AV411071 Lotus japonicus young plants (two...
                                                                         78 4e-14
45
      emb|AV411588|AV411588 AV411588 Lotus japonicus young plants (two...
      emb|AI496419|AI496419 sb04e01.yl Gm-c1004 Glycine max cDNA clone... 69 le-13
      emb|AI507807|AI507807 sb12h09.y1 Gm-c1004 Glycine max cDNA clone...
      emb|AI772831|AI772831 EST253931 tomato resistant, Cornell Lycope... 65 2e-13
      emb|AI776903|AI776903 EST258003 tomato resistant, Cornell Lycope... 65 2e-13
50
      emb|AW650068|AW650068 EST328522 tomato germinating seedlings, TA... 75 2e-13
      emb|AW650542|AW650542 EST328996 tomato germinating seedlings, TA... 65 2e-13
      emblAI967649|AI967649 Ljirnpest08-651-c10 Ljirnp Lambda HybriZap... 65 2e-13
      emb|AW092951|AW092951 EST286131 tomato mixed elicitor, BTI Lycop... 65 2e-13
      emb|AI442516|AI442516 sa32e08.y1 Gm-c1004 Glycine max cDNA clone... 69 2e-13
55
      emb|AI736269|AI736269 sb26b02.yl Gm-c1008 Glycine max cDNA clone... 69 3e-13
      emb|AW830131|AW830131 sm23c07.yl Gm-c1028 Glycine max cDNA clone... 69 3e-13
      emb|AW152920|AW152920 se32g01.yl Gm-c1015 Glycine max cDNA clone... 69 3e-13
      gb|BE020655|BE020655 sm51h06.yl Gm-c1028 Glycine max cDNA clone ... 69 3e-13
      emb|AW570545|AW570545 sj63d10.yl Gm-c1033 Glycine max cDNA clone... 69 3e-13
60
```

PCT/US01/28506 WO 02/22675

emb|caa65053.1| (x95738) proline transporter 2 [arabidopsis thaliana] /blast score 0 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|x95738|/ncgi http://www.ncgr.org/cgi-bin/ff?x95738 (1579 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

10

Searching......done Score Sequences producing significant alignments: (bits) Value 15 emb|AF014809|AF014809 Lycopersicon esculentum proline transporte... 677 0.0 emb|AF014810|AF014810 Lycopersicon esculentum proline transporte... 676 0.0 emb|AF014808|AF014808 Lycopersicon esculentum proline transporte... 668 0.0 emb|AW563318|AW563318 LG1 228 A07.g1 A002 Light Grown 1 (LG1) So... 173 9e-66 20 emb|AI054471|AI054471 coau0001B09 Cotton Boll Abscission Zone cD... 168 3e-53 emb|AI895644|AI895644 EST265087 tomato callus, TAMU Lycopersicon... 206 3e-52 emb|AW691556|AW691556 NF046C09ST1F1000 Developing stem Medicago ... 178 8e-52 emb|AW287445|AW287445 LG1 228 A07.b1 A002 Light Grown 1 (LG1) So... 201 1e-50 emb|AW428965|AW428965 EST306505 tomato flower buds 0-3 mm, Corne... 198 9e-50 25 emb|AW672225|AW672225 LG1_358_C11.b1_A002 Light Grown 1 (LG1) So... 192 6e-48 emb|AW102341|AW102341 sd86d12.yl Gm-c1009 Glycine max cDNA clone... 186 4e-46 emb|AW063020|AW063020 SBcD66 Sugar beet leaf cDNA library Beta v... 133 3e-44 emb|AW686923|AW686923 NF004A10RT1F1072 Developing root Medicago ... 91 2e-40 emb|AW773932|AW773932 EST332918 KV3 Medicago truncatula cDNA clo... 91 6e-35 30 emb|AW011298|AW011298 ST19B09 Pine TriplEx shoot tip library Pin... 83 2e-32 emb|AW694902|AW694902 NF081C08ST1F1065 Developing stem Medicago ... 88 1e-24 emb|AW754669|AW754669 PC04H09 Pine TriplEx pollen cone library P... 113 4e-24 emb|AW034884|AW034884 EST279113 tomato callus, TAMU Lycopersicon... 82 1e-14 emb|AW279551|AW279551 sf95a10.y1 Gm-c1019 Glycine max cDNA clone... 58 7e-14 35 gb U31932 NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 58 6e-11 emb|AW690084|AW690084 NF028B08ST1F1000 Developing stem Medicago ... 48 6e-09 emb|AI776947|AI776947 EST258047 tomato resistant, Cornell Lycope... 58 2e-07 emb|AJ007574|RCO7574 Ricinus communis mRNA for amino acid carrier. emb|AW306512|AW306512 se51h04.y1 Gm-c1017 Glycine max cDNA clone... 54 4e-06 40 emb|AJ132228|RCO132228 Ricinus communis mRNA for amino acid carr... 48 5e-06 emb|Y09825|STAAP1 S.tuberosum mRNA for amino acid transporter AA... 48 7e-06 emb|AJ004959|CAA004959 Cicer arietinum mRNA for hypothetical pro... 52 9e-06 emb|AF080542|AF080542 Nepenthes alata amino acid transporter (AA... 47 2e-05 emb|AW164093|AW164093 Ljirnpest19-543-g11 Ljirnp Lambda HybriZap... 50 Se-05 45 emb|AW309945|AW309945 sf27a03.x1 Gm-c1028 Glycine max cDNA clone... 50 5e-05 emb|AF080544|AF080544 Nepenthes alata amino acid transporter (AA... 45 6e-05 gb|U64823|NSU64823 Nicotiana sylvestris amino acid permease (nsa... 50 6e-05 emb|AJ238635|CPR238635 Chlorella protothecoides partial mRNA for... 49 1e-04 emb|AI974813|AI974813 T113295e KV2 Medicago truncatula cDNA clon... 49 1e-04 50 emb|AI773761|AI773761 EST254861 tomato resistant, Cornell Lycope... 48 2e-04 emb|AW736648|AW736648 EST333140 KV3 Medicago truncatula cDNA clo... 47 3e-04 emb|AW255060|AW255060 ML1355 peppermint glandular trichome Menth... 40 4e-04 emb[Y09591|VFAMACTRA V.faba mRNA for amino acid transporter. emb|AI441371|AI441371 sa64f02.yl Gm-c1004 Glycine max cDNA clone... 46 6e-04 55 emb|AW396191|AW396191 sh02e09.y1 Gm-c1026 Glycine max cDNA clone... 46 6e-04 emb|AW395873|AW395873 sh01d01.y1 Gm-c1026 Glycine max cDNA clone... 37 0.003 emb|AI166826|AI166826 xylem.est.62 Poplar xylem Lambda ZAPII lib... 44 0.003 emb|AW830239|AW830239 sm24g01.yl Gm-c1028 Glycine max cDNA clone... 44 0.004 emb[AF074703]AF074703 Glycine max pA381 marker, sequence tagged ... 43 0.005 60 emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 43 0.005

gb[BE022301]BE022301 sm73b09.yl Gm-c1028 Glycine max cDNA clone ... 43 0.007

PCT/US01/28506 WO 02/22675

	emb AW102174 AW102174 sd84c08.yl Gm-c1009 Glycine max cDNA clone 42 0.010 emb AI166882 AI166882 xylem.est.670 Poplar xylem Lambda ZAPII li 41 0.019 emb Y09826 STAAP2 S.tuberosum mRNA for amino acid transporter AA 36 0.020
5	emb AW307208 AW307208 sf54b08.y1 Gm-c1009 Glycine max cDNA clone 41 0.026
3	emb AF080543 AF080543 Nepenthes alata amino acid transporter (AA 40 0.049 emb AW096758 AW096758 EST289938 tomato mixed elicitor, BTI Lycop 40 0.068
	emb AI727855 AI727855 BNLGHi9274 Six-day Cotton fiber Gossypium 29 0.17
	emb AI487167 AI487167 EST245489 tomato ovary, TAMU Lycopersicon 38 0.18
	emb AW649763 AW649763 EST328217 tomato germinating seedlings, TA 38 0.18
10	emb AW310916 AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone 38 0.24
	emb AJ400848 SOL400848 Spinacia oleracea complete chloroplast ge 37 0.46
	emb AW203255 AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone 36 0.63
	emb AI778004 AI778004 EST258883 tomato susceptible, Cornell Lyco 36 0.86
	emb AW649841 AW649841 EST328295 tomato germinating seedlings, TA 36 0.86
15	emb AF061435 AF061435 Vicia faba amino acid transporter b (AAPB) 35 1.2
	emb AQ492251 AQ492251 V109G12 mTn-3xHA/lacZ Insertion Library Sa 35 1.2
	emb AI779305 AI779305 EST260184 tomato susceptible, Cornell Lyco 35 1.2
	emb AI779304 AI779304 EST260183 tomato susceptible, Cornell Lyco 35 1.2
••	emb AW982545 AW982545 HVSMEg0003I22f Hordeum vulgare pre-anthesi 29 1.4
20	emb AQ874703 AQ874703 V113C6 mTn-3xHA/lacZ Insertion Library, st 35 1.6
	emb AV428014 AV428014 AV428014 Lotus japonicus young plants (two 35 1.6
	emb AI856198 AI856198 sb39a11.x1 Gm-c1014 Glycine max cDNA clone 35 1.6
	gb L28920 YSCCHR1RAA Saccharomyces cerevisiae chromosome I right 35 2.2
25	emb AQ874913 AQ874913 V118E8 mTn-3xHA/lacZ Insertion Library, st 35 2.2 emb AF061434 AF061434 Vicia faba amino acid transporter a (AAPA) 35 2.2
23	emb AF061434 AF061434 Vicia faba amino acid transporter a (AAPA) 35 2.2 emb AQ876251 AQ876251 V153B8 mTn-3xHA/lacZ Insertion Library, st 35 2.2
	emb AQ874228 AQ874228 V105B1 mTn-3xHA/lacZ Insertion Library, st 35 2.2
	emb X74552 SCSWH1 S.cerevisiae SWH1 gene. 35 2.2
	emb AQ876104 AQ876104 V133C7 mTn-3xHA/lacZ Insertion Library, st 35 2.2
30	emb AQ876111 AQ876111 V133D2 mTn-3xHA/lacZ Insertion Library, st 35 2.2
	emb AQ875710 AQ875710 V128E8 mTn-3xHA/lacZ Insertion Library, st 35 2.2
	emb AW092708 AW092708 EST285888 tomato mixed elicitor, BTI Lycop 34 3.1
	emb AI938816 AI938816 sc60f01.yl Gm-c1016 Glycine max cDNA clone 34 4.2
	emb AW704460 AW704460 sk53c11.yl Gm-c1019 Glycine max cDNA clone 34 4.2
35	emb AI965655 AI965655 sc75b03.yl Gm-c1018 Glycine max cDNA clone 34 4.2
	emb AW010573 AW010573 ST08D02 Pine TriplEx shoot tip library Pin 34 4.2
	emb AJ277985 NTA277985 Nicotiana tabacum drepp1 gene, exons 1-4. 33 5.8
	emb AL049559 SPCC1450 S.pombe chromosome III cosmid c1450. 33 8.0
40	emb Z72791 SCYGR006W S.cerevisiae chromosome VII reading frame O 33 8.0 emb Z34930 TV18SRRN T.violaceum (var. violaceum) gene for 18S rRNA. 33 8.0
TU	emb Z34930 TV18SRRN T.violaceum (var. violaceum) gene for 18S rRNA. 33 8.0 gb U42663 TGU42663 Tuber gibbosum 18S small subunit ribosomal RN 33 8.0
	emb AQ940191 AQ940191 Sheared DNA-42C20.TF Sheared DNA Trypanoso 33 8.0
	emb AA274279 AA274279 TgESTzz24b06.s1 TgME49 invivo Bradyzoite c 33 8.0
	emb AU006886 AU006886 AU006886 Schizosaccharomyces pombe late lo 33 8.0
45	emb AW926892 AW926892 HVSMEg0008N19 Hordeum vulgare pre-anthesis 33 8.0
	dbj D64123 D64123 Fibulobasidium inconspicuum DNA for small subu 33 8.0
· ·	
	Query= AC002335.160_at 19171_at /id_source genbank /description
50	gb aab64325.1 (ac002335) putative trypsin inhibitor [arabidopsis
	thaliana] /blast_score 7.00e-40 /ec_number /family /chip nova
	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac002335 /ncgi
55	http://www.ncgr.org/cgi-bin/ff?ac002335
55	(449 letters)
	Database: plantfingel
	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	001,010 sequences, 420,114,510 total fellets
60	Searchingdone

Searching.....done

Score Ε

Sequences producing significant alignments: (bits) Value emb|Y16190|SAMTI2 Sinapsis alba mRNA for trypsin inhibitor 2. 161 2e-39 5 emb|X84208|SSAMTI2 Sinapis alba mti-2 gene for trypsin inhibitor 2. 161 3e-39 emb|AT002119|AT002119 AT002119 Flower bud cDNA Brassica rapa sub... 72 5e-14 gb|L33539|L33539 BNAESTF178 Mustard flower buds Brassica rapa cD... 72 6e-14 emb|AF025857|AF025857 Aegilops caudata RAPD marker generated by ... 36 0.18 emb|AI065316|AI065316 TENU2203 T. cruzi epimastigote normalized ... 31 0.42 emb|AF066077|AF066077 Helianthus annuus RPL5A-related protein (R... 34 0.89 10 emb|AL356173|NCB14D6 Neurospora crassa DNA linkage group II BAC ... 34 0.89 emb|AF242188|AF242188 Plasmodium falciparum membrane protein Pf1... 34 0.89 gb|M28889|PFAMEM12A P.falciparum membrane protein Pf12 gene, com... 34 0.89 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 33 1.2 15 gb|U47092|U47092 DCU47092 Carrot somatic embryos Daucus carota c... 33 1.2 emb|AL354533|LMFL6294 Leishmania major Friedlin chromosome 21 co... 33 1.2 emb|AW278233|AW278233 sf41d09.y1 Gm-c1009 Glycine max cDNA clone... 33 1.2 emb|AQ849793|AQ849793 LMAJFVI_lm49f04.x1 Leishmania major FV1 ra... 33 1.2 gb|U91982|SHU91982 Stylosanthes hamata EREBP-3 homolog mRNA, com... 33 1.7 20 emb|AW727560|AW727560 GA_Ea0012P04 Gossypium arboreum 7-10 dpa ... 33 1.7 emb|AQ848503|AQ848503 LMAJFV1 lm10a08.x1 Leishmania major FV1 ra... 33 1.7 emb|AW668496|AW668496 GA_Ea0014C23 Gossypium arboreum 7-10 dpa ... 33 1.7 emb|AL136236|SPAPJ696 S.pombe chromosome I PCR product p696. emb|AL133359|SPAP696 S.pombe chromosome I PCR product p696. 25 emb|AW099428|AW099428 sd40c12.yl Gm-c1016 Glycine max cDNA clone... 32 2.3 emb|AV389315|AV389315 AV389315 Chlamydomonas reinhardtii C9 Chla... 32 2.3 emb|AW707869|AW707869 832013D08.y1 C. reinhardtii CC-125 nutrien... 32 2.3 emb|AC068564|AC068564 Filobasidiella neoformans var. neoformans,... 32 3.2 30 emb Z38058 LMCLPB L.major (MHOM/SU/5ASKH) DNA for 100 kDa heat s... 32 3.2 emb|AW932211|AW932211 EST358054 tomato fruit mature green, TAMU ... 32 3.2 emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 32 3.2 emb|AQ445563|AQ445563 GSSTc0014 Trypanosoma cruzi random genomic... 32 3.2 emb|AF263283|AF263283 Filobasidiella neoformans var. neoformans ... 32 3.2 35 emb|X95256|HVXYLISOG H.vulgare xylose isomerase gene. emb|AW217087|AW217087 EST295801 tomato callus, TAMU Lycopersicon... 32 3.2 emb|X62675|TRMINEX5S T.rangeli DNA for mini-exon and 5S rRNA. emb|AW745480|AW745480 WS1_35_H03.b1_A002 Water-stressed 1 (WS1) ... 31 4.4 emb|AW705201|AW705201 sk43a03.yl Gm-c1019 Glycine max cDNA clone... 31 4.4 40 emb|AI496396|AI496396 sb04b11.yl Gm-c1004 Glycine max cDNA clone... 31 4.4 emb|AW694532|AW694532 NF077E02ST1F1017 Developing stem Medicago ... 31 4.4 emb|AW598155|AW598155 sj89b07.yl Gm-c1034 Glycine max cDNA clone... 31 4.4 emb|AW508121|AW508121 si51a09.yl Gm-r1030 Glycine max cDNA clone... 31 4.4 emb|AW317929|AW317929 sg59a02.yl Gm-c1007 Glycine max cDNA clone... 31 4.4 45 emb|AW185756|AW185756 se59c04.yl Gm-c1019 Glycine max cDNA clone... 31 4.4 emb|AW119645|AW119645 sd50d05.yl Gm-c1016 Glycine max cDNA clone... 31 4.4 emb|AI522947|AI522947 sa92d09.y1 Gm-c1004 Glycine max cDNA clone... 31 4.4 gb|L38627|GYNRGNA Gymnodinium catenatum 24S ribosomal RNA (24S r... 31 4.4

emb|AW926726|AW926726 HVSMEg0007P17 Hordeum vulgare pre-anthesis... 31 4.4 50 emb|AW307483|AW307483 sf57e09.y1 Gm-c1009 Glycine max cDNA clone... 31 4.4 emb|AW307220|AW307220 sf54c09.yl Gm-c1009 Glycine max cDNA clone... 31 4.4 emb|AI437852|AI437852 sa40e07.yl Gm-c1004 Glycine max cDNA clone... 31 4.4 emb|AW733531|AW733531 sk74g09.yl Gm-c1016 Glycine max cDNA clone... 31 4.4 emb|AW186505|AW186505 se68f10.yl Gm-c1019 Glycine max cDNA clone... 31 4.4 55 emb|AW099682|AW099682 sd29g03.y2 Gm-c1012 Glycine max cDNA clone... 31 4.4 emb|AW761228|AW761228 sl64h04.yl Gm-c1027 Glycine max cDNA clone... 31 4.4 emb|AI900314|AI900314 sc03h10.yl Gm-c1012 Glycine max cDNA clone... 31 4.4 emb|AF031065|AF031065 Dipsacomyces acuminosporus 28S ribosomal R... 31 4.4 emb|AW099689|AW099689 sd29h03.y2 Gm-c1012 Glycine max cDNA clone... 31 4.4 60 emb|AI494951|AI494951 sa93a10.yl Gm-c1004 Glycine max cDNA clone... 31 4.4 emb|AI988406|AI988406 sd01f04.yl Gm-c1020 Glycine max cDNA clone... 31 4.4 401

5	emb AW782121 AW782121 sm01g01.y1 Gm-c1027 Glycine max cDNA clone 31 4.4 emb AW100084 AW100084 sd20b03.y2 Gm-c1012 Glycine max cDNA clone 31 4.4 emb AI939026 AI939026 sc64f02.y1 Gm-c1016 Glycine max cDNA clone 31 4.4 emb AI736322 AI736322 sb27a03.y1 Gm-c1009 Glycine max cDNA clone 31 4.4 emb AI965890 AI965890 sc79c09.y1 Gm-c1018 Glycine max cDNA clone 31 4.4 emb AI901200 AI901200 sc22a07.y1 Gm-c1013 Glycine max cDNA clone 31 4.4 emb AI736604 AI736604 sb31b04.y1 Gm-c1012 Glycine max cDNA clone 31 4.4 emb AW666300 AW666300 sk34h06.y1 Gm-c1028 Glycine max cDNA clone 31 6.0
10	emb AW831353 AW831353 sm32e10.y1 Gm-c1028 Glycine max cDNA clone 31 6.0 gb L37877 CPCRPL27P Cryptococcus neoformans ribosomal protein L2 31 6.0 emb Z75290 SCYOR382W S.cerevisiae chromosome XV reading frame OR 31 6.0 emb AQ850290 AQ850290 LMAJFV1_lm28c06.x1 Leishmania major FV1 ra 31 6.0 gb L26508 CPCAAA Filobasidiella neoformans CAP59 gene, complete 31 6.0 emb AQ847349 AQ847349 LMAJFV1_lm30a04.x1 Leishmania major FV1 ra 31 6.0
15	emb AC008241 AC008241 Leishmania major clone L952b strain Friedl 31 6.0 emb AW667667 AW667667 GA_Ea0010C24 Gossypium arboreum 7-10 dpa 31 6.0 emb AF031066 AF031066 Martensiomyces pterosporus 28S ribosomal R 31 6.0 emb AQ398504 AQ398504 mgxb0019M20f CUGI Rice Blast BAC Library P 31 6.0 emb AZ215468 AZ215468 Sheared DNA-79C4.TF Sheared DNA Trypanosom 25 7.1
20	dbj D50617 YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp 30 8.3 dbj D44598 YSCF4121F Saccharomyces cerevisiae chromosome VI phag 30 8.3 dbj D87895 D87895 Aspergillus nidulans chiA gene for chitinase, 30 8.3 emb AQ162420 AQ162420 mgxb0012N11r CUGI Rice Blast BAC Library P 30 8.3
25	gb BE036961 BE036961 MP09G07 MP Mesembryanthemum crystallinum cD 30 8.3 emb AW101721 AW101721 sd69c10.y1 Gm-c1008 Glycine max cDNA clone 30 8.3 emb AW980894 AW980894 EST392047 GVN Medicago truncatula cDNA clo 30 8.3 emb AQ447068 AQ447068 mgxb0004O05f CUGI Rice Blast BAC Library P 30 8.3 emb AW727134 AW727134 GA_Ea0023J07 Gossypium arboreum 7-10 dpa 26 8.7
30	gb BE053868 BE053868 GA_Ea0013O20f Gossypium arboreum 7-10 dpa 27 8.9
35	Query= X99923.1_at 19177_at /id_source genbank /description emb caa68191.1 (x99923) male sterility 2-like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb x99923 /ncgi http://www.ncgr.org/cgi-bin/ff?x99923 (1710 letters)
40	Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
45	Score E Sequences producing significant alignments: (bits) Value
50	emb AF149917 AF149917 Simmondsia chinensis acyl CoA reductase mR 158 e-144 emb X99922 BNMS2PROT B.napus mRNA for male sterility protein 2. 137 2e-74 emb A45743 A45743 Sequence 22 from Patent WO9520668. 137 2e-74 emb AW615992 AW615992 EST325442 tomato flower buds 0-3 mm, Corne 277 2e-73 emb AI730540 AI730540 BNLGHi7015 Six-day Cotton fiber Gossypium 153 4e-59
55	emb AW738637 AW738637 EST340064 tomato flower buds, anthesis, Co 158 3e-51 emb AW931162 AW931162 EST357005 tomato fruit mature green, TAMU 201 1e-50 emb AW616784 AW616784 EST323195 L. hirsutum trichome, Cornell Un 200 3e-50 emb AW308800 AW308800 sf72b03.yl Gm-c1013 Glycine max cDNA clone 141 7e-50 emb AW278653 AW278653 sf63e03.yl Gm-c1013 Glycine max cDNA clone 110 1e-46
60 _.	emb AI727421 AI727421 BNLGHi7945 Six-day Cotton fiber Gossypium 106 3e-46 emb AI901240 AI901240 sc22e07.y1 Gm-c1013 Glycine max cDNA clone 166 3e-40 emb AW306151 AW306151 se46e08.y1 Gm-c1017 Glycine max cDNA clone 145 2e-39 emb AW688482 AW688482 NF008B06ST1F1000 Developing stem Medicago 127 6e-38

```
emb|AW648210|AW648210 EST326664 tomato germinating seedlings, TA... 107 1e-37
      emb|AW279265|AW279265 sf68h11.yl Gm-c1013 Glycine max cDNA clone... 123 3e-37
      emb|AW671408|AW671408 LG1 343 A01.b1 A002 Light Grown 1 (LG1) So... 156 4e-37
      emb|AW306626|AW306626 se53c07.yl Gm-c1017 Glycine max cDNA clone... 145 5e-37
      emb|AW624291|AW624291 EST322152 tomato flower buds 3-8 mm, Corne... 121 1e-32
      emblAW688474|AW688474 NF008A09ST1F1000 Developing stem Medicago ... 106 5e-31
      emb|AW781535|AW781535 sl81d04.yl Gm-c1037 Glycine max cDNA clone... 109 7e-30
      emb|AW622996|AW622996 EST320941 tomato flower buds 3-8 mm, Corne... 128 1e-28
      emb|AI055562|AI055562 coau0004F11 Cotton Boll Abscission Zone cD... 98 1e-27
10
      emb|AW287082|AW287082 LG1_265_C07.b2_A002 Light Grown 1 (LG1) So... 119 7e-26
      emb|AW691252|AW691252 NF042F05ST1F1000 Developing stem Medicago ... 100 3e-25
      emb|AW649410|AW649410 EST327864 tomato germinating seedlings, TA... 115 1e-24
      emb|AW705269|AW705269 sk59a03.yl Gm-c1019 Glycine max cDNA clone... 70 3e-18
      emb|AW217786|AW217786 EST296500 tomato flower buds 8 mm to pre-a... 92 6e-18
15
      emb|AW217788|AW217788 EST296502 tomato flower buds 8 mm to pre-a... 91 8e-18
      emb|AW217787|AW217787 EST296501 tomato flower buds 8 mm to pre-a... 91 3e-17
      emb|AW928598|AW928598 EST337386 tomato flower buds 8 mm to pre-a... 86 1e-16
      emb|Z11889|MITTARRNG T.aestivum mitochondrion rrn26 gene for rRN... 88 2e-16
      emb|AW565061|AW565061 LG1_320_C11.b1_A002 Light Grown 1 (LG1) So... 78 2e-13
20
      emb|AW980920|AW980920 EST392073 GVN Medicago truncatula cDNA clo... 50 3e-13
      emb|AV428628|AV428628 AV428628 Lotus japonicus young plants (two... 71 2e-11
      emb|AV419850|AV419850 AV419850 Lotus japonicus young plants (two... 68 2e-10
      emb|AF076792|AF076792 Irvingia gabonensis clone BM35, genomic su... 51 2e-08
      emb|AW056631|AW056631 ST53H08 Pine TriplEx shoot tip library Pin... 36 7e-05
25
      emb|AW289724|AW289724 NXNV005H02F Nsf Xylem Normal wood Vertical... 48 2e-04
      gb|BE057395|BE057395 sn02f06.yl Gm-c1015 Glycine max cDNA clone ... 44 2e-04
      emb|AZ050471|AZ050471 GSSTc11316 Trypanosoma cruzi random genomi... 48 2e-04
      emb|AW758790|AW758790 NXNV 089 G03 F Nsf Xylem Normal wood Verti... 47 5e-04
      emb|AA952454|AA952454 TENS1392 T. cruzi epimastigote normalized ... 46 0.001
30
      emblAQ361876|AQ361876 mgxb0005G07r CUGI Rice Blast BAC Library P... 42 0.015
      emb|AI069380|AI069380 mgae0006dC11f Magnaporthe grisea Appressor... 42 0.015
      emb|AW649203|AW649203 EST327657 tomato germinating seedlings, TA... 41 0.021
      emb|Y13967|PCLYS2 Penicillium chrysogenum lys2 gene.
                                                                  41 0.021
      emb|AW929360|AW929360 EST338148 tomato flower buds 8 mm to pre-a... 40 0.074
35
      emb|AW564691|AW564691 LG1 _300_C05.b1 _ A002 Light Grown 1 (LG1) So... 37 0.50
      emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 37 0.50
      gb|BE033566|BE033566 MF03E04 MF Mesembryanthemum crystallinum cD... 36 0.69
      emb|AI488290|AI488290 EST246612 tomato ovary, TAMU Lycopersicon ... 36 0.94
      emb|AW932683|AW932683 EST358526 tomato fruit mature green, TAMU ... 36 0.94
40
      emb|AW932440|AW932440 EST358283 tomato fruit mature green, TAMU ... 36 0.94
      emb|AQ874417|AQ874417 V108D3 mTn-3xHA/lacZ Insertion Library, st... 35 1.3
      emb|AF156928|AF156928 Candida albicans folylpolyglutamate synthe... 28 1.4
      emb|AW720470|AW720470 LjNEST19f2r Lotus japonicus nodule library... 35 1.8
      emblAW397976|AW397976 sg70f10.yl Gm-c1007 Glycine max cDNA clone... 35 1.8
45
      emb|AV409049|AV409049 AV409049 Lotus japonicus young plants (two... 35 1.8
      emb|AL353821|NC68B2 Neurospora crassa DNA linkage group V Cosmid... 35 2.4
      emb|AW775233|AW775233 EST331955 GVN Medicago truncatula cDNA clo... 35 2.4
      emb|AW694088|AW694088 NF072C08ST1F1065 Developing stem Medicago ... 35 2.4
      emb|AW693849|AW693849 NF069G11ST1F1087 Developing stem Medicago ... 35 2.4
50
      emb|AW694067|AW694067 NF072D11ST1F1093 Developing stem Medicago ... 35 2.4
      emb|AW773778|AW773778 EST332764 KV3 Medicago truncatula cDNA clo... 35 2.4
      emb|AW774799|AW774799 EST333950 KV3 Medicago truncatula cDNA clo... 35 2.4
      emb|AW774591|AW774591 EST333742 KV3 Medicago truncatula cDNA clo... 35 2.4
      emb|AW689574|AW689574 NF021H08ST1F1000 Developing stem Medicago ... 35 2.4
55
      emb|AW694736|AW694736 NF079D09ST1F1077 Developing stem Medicago ... 35 2.4
      emb|AI075585|AI075585 TENU3007 T. cruzi epimastigote normalized ... 35 2.4
      emb|AW691920|AW691920 NF050F11ST1F1000 Developing stem Medicago ... 35 2.4
      emb|AW690529|AW690529 NF035F03ST1F1000 Developing stem Medicago ... 35 2.4
      emb|AA660549|AA660549 00435 MtRHE Medicago truncatula cDNA 5' si... 35 2.4
60
      emb|AQ841091|AQ841091 T132045b Medicago truncatula BAC library M... 35 2.4
      emb|AW695358|AW695358 NF093H05ST1F1047 Developing stem Medicago ... 35 2.4
```

-----PCT/US01/28506

emb|AW299108|AW299108 EST305782 KV2 Medicago truncatula cDNA clo... 35 2.4 gb[U46545]HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 34 3.4 emb|AW309167|AW309167 sg05b03.y1 Gm-c1019 Glycine max cDNA clone... 34 3.4 emb|AW234839|AW234839 sf19g08.yl Gm-c1028 Glycine max cDNA clone... 34 3.4 5 emb|AI960722|AI960722 sc89e06.y1 Gm-c1019 Glycine max cDNA clone... 34 3.4 emb|AF233374|AF233374 Volvox carteri argininosuccinate lyase (VA... 34 4.6 emb|AW925731|AW925731 HVSMEg0005F22 Hordeum vulgare pre-anthesis... 34 4.6 emb|AI213767|AI213767 z5b08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.6 10 gb|U58133|CAU58133 Candida albicans alpha-aminoadipate reductase... 26 6.1 emb|AW686938|AW686938 NF004C01RT1F1004 Developing root Medicago ... 33 6.3 emb|Z46881|SC3299 S.cerevisiae chromosome IX cosmid 3299. 33 6.3 emb|AV391768|AV391768 AV391768 Chlamydomonas reinhardtii C9 Chla... 33 6.3 emb|AW933793|AW933793 EST359636 tomato fruit mature green, TAMU ... 33 6.3 15 emb|AW618444|AW618444 EST320430 L. pennellii trichome, Cornell U... 33 6.3 emb|AF082993|AF082993 Cryptosporidium parvum type I fatty acid s... 33 6.3 emb|AZ220106|AZ220106 Sheared DNA-63H10.TR Sheared DNA Trypanoso... 33 6.3 emb|AF072272|AF072272 Lactuca sativa resistance protein candidat... 33 6.3 20 emb|AB012945|AB012945 Aspergillus oryzae gene for amyRp, complet... 33 8.7 emb|AF180560|AF180560 Emericella nidulans sgdA gene, partial seq... 33 8.7 dbi|D29761|YSACSII Candida maltosa gene for chitin synthase 2, p... 33 8.7 emb|AJ273086|AJ273086 AJ273086 Metarhizium anisopliae ARSEF 2575... dbj|E12507|E12507 Promoter region of the agdA gene. 33 8.7 25 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... Query= AL031804.245 at 19182 at /id source genbank /description emb|caa21214.1| (al031804) putative protein [arabidopsis thaliana] 30 /blast score 0 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|al031804| /ncgi http://www.ncgr.org/cgi-bin/ff?al031804 (1467 letters) 35 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 40 E Score Sequences producing significant alignments: (bits) Value emb|AI894665|AI894665 EST264108 tomato callus, TAMU Lycopersicon... 341 6e-93 45 emb|AW032812|AW032812 EST276371 tomato callus, TAMU Lycopersicon... 325 5e-88 emb[AW035000]AW035000 EST279229 tomato callus, TAMU Lycopersicon... 297 2e-79 emb|AI896184|AI896184 EST265627 tomato callus, TAMU Lycopersicon... 282 5e-75 emb|AI896887|AI896887 EST266330 tomato callus, TAMU Lycopersicon... 178 1e-72 emb[AW030421]AW030421 EST273676 tomato callus, TAMU Lycopersicon... 254 1e-66 50 gb|BE059595|BE059595 sn34c09.y1 Gm-c1016 Glycine max cDNA clone ... 177 2e-43 emb|AW234683|AW234683 sf18a11.y1 Gm-c1028 Glycine max cDNA clone... 166 4e-40 emb|AW687734|AW687734 NF012H03RT1F1031 Developing root Medicago ... 105 7e-39 emb|AI728318|AI728318 BNLGHi10452 Six-day Cotton fiber Gossypium... 154 2e-36 emb|AT000486|AT000486 AT000486 Brassica rapa guard cell Brassica... 92 1e-32 55 emb|AI487311|AI487311 EST245633 tomato ovary, TAMU Lycopersicon ... 79 2e-30 emb|AW220379|AW220379 EST302862 tomato root during/after fruit s... 133 2e-30 emb|AI166722|AI166722 xylem.est.526 Poplar xylem Lambda ZAPII li... 103 3e-29 emb|AW830251|AW830251 sm33a02.y1 Gm-c1028 Glycine max cDNA clone... 128 8e-29

emb|AW777089|AW777089 M110842e GVSN Medicago truncatula cDNA clo... 126 5e-28

emb|AT000492|AT000492 AT000492 Brassica rapa guard cell Brassica... 92 6e-28 emb|AI895477|AI895477 EST264920 tomato callus, TAMU Lycopersicon... 125 1e-27

60

--WO 02/22675 -- PCT/US01/28506

	emb AV409317 AV409317 AV409317 Lotus japonicus young plants (two 123 4e-27
	emb AI487156 AI487156 EST245478 tomato ovary, TAMU Lycopersicon 80 1e-25
	ombla VIA 708 I A
	emb AV427085 AV427085 AV427085 Lotus japonicus young plants (two 111 1e-23
_	emb AT000641 AT000641 AT000641 Brassica rapa guard cell Brassica 110 3e-23
5	emb AW685452 AW685452 NF029F12NR1F1000 Nodulated root Medicago t 104 2e-21
٠.,	emb AW719903 AW719903 LjNEST11g5r Lotus japonicus nodule library 77 2e-21
	emb AI966612 AI966612 sc53d04.y1 Gm-c1015 Glycine max cDNA clone 86 3e-19
	emb AW647985 AW647985 EST326439 tomato germinating seedlings, TA 95 9e-19
	emb AI966597 AI966597 sc52h04.y1 Gm-c1015 Glycine max cDNA clone 82 5e-18
10	emb AW278350 AW278350 sf43a03.y1 Gm-c1009 Glycine max cDNA clone 90 3e-17
10	emb AW687571 AW687571 NF011A10RT1F1072 Developing root Medicago 90 3e-17
	emb AT000935 AT000935 AT000935 Brassica rapa guard cell Brassica 89 1e-16
	emb AW684018 AW684018 NF011C08NR1F1000 Nodulated root Medicago t 68 6e-16
	gb BE059565 BE059565 sn33g08.yl Gm-c1016 Glycine max cDNA clone 78 3e-15
15	emb AW934333 AW934333 EST360176 tomato fruit mature green, TAMU 84 4e-15
	emb AI781643 AI781643 EST262522 tomato susceptible, Cornell Lyco 84 4e-15
	emb AW699630 AW699630 gb29d11.yl Moss EST library PPN Physcomitr 83 7e-15
	emb AW686556 AW686556 NF039E01NR1F1000 Nodulated root Medicago t 81 2e-14
	emb AI736754 AI736754 sb33a10.y1 Gm-c1012 Glycine max cDNA clone 68 6e-14
20	
	emb AW687218 AW687218 NF007C06RT1F1049 Developing root Medicago 78 2e-13
	emb AI496521 AI496521 sb08h01.yl Gm-c1004 Glycine max cDNA clone 76 8e-13
	emb AQ448299 AQ448299 mgxb0020C15f CUGI Rice Blast BAC Library P 75 1e-12
	emb AI731601 AI731601 BNLGHi10195 Six-day Cotton fiber Gossypium 70 5e-11
	emb AW719552 AW719552 LjNEST6b3r Lotus japonicus nodule library, 64 4e-10
25	emb AI485751 AI485751 EST244072 tomato ovary, TAMU Lycopersicon 64 2e-09
	emb AL113765 CNS01B4D Botrytis cinerea strain T4 cDNA library un 62 8e-09
	emb AW671559 AW671559 LG1 348 E04.b1 A002 Light Grown 1 (LG1) So 62 1e-08
	emb AI484941 AI484941 EST243204 tomato ovary, TAMU Lycopersicon 60 5e-08
	emb A1486383 A1486383 EST244704 tomato ovary, TAMU Lycopersicon 58 2e-07
30	emb AW564851 AW564851 LG1_310_D10.b1 A002 Light Grown 1 (LG1) So 54 2e-06
טט	- EMDIA WOD4XO DA WOD4XO ELLO ESTE SUL ESTE DE LA CONTENTA DE LA COLOR DE SA PA-ON
-	
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024
35	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 gb M27164 TRBPOLI Trypanosoma brucei RNA polymerase I largest su 37 0.42
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 gb M27164 TRBPOLI Trypanosoma brucei RNA polymerase I largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58
35	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW98514 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79
	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW985394 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1
35	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW98514 AW985394 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1
35	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW985394 AW985394 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1
35	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AI328270 AI328270 a2b05ne.rl Neurospora crassa evening cDNA 35 2.1
35 40	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AI328270 AI328270 a2b05ne.rl Neurospora crassa evening cDNA 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8
35	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AI328270 AI328270 a2b05ne.rl Neurospora crassa evening cDNA 35 2.1
35 40	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AY931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5O22 Neurospora crassa DNA linkage group II BAC 34 3.9
35 40	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AY931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5O22 Neurospora crassa DNA linkage group II BAC 34 3.9
35 40	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AU355932 NCB5O22 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3
35 40	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AY931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AW283985 AW283985 LG1_264_D01.g1_A002 Light Grown 1 (LG1) So 33 5.3
35 40 45	emb AW703782 AW703782 sk12e01.y1 Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.y1 Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AY931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb AK9461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AW283985 AW283985 LG1_264_D01.g1_A002 Light Grown 1 (LG1) So 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3
35 40	emb AW703782 AW703782 sk12e01.y1 Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.y1 Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb AK93461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AK9461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AW283985 AW283985 LG1_264_D01.g1_A002 Light Grown 1 (LG1) So 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AK9461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AW283985 AW283985 LG1_264_D01.g1_A002 Light Grown 1 (LG1) So 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb Z36169 SCYBR300C S.cerevisiae chromosome II reading frame OR 33 5.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AW69451 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AW61229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AW283985 AW283985 LG1_264_D01.g1_A002 Light Grown 1 (LG1) So 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb AG655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AQ655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AQ655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb AU35932 NCB5022 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb AG655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AG655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AF107804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb A1960597 A1960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 gb M27164 TRBPOL1 Trypanosoma brucei RNA polymerase I largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb A1276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb AF107804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF107804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF007865 AC007865 Trypanosoma brucei chromosome II clone RPC 33 7.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86ft09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 gb M27164 TRBPOL1 Trypanosoma brucei RNA polymerase I largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF104916 AF104916 Chadida albicans protein mannosyltransfera 33 5.3 emb AF04916 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF07804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF07804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC 33 7.3 gb U13054 LEU13054 Lycopersicon esculentum endo-1,4-beta-glucana 33 7.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.b1_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb A1960597 A1960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 gb M27164 TRBPOL1 Trypanosoma brucei RNA polymerase I largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb A1276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb AF164200 AF164200 Trypanosoma brucei putative DNA replicatio 33 5.3 emb AF107804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF107804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF007865 AC007865 Trypanosoma brucei chromosome II clone RPC 33 7.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1_360_D10.bl_A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86ft09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 gb M27164 TRBPOL1 Trypanosoma brucei RNA polymerase I largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW461229 AW461229 NXNV052C08F Nsf Xylem Normal wood Vertical 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AF104916 AF104916 Chadida albicans protein mannosyltransfera 33 5.3 emb AF04916 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF07804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF07804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC 33 7.3 gb U13054 LEU13054 Lycopersicon esculentum endo-1,4-beta-glucana 33 7.3
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW981534 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AJ28270 AI328270
35 40 45	emb AW703782 AW703782 sk12e01.y1 Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.b1 A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-0 emb AU960597 AI960597 sc86f09.y1 Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW985394 AW985394 NXNV 134 H05 F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei RNA polymerase I largest su 37 0.42 emb AW401287 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AW931221 AW931221 EST357064 tomato fruit mature green, TAMU 34 2.8 emb X69461 HPURA3 H.polymorpha URA3 gene. 34 2.8 emb AL355932 NCB5022 Neurospora crassa DNA linkage group II BAC 34 3.9 emb AW283985 AW283985 LG1 264 D01.g1 A002 Light Grown 1 (LG1) So 33 5.3 emb AW283985 AW283985 LG1 264 D01.g1 A002 Light Grown 1 (LG1) So 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AG655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AG655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AG055061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 5.3 emb AF104916 AF107804 AF107804 Pleospora herbarum DNA-dependent RNA polym 33 5.3 emb AF104916 AF104916 Candida albicans protein mannosyltransfera 33 5.3 emb AG655061 AQ655061 Sheared DNA-27K12.TF Sheared DNA Trypanoso 33 7.3 emb AG647629 AQ647629 AQ647629 RPC193-EcoRI-6K22.TI RPC193-EcoRI Trypanoso 33 7.3 emb AQ647629 AQ647629 RPC193-EcoRI-6K22.TI RPC193-EcoRI Trypanoso 33 7.3 emb AQ660459
35 40 45	emb AW703782 AW703782 sk12e01.yl Gm-c1023 Glycine max cDNA clone 54 3e-06 emb AW672524 AW672524 LG1 360 D10.bl A002 Light Grown 1 (LG1) So 49 8e-05 emb AW348926 AW348926 GM210010A20D1R Gm-r1021 Glycine max cDNA 3 47 3e-04 emb AI960597 AI960597 sc86f09.yl Gm-c1018 Glycine max cDNA clone 41 0.024 emb AW985394 AW985394 NXNV_134_H05_F Nsf Xylem Normal wood Verti 39 0.12 emb X14399 TBRNPOL1 Trypanosoma brucei Trp11 gene for largest su 37 0.42 emb AW981534 AW401287 LamdiGest487est L.digitata gametophyte Lam 36 0.58 emb AJ276509 TAE276509 Triticum aestivum grp1 gene for glycine-r 36 0.79 emb AL133468 LMFL3238 Leishmania major Friedlin chromosome 19 co 35 1.1 emb AL353820 NC13E11 Neurospora crassa DNA linkage group V Cosmi 35 2.1 emb AQ947099 AQ947099 Sheared DNA-44E22.TF Sheared DNA Trypanoso 35 2.1 emb AJ28270 AI328270

emb|AZ217295|AZ217295 Sheared DNA-112B7.TF Sheared DNA Trypanoso... 33 7.3 emb|AW287840|AW287840 N100683e rootphos(-) Medicago truncatula c... 33 7.3

Query= AC003027.39_at 19229_at /id_source genbank /description gb|aad10694.1| (ac003027) lcl|prt_seq no definition line found [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003027| /ncgi http://www.ncgr.org/cgi-bin/ff?ac003027 (1743 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E Sequences producing significant alignments: (bits) Value 20 emblAW218224|AW218224 EST303405 tomato radicle, 5 d post-imbibit... 270 4e-81 emb|AW775278|AW775278 EST334343 DSIL Medicago truncatula cDNA cl... 276 6e-80 emb|AW443927|AW443927 EST308857 tomato mixed elicitor, BTI Lycop... 225 3e-78 emb|AW560040|AW560040 EST315088 DSIR Medicago truncatula cDNA cl... 276 1e-77 25 emb|AW560039|AW560039 EST315087 DSIR Medicago truncatula cDNA cl... 276 3e-73 gb|BE033452|BE033452 ME02B10 ME Mesembryanthemum crystallinum cD... 264 2e-72 emb|AI487716|AI487716 EST246038 tomato ovary, TAMU Lycopersicon ... 271 1e-71 emb|AI486962|AI486962 EST245284 tomato ovary, TAMU Lycopersicon ... 269 4e-71 emb|AW441974|AW441974 EST311370 tomato fruit red ripe, TAMU Lyco... 242 8e-71 30 emb|AW099977|AW099977 sd19c07.y2 Gm-c1012 Glycine max cDNA clone... 253 7e-69 emb[AW733661]AW733661 sk83d11.y1 Gm-c1016 Glycine max cDNA clone... 223 4e-65 emb|AW164658|AW164658 se75h05.y1 Gm-c1023 Glycine max cDNA clone... 162 1e-64 emb|AW689466|AW689466 NF019F01ST1F1000 Developing stem Medicago ... 159 1e-62 emb|AI441647|AI441647 sa65a03.yl Gm-c1004 Glycine max cDNA clone... 212 9e-58 35 emb|AI729737|AI729737 BNLGHi14077 Six-day Cotton fiber Gossypium... 128 7e-55 emb|AI771313|AI771313 EST252329 tomato ovary, TAMU Lycopersicon ... 137 3e-46 emb|AW033056|AW033056 EST276615 tomato callus, TAMU Lycopersicon... 177 3e-43 emb|AW623019|AW623019 EST320964 tomato flower buds 3-8 mm, Corne... 76 2e-41 emb|AI728350|AI728350 BNLGHi10536 Six-day Cotton fiber Gossypium... 76 5e-40 40 emb[AW922217]AW922217 DG1 17 D01.b1 A002 Dark Grown 1 (DG1) Sorg... 162 6e-39 emb|AI731527|AI731527 BNLGHi9654 Six-day Cotton fiber Gossypium ... 158 1e-37 gb|BE056576|BE056576 894010C07.yl C. reinhardtii CC-1690, normal... 129 9e-36 emb|AI165184|AI165184 A077p80u Hybrid aspen plasmid library Popu... 142 1e-32 emb|Z98600|SPAC20G4 S.pombe chromosome I cosmid c20G4. 45 emb|AW056437|AW056437 ST51H06 Pine TriplEx shoot tip library Pin... 68 4e-27 gb|BE020433|BE020433 sm40f12.yl Gm-c1028 Glycine max cDNA clone ... 65 1e-26 gb|BE053819|BE053819 GA_Ea0035C17f Gossypium arboreum 7-10 dpa ... 74 9e-26 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... 113 5e-24 50 dbj|D44595|YSCF6781C Saccharomyces cerevisiae chromosome VI phag... 113 5e-24 emb|AA520817|AA520817 TgESTzz64d12.rl TgME49 invivo Bradyzoite c... 80 1e-23 emb|AW683126|AW683126 NF007H02LF1F1026 Developing leaf Medicago ... 66 2e-21 emb|AW564299|AW564299 LG1_289_C04.b1_A002 Light Grown 1 (LG1) So... 47 4e-21 emb|AW745946|AW745946 WS1_38_H09.b1_A002 Water-stressed 1 (WS1) ... 57 9e-21 55 emb|AW651005|AW651005 EST329459 tomato germinating seedlings, TA... 99 1e-19 emb|AW760155|AW760155 sl58g05.yl Gm-c1027 Glycine max cDNA clone... 94 7e-19 emb|AW677014|AW677014 DG1_3_C03.b1_A002 Dark Grown 1 (DG1) Sorgh... 92 1e-17 emb|AA556650|AA556650 505 Loblolly pine C Pinus taeda cDNA clone... 68 2e-16 emb|AW681004|AW681004 WS1 9 D01.b1 A002 Water-stressed 1 (WS1) S... 73 3e-15 60 emb|AW686988|AW686988 NF004G03RT1F1023 Developing root Medicago ... 69 4e-15 emb|AW650999|AW650999 EST329453 tomato germinating seedlings, TA... 83 6e-15

emb|AI055048|AI055048 coau0002O07 Cotton Boll Abscission Zone cD... 75 6e-13 emb|AW200862|AW200862 se94e02.y1 Gm-c1027 Glycine max cDNA clone... 53 1e-10 emb|AW693163|AW693163 NF062G06ST1F1000 Developing stem Medicago ... 56 4e-10 emb|AL111305|CNS01981 Botrytis cinerea strain T4 cDNA library un... 60 2e-09 emb|AW284408|AW284408 LG1_289_C04.g1_A002 Light Grown 1 (LG1) So... 47 2e-07 emb|AQ659916|AQ659916 Sheared DNA-16N2.TR Sheared DNA Trypanosom... 45 2e-07 emb|X79680|CAORF C.arietinum mRNA for open reading frame. gb|U19971|SCU19971 Saccharomyces cerevisiae ATP binding cassette... 54 4e-06 dbi|D44599|YSCF4233G Saccharomyces cerevisiae chromosome VI phag... 54 4e-06 10 emb|AW266043|AW266043 L30-2716T3 Ice plant Lambda Uni-Zap XR exp... 51 4e-05 emb|AA962925|AA962925 L30-456T3 Ice plant Lambda Uni-Zap XR expr... 42 5e-05 emb|AW982522|AW982522 HVSMEg0003H22f Hordeum vulgare pre-anthesi... 50 7e-05 emb|AQ953753|AQ953753 Sheared DNA-52P9.TF Sheared DNA Trypanosom... 49 1e-04 emb|AI776285|AI776285 EST257385 tomato resistant, Cornell Lycope... 48 2e-04 15 emb|AQ649643|AQ649643 Sheared DNA-16E5.TR Sheared DNA Trypanosom... 33 4e-04 emb|Z74816|SCYOL074C S.cerevisiae chromosome XV reading frame OR... 47 5e-04 47 5e-04 emb|AL122011|SPCC825 S.pombe chromosome III cosmid c825. gb|T38919|T38919 EST104485 S. cerevisiae strain X2180-1A Sacchar... 46 9e-04 emb|Z99168|SPAC8C9 S.pombe chromosome I cosmid c8C9. 46 9e-04 20 emb|Z97208|SPAC15A10 S.pombe chromosome I cosmid c15A10. 46 9e-04 emb|AW746912|AW746912 WS1 56 G02.b1 A002 Water-stressed 1 (WS1) ... 46 0.001 emb|AC005893|AC005893 Leishmania major chromosome 3 clone L822 s... 46 0.001 emb|AC005767|AC005767 Leishmania major chromosome 3 clone L7535 ... 46 0.001 emb|AC005766|AC005766 Leishmania major chromosome 3 clone L4625 ... 46 0.001 25 emb|AQ640246|AQ640246 927P1-18B11.TP 927P1 Trypanosoma brucei ge... 45 0.002 emb|AQ642395|AQ642395 RPCI93-DpnII-29C18.TJ RPCI93-DpnII Trypano... 45 0.002 emb|AW043038|AW043038 ST28E05 Pine TriplEx shoot tip library Pin... 45 0.002 emb|AW226288|AW226288 ST80F04 Pine TriplEx shoot tip library Pin... 45 0.002 emb|AW870068|AW870068 NXNV 123 G02 F Nsf Xylem Normal wood Verti... 45 0.002 30 gb[U52079|STU52079 Solanum tuberosum P-glycoprotein (pmdr1) mRNA... 44 0.003 emb|AI780527|AI780527 EST261406 tomato susceptible, Cornell Lyco... 44 0.004 emb|AW934240|AW934240 EST360083 tomato fruit mature green, TAMU ... 44 0.004 emb|AV423490|AV423490 AV423490 Lotus japonicus young plants (two... 44 0.004 emb|AI328856|AI328856 a7c03ne.fl Neurospora crassa evening cDNA ... 44 0.004 35 emb|AI485412|AI485412 EST243733 tomato ovary, TAMU Lycopersicon ... 44 0.004 emb|AW625153|AW625153 EST319060 tomato radicle, 5 d post-imbibit... 44 0.004 gb|BE122564|BE122564 Ljimpest29-339-f11 Ljimp Lambda HybriZap ... 44 0.004 emb|AV419032|AV419032 AV419032 Lotus japonicus young plants (two... 44 0.004 emb|AW010587|AW010587 ST08E04 Pine TriplEx shoot tip library Pin... 44 0.004 40 emb|AW308969|AW308969 sf92d12.yl Gm-c1019 Glycine max cDNA clone... 43 0.006 gb|BE021188|BE021188 sm47h12.yl Gm-c1028 Glycine max cDNA clone ... 43 0.006 emb|AQ659914|AQ659914 Sheared DNA-16N2.TF Sheared DNA Trypanosom... 43 0.006 emb|AQ841079|AQ841079 T132031b Medicago truncatula BAC library M... 43 0.008 emb|AF137379|AF137379 Nephroselmis olivacea chloroplast DNA, com... 42 0.011 45 emb|AQ254520|AQ254520 CpG0676A CpIOWAgDNA1 Cryptosporidium parvu... 42 0.011 emb|AW761021|AW761021 sl70a03.yl Gm-c1027 Glycine max cDNA clone... 42 0.011 gb|BE022040|BE022040 sm65g07.yl Gm-c1028 Glycine max cDNA clone ... 42 0.011 emb|AW621316|AW621316 EST312114 tomato root during/after fruit s... 42 0.011 emb|Z14055|SPHMT1M S.pombe mRNA for HMT1. 42 0.016 50 emb|AB041505|AB041505 Populus nigra PnATH mRNA for ABC transport... 42 0.016 emb|AL109988|SPAC323 S.pombe chromosome I cosmid c323. 42 0.016 emb|Z98951|SPCC10D6 S.pombe chromosome I cosmid c10D6. 42 0.016 emb|AL031546|SPCC737 S.pombe chromosome III cosmid c737. 42 0.016 emb[Y10099]HVPGLYH H.vulgare mRNA for novel P-glycoprotein homol... 41 0.021 55 emb|AQ852914|AQ852914 LMAJFV1 lm93e10.yl Leishmania major FV1 ra... 41 0.021 emb|AV410111|AV410111 AV410111 Lotus japonicus young plants (two... 41 0.029 emb|Z49212|SC9952X S.cerevisiae chromosome XIII cosmid 9952. 41 0.029 emb|X81715|SCMDYGENE S.cerevisiae partial MDY gene. 41 0.029 emb|AF166114|AF166114 Mesostigma viride chloroplast DNA, complet... 41 0.029 60

emb|cab45805.1| (al080253) putative protein [arabidopsis thaliana] /blast_score 7.00e-83 /ec_number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbin-5 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al080253| /ncgi http://www.ncgr.org/cgi-bin/ff?al080253 (594 letters) Database: plantfungal 10 661,018 sequences; 426,114,510 total letters Searching.....done Score E 15 Sequences producing significant alignments: (bits) Value emb|Z99969|MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl... 62 3e-09 gb|BE033791|BE033791 MF06E10 MF Mesembryanthemum crystallinum cD... 58 5e-08 20 gb|BE034803|BE034803 ML04E10 ML Mesembryanthemum crystallinum cD... 58 5e-08 emb|AI728744|AI728744 BNLGHi11492 Six-day Cotton fiber Gossypium... 35 2e-07 emb|AW394608|AW394608 sh33e11.yl Gm-c1017 Glycine max cDNA clone... 41 1e-06 emb|AW687017|AW687017 NF005A10RT1F1072 Developing root Medicago ... 40 2e-06 emb|AW685774|AW685774 NF035A03NR1F1000 Nodulated root Medicago t... 40 2e-06 25 emb|AW220014|AW220014 EST302497 tomato root during/after fruit s... 45 2e-06 emb|AW277478|AW277478 sf82e11.y1 Gm-c1019 Glycine max cDNA clone... 37 8e-06 emb|AW728453|AW728453 GA_ Ea0016L16 Gossypium arboreum 7-10 dpa ... 34 1e-05 emb|AW625648|AW625648 EST319555 tomato radicle, 5 d post-imbibit... 45 1e-05 emb|AW775954|AW775954 EST335019 DSIL Medicago truncatula cDNA cl... 39 2e-05 30 emb|AW299135|AW299135 EST305809 KV2 Medicago truncatula cDNA clo... 47 1e-04 gb|BE033951|BE033951 MG02E05 MG Mesembryanthemum crystallinum cD... 46 2e-04 emb|AW697566|AW697566 ST64E03 Pine TriplEx shoot tip library Pin... 34 8e-04 emb|AI812453|AI812453 11C3 Pine Lambda Zap Xylem library Pinus t... 44 0.001 emb|AW687794|AW687794 NF013E08RT1F1066 Developing root Medicago ... 32 0.003 35 emb|AW423428|AW423428 sh66f08.yl Gm-c1015 Glycine max cDNA clone... 38 0.003 emb|AW310121|AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone... emb|AW704218|AW704218 sk17c12.y1 Gm-c1028 Glycine max cDNA clone... 38 0.004 emb|AW704640|AW704640 sk54f05.y1 Gm-c1019 Glycine max cDNA clone... 36 0.004 emb|AW395252|AW395252 sh45g06.yl Gm-c1017 Glycine max cDNA clone... 36 0.004 40 emb[AW704612]AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone... 36 0.004 emb|AW284126|AW284126 LG1_262_A05.g1_A002 Light Grown 1 (LG1) So... 41 0.008 emb|AW923658|AW923658 DG1 57 B06.g1 A002 Dark Grown 1 (DG1) Sorg... 39 0.040 emb|AW423359|AW423359 sh06g04.y1 Gm-c1016 Glycine max cDNA clone... 38 0.076 emb|AW649685|AW649685 EST328139 tomato germinating seedlings, TA... 28 0.35 45 emb|AA520781|AA520781 TgESTzz64a03.r1 TgME49 invivo Bradyzoite c... 35 0.37 emb|AW620830|AW620830 sj47b03.y1 Gm-c1033 Glycine max cDNA clone... 30 0.48 emb|X65608|SCPDC2G S.cerevisiae PDC2 gene. 35 0.51 emb|Z74377|SCYDR081C S.cerevisiae chromosome IV reading frame OR... 35 0.51 emb|Z46796|SC8554 S.cerevisiae chromosome IV cosmid 8554. 35 0.51 50 emb|X82086|SCCHROIV S.cerevisiae DNA for right arm of chromosome... 35 0.51 gb|L19880|YSCPDC2A Saccharomyces cerevisiae pdc2 gene, complete ... 35 0.51 emb|AW299176|AW299176 EST305986 KV2 Medicago truncatula cDNA clo... 35 0.70 emb|AW310120|AW310120 sf31d06.x1 Gm-c1028 Glycine max cDNA clone... 35 0.70 emb|AW309936|AW309936 sf26g12.x1 Gm-c1028 Glycine max cDNA clone... 35 0.70 55 emb|AW278505|AW278505 sf45c08.yl Gm-c1009 Glycine max cDNA clone... 35 0.70 emb|AW310598|AW310598 sg21h03.x1 Gm-c1024 Glycine max cDNA clone... 34 0.96 emb|AW233878|AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone... 34 0.96 gb|BE125775|BE125775 DG1_57 B06.b1 A002 Dark Grown 1 (DG1) Sorgh... gb|M13237|BLYGLUCB Barley beta glucanase mRNA. 60 gb[M62740]BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan... 34 0.96 emb|AW747074|AW747074 WS1 65 A07.g1 A002 Water-stressed 1 (WS1) ... 34 1.3

Query= AL080253.32_at 19415_at /id_source genbank /description

---WO-02/22675 PCT/US01/28506

	emb AJ228137 NTJ228137 Nicotiana tomentosiformis DNA for Tnt1 re 34 1.3
	emb AJ228118 NTJ228118 Nicotiana tomentosiformis DNA for Tnt1 re 34 1.3
	emb AE001365 AE001365 Plasmodium falciparum chromosome 2, sectio 33 1.8
	emb AW233798 AW233798 sf26g12.yl Gm-c1028 Glycine max cDNA clone 33 2.5
5	emb AV393790 AV393790 AV393790 Chlamydomonas reinhardtii C9 Chla 33 2.5
-	
	emb AI920265 AI920265 1795 Pine Lambda Zap Xylem library Pinus t 32 3.4
	emb AL157415 LMFL8325 Leishmania major Friedlin chromosome 5 cos 32 3.4
	emb AQ935443 AQ935443 CpG2473A CpIOWAgDNA1 Cryptosporidium parvu 32 3.4
	emb AW686346 AW686346 NF040F08NR1F1000 Nodulated root Medicago t 32 3.4
10	emb AW687188 AW687188 NF006H09RT1F1079 Developing root Medicago 32 3.4
	emb AW684973 AW684973 NF023G04NR1F1000 Nodulated root Medicago t 32 3.4
	emb AW687098 AW687098 NF006A02RT1F1007 Developing root Medicago 32 3.4
1.0	emb AQ855101 AQ855101 CpG1965B CpIOWAgDNA1 Cryptosporidium parvu 32 3.4
15	emb Y08937 CRNII1 Chlamydomonas reinhardtii mRNA for nitrite red 32 3.4
	gb C96140 C96140 C96140 Marchantia polymorpha immature sex organ 32 4.7
	emb AI162427 AI162427 A017P38U Hybrid aspen plasmid library Popu 31 6.5
	emb Z98549 PFSC03014 Plasmodium falciparum DNA *** SEQUENCING IN 31 6.5
•	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC 31 6.5
20	4 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC 31 6.5
	emb AW696295 AW696295 NF105E11ST1F1086 Developing stem Medicago 31 6.5
	emb AI213146 AI213146 y8b01al.rl Aspergillus nidulans 24hr asexu 31 6.5
	emb AC009259 AC009259 Trypanosoma brucei chromosome VI clone RPC 31 6.5
25	emb AC007863 AC007863 Trypanosoma brucei chromosome VI clone RPC 31 6.5
	emb AV418253 AV418253 AV418253 Lotus japonicus young plants (two 31 6.5
	emb A85864 A85864 Sequence 523 from Patent EP0866129. 31 6.5
	a long a selection of a second
	emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque 31 6.5
20	gb BE056773 BE056773 894011F02.y1 C. reinhardtii CC-1690, normal 31 6.5
30	emb AQ945249 AQ945249 Sheared DNA-54D15.TR Sheared DNA Trypanoso 31 6.5
	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC 31 6.5
	emb AF226997 AF226997 Cladosporium fulvum methionine synthase ge 31 8.9
	emb AW687565 AW687565 NF011A04RT1F1024 Developing root Medicago 31 8.9
	emb AF186185 AF186185 Glycine max retrovirus-like element Calyps 31 8.9
35	emb AW569976 AW569976 si85a11.yl Gm-c1031 Glycine max cDNA clone 31 8.9
	emb AI441553 AI441553 sa67c12.yl Gm-c1004 Glycine max cDNA clone 31 8.9
	emb AI759235 AI759235 EtESTea26d12.yl Eimeria S5-2 Sporozoite st 27 9.6
	O
40	Query= X98321.2 i at 19594 i at /id source genbank /description
40	emb caa66965.1 (x98321) peroxidase [arabidopsis thaliana]
	/blast_score 1.00e-174 /ec_number /family peroxidase /chip nova
	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb x98321 /ncgi
	http://www.ncgr.org/cgi-bin/ff?x98321
45	(1212 letters)
	(1212 101020)
	DatabassIsraelin1
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
50	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
55	gb[U51191]GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA 388 e-129
33	
	gb[U51192 GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA 385 e-128
	gb L13653 TOMTPX2A Lycopersicon esculentum peroxidase (TPX2) mRN 326 e-122
	gb L13654 TOMTPX1A Lycopersicon esculentum peroxidase (TPX1) mRN 204 e-118
	emb[Y16776]SOY16776 Spinacia oleracea mRNA for peroxidase, prx10 210 e-113
60	emb Z22920 SPPEROXDS S.polyrrhiza mRNA for peroxidase. 183 5e-90
	emb AI495190 AI495190 sa89c07.yl Gm-c1004 Glycine max cDNA clone 325 6e-88
	, ————————————————————————————————————

```
emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 212 5e-85
       emb|AW621449|AW621449 EST312247 tomato root during/after fruit s... 212 7e-85
       emb|AW625780|AW625780 EST319687 tomato radicle, 5 d post-imbibit... 211 1e-84
       emb|AW622057|AW622057 EST312855 tomato root during/after fruit s... 182 2e-83
       emb|AW329363|AW329363 N200592e rootphos(-) Medicago truncatula c... 307 1e-82
       emb|AW647641|AW647641 EST307119 tomato germinating seedlings, TA... 190 9e-82
       emb|AW625441|AW625441 EST319348 tomato radicle, 5 d post-imbibit... 187 7e-80
       emb|AW621198|AW621198 EST311996 tomato root during/after fruit s... 206 9e-80
      emb|AW704698|AW704698 sk39d06.y1 Gm-c1028 Glycine max cDNA clone... 297 1e-79
10
      emb|AW219160|AW219160 EST301642 tomato root during/after fruit s... 190 2e-79
      emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 205 2e-79
      emb|AW622593|AW622593 EST313393 tomato root during/after fruit s... 188 1e-77
      emb|AW626302|AW626302 EST320209 tomato radicle, 5 d post-imbibit... 205 1e-77
      emb|AW621202|AW621202 EST312000 tomato root during/after fruit s... 187 3e-77
15
      emb|AW220017|AW220017 EST302500 tomato root during/after fruit s... 197 7e-77
      emb|AB024437|AB024437 Scutellaria baicalensis mRNA for peroxidas... 212 6e-76
      emb|AW622066|AW622066 EST312864 tomato root during/after fruit s... 211 6e-76
      emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 196 6e-76
      emb|AW625860|AW625860 EST319767 tomato radicle, 5 d post-imbibit... 181 2e-75
20
      emb|AI771103|AI771103 EST252203 tomato ovary, TAMU Lycopersicon ... 190 8e-75
      emb|AW218917|AW218917 EST301399 tomato root during/after fruit s... 180 2e-74
      emb[AW831524]AW831524 sm27c05.yl Gm-c1028 Glycine max cDNA clone... 279 3e-74
      emb|AW220442|AW220442 EST302925 tomato root during/after fruit s... 192 9e-73
      gb|BE020787|BE020787 sm52h01.yl Gm-c1028 Glycine max cDNA clone ... 274 1e-72
25
      emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 178 3e-71
      emb|AW219955|AW219955 EST302438 tomato root during/after fruit s... 178 3e-71
      gb|BE020269|BE020269 sm42f09.yl Gm-c1028 Glycine max cDNA clone ... 165 3e-71
      emb|AW219743|AW219743 EST302225 tomato root during/after fruit s... 173 9e-70
      emb|AW218390|AW218390 EST303573 tomato radicle, 5 d post-imbibit... 191 8e-69
30
      gb|BE020135|BE020135 sm41f03.yl Gm-c1028 Glycine max cDNA clone ... 184 1e-68
      emblAI895098|AI895098 EST264541 tomato callus, TAMU Lycopersicon... 169 2e-68
      emb|AW219511|AW219511 EST301909 tomato root during/after fruit s... 193 6e-68
      emb|AW154826|AW154826 EST290219 tomato root deficiency, Cornell ... 154 1e-67
      gb|L36112|SSNPEROXIC Stylosanthes humilis peroxidase mRNA.
35
      emb|AW625509|AW625509 EST319416 tomato radicle, 5 d post-imbibit... 167 2e-65
      dbj|D42065|TOBCPI40KB Tobacco mRNA for cationic peroxidase isozy... 122 3e-65
      gb|U51193|GMU51193 Glycine max peroxidase (sEPb1) mRNA, partial ... 95 5e-65
      dbj|D42064|TOBCPI38KA Tobacco mRNA for cationic peroxidase isozy... 119 6e-65
      gb|U51194|GMU51194 Glycine max peroxidase (sEPb2) mRNA, partial ... 100 6e-65
40
      emb|AW621545|AW621545 EST312343 tomato root during/after fruit s... 166 8e-65
      emb|AW704193|AW704193 sk17a09.yl Gm-c1028 Glycine max cDNA clone... 244 8e-64
      gb|M37637|ARCPNC2 A.hypogaea cationic peroxidase mRNA, complete ... 100 2e-63
      emb|X90694|MSRNAPE1C M.sativa mRNA for peroxidase 1C.
                                                                        164 3e-63
      emb|AW621842|AW621842 EST312640 tomato root during/after fruit s... 151 4e-63
45
      emb|X94943|LECEVI16G L.esculentum mRNA for peroxidase.
                                                                       104 4e-63
      emb|AI487546|AI487546 EST245868 tomato ovary, TAMU Lycopersicon ... 150 5e-63
      emb|AW625242|AW625242 EST319245 tomato radicle, 5 d post-imbibit... 149 9e-63
      emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 100 2e-62
      emb|AW621971|AW621971 EST312769 tomato root during/after fruit s... 147 6e-62
50
      emb|AW218589|AW218589 EST303772 tomato radicle, 5 d post-imbibit... 147 6e-62
      emb|AW621728|AW621728 EST312526 tomato root during/after fruit s... 136 8e-62
      gb|L36157|ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... 151 2e-61
      emb|AW569722|AW569722 si79f03.yl Gm-c1031 Glycine max cDNA clone... 160 2e-61
      emb|AW649624|AW649624 EST328078 tomato germinating seedlings, TA... 145 2e-61
55
      emb|AW621885|AW621885 EST312683 tomato root during/after fruit s... 145 2e-61
      gb|J02979|TOBPXDLF Nicotiana tabacum lignin-forming peroxidase m... 235 6e-61
      emb|AW625097|AW625097 EST313914 tomato radicle, 5 d post-imbibit... 143 8e-61
      emb|AB027753|AB027753 Nicotiana tabacum mRNA for peroxidase, com... 105 1e-60
      emb[Y16778|SPY16778 Spinacia oleracea mRNA for peroxidase, prx11... 109 3e-60
60
      emb X71593 LECEVIIA L.esculentum CEVI-1 mRNA.
                                                                     174 4e-60
      emb|X90693|MSRNAPE1B M.sativa mRNA for peroxidase 1B.
                                                                        153 6e-60
```

WO 02/22675 ---- PCT/US01/28506

gb|BE057477|BE057477 sm58f06.y1 Gm-c1028 Glycine max cDNA clone ... 231 6e-60 emb|X90692|MSRNAPE1A M.sativa mRNA for peroxidase 1A. 149 9e-60 emb|AW666051|AW666051 sk31e03.y1 Gm-c1028 Glycine max cDNA clone... 154 3e-59

5	emb AW219008 AW219008 EST301490 tomato root during/after fruit s 149 2e-58 gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 161 2e-58 emb AW351229 AW351229 GM210011A10H11R Gm-r1021 Glycine max cDNA 149 2e
	58 emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor 151 3e-58 emb AW666205 AW666205 sk33f10.y1 Gm-c1028 Glycine max cDNA clone 199 3e-58
10	emb X56011 TAPERO Wheat mRNA for peroxidase. 146 6e-58 emb AW132575 AW132575 se05h10.yl Gm-c1013 Glycine max cDNA clone 102 7e-58 emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod 154 1e-57
	emb AW218512 AW218512 EST303695 tomato radicle, 5 d post-imbibit 124 4e-57 emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1) 157 6e-57
15	emb AB024438 AB024438 Scutellaria baicalensis mRNA for peroxidas 141 6e-57 emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g 109 8e-57 emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl 154 1e-56
20	emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo 154 1e-56 emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl 154 1e-56 emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl 154 1e-56
	emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs 171 2e-56 emb Y10467 SOPRXR6 S.oleracea mRNA for peroxidase, clone PC23. 151 4e-56 emb AW035958 AW035958 EST282817 tomato callus, TAMU Lycopersicon 106 3e-55
25	emb X91232 MARNAPRX M.annua mRNA for peroxidase. 163 4e-55 emb AW625144 AW625144 EST319051 tomato radicle, 5 d post-imbibit 123 8e-55 emb AF049881 AF049881 Linum usitatissimum peroxidase FLXPER4 (PE 146 1e-54
30	gb L36158 ALFPXDD Medicago sativa peroxidase (pxdD) mRNA, 3' end. 136 1e-54 emb AW441632 AW441632 EST311028 tomato fruit red ripe, TAMU Lyco 165 2e-54 emb Y10468 SOPRXR7 S.oleracea mRNA for peroxidase, clone PC36. 96 2e-54
30	emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per 158 2e-54 emb AW218519 AW218519 EST303702 tomato radicle, 5 d post-imbibit 122 2e-54 emb AW622418 AW622418 EST313205 tomato root during/after fruit s 122 2e-54 emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor 141 3e-54
35	omoral 192200 km 192200 kmasoolas valgaris peroxidase 3 preciasor 141 36-34
	Query= AC004561.78_at 19640_at /id_source genbank /description gb aac95192.1 (ac004561) putative glutathione s-transferase [arabidopsis thaliana] /blast_score 1.00e-118 /ec_number /family
40	transferase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac004561 /ncgi http://www.ncgr.org/cgi-bin/ff?ac004561
45	(675 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters
	Searchingdone
50	Score E Sequences producing significant alignments: (bits) Value
55	emb AW624985 AW624985 EST313814 tomato radicle, 5 d post-imbibit 73 1e-42 emb AW041029 AW041029 EST283893 tomato mixed elicitor, BTI Lycop 110 7e-41 emb AW728749 AW728749 GAEa0028D12 Gossypium arboreum 7-10 dpa 112 5e-40 emb AW622625 AW622625 EST313425 tomato root during/after fruit s 73 6e-40
. 0	emb AW267974 AW267974 EST306196 DSIR Medicago truncatula cDNA cl 115 1e-39 emb AW224728 AW224728 EST303171 tomato root, plants pre-anthesis 88 1e-37 emb AW597347 AW597347 si91f07.yl Gm-c1031 Glycine max cDNA clone 92 2e-36
60	emb AW186185 AW186185 se64f07.y1 Gm-c1019 Glycine max cDNA clone 112 3e-36 emb AW760657 AW760657 sl53c04.y1 Gm-c1027 Glycine max cDNA clone 89 2e-35

	gb BE021138 BE021138 sm55h05.y1 Gm-c1028 Glycine max cDNA clone 89 2e-35
	gb BE021010 BE021010 sm54f05.yl Gm-c1028 Glycine max cDNA clone 89 2e-35
	emb AW569900 AW569900 si83a10.y1 Gm-c1031 Glycine max cDNA clone 89 2e-35
	emb AW423852 AW423852 sh52g05.y1 Gm-c1017 Glycine max cDNA clone 86 4e-35
5	gb[U20809]VRU20809 Vigna radiata clone MII-4 auxin-induced prote 75 4e-35
•	emb AW234458 AW234458 sf25d08.y1 Gm-c1028 Glycine max cDNA clone 89 5e-35
	emb AV422068 AV422068 AV422068 Lotus japonicus young plants (two 93 1e-34

10	
10	gb BE057428 BE057428 sm58a10.y1 Gm-c1028 Glycine max cDNA clone 89 2e-34
	emb X56264 NTAUX110 N.tabacum auxin-induced mRNA (pCNT110). 82 7e-34
	emb AW761562 AW761562 sl69c11.yl Gm-c1027 Glycine max cDNA clone 89 7e-34
	emb AW704357 AW704357 sk18c09.yl Gm-c1028 Glycine max cDNA clone 82 7e-34
نہ ۔	gb BE020410 BE020410 sm43h07.y1 Gm-c1028 Glycine max cDNA clone 85 9e-34
15	emb AW234420 AW234420 sf25a01.yl Gm-c1028 Glycine max cDNA clone 89 9e-34
	emb X56265 NTAUX111 N.tabacum auxin-induced mRNA (pCNT111). 83 2e-33
	emb X56263 NTAUX103 N.tabacum auxin-induced mRNA (pCNT103). 79 2e-33
	emb AV417399 AV417399 AV417399 Lotus japonicus young plants (two 89 2e-33'
	emb AW569893 AW569893 si82h12.yl Gm-c1031 Glycine max cDNA clone 93 3e-33
20 .	emb AW981250 AW981250 EST392403 DSIL Medicago truncatula cDNA cl 84 4e-33
	gb BE057291 BE057291 sn01b03.yl Gm-c1015 Glycine max cDNA clone 89 1e-32
	emb AW560886 AW560886 EST315934 DSIR Medicago truncatula cDNA cl 84 4e-32
	emb AV427433 AV427433 AV427433 Lotus japonicus young plants (two 84 4e-32
	emb AW626046 AW626046 EST319953 tomato radicle, 5 d post-imbibit 88 7e-32
25	emb AW776845 AW776845 EST335910 DSIL Medicago truncatula cDNA cl 84 2e-31
	emb AW776620 AW776620 EST335685 DSIL Medicago truncatula cDNA cl 79 2e-31
	emb AV422089 AV422089 AV422089 Lotus japonicus young plants (two 115 3e-31
	emb AW234602 AW234602 sf17b10.yl Gm-c1028 Glycine max cDNA clone 85 4e-31

30	4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
50	4 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	* * · * · * · · · · · · · · · · · · · ·
	emb AW306150 AW306150 se46e07.yl Gm-c1017 Glycine max cDNA clone 85 7e-30
35	emb AW397802 AW397802 sg68e08.y1 Gm-c1007 Glycine max cDNA clone 81 1e-29
33	emb AW234580 AW234580 sf15h12.yl Gm-c1028 Glycine max cDNA clone 81 2e-29
	emb AW690032 AW690032 NF027E09ST1F1000 Developing stem Medicago 79 2e-29
	emb AW569497 AW569497 si87h06.yl Gm-c1031 Glycine max cDNA clone 83 3e-29
	gb[M20363 SOYHSP Soybean heat-shock protein (Gmhsp26-A) gene, co 90 3e-29
40	emb AW350224 AW350224 GM210007B10H2R Gm-r1021 Glycine max cDNA 3 107 3e
40	29
	emb AF239928 AF239928 Euphorbia esula glutathione S-transferase 84 4e-29
	emb AW907271 AW907271 EST343394 potato stolon, Cornell Universit 81 5e-29
	emb AW980323 AW980323 EST391476 GVN Medicago truncatula cDNA clo 84 6e-29
٠.	emb AW569022 AW569022 si74e07.yl Gm-c1031 Glycine max cDNA clone 85 7e-29
45	emb AW218869 AW218869 EST301351 tomato root during/after fruit s 62 8e-29
	emb AW224727 AW224727 EST303170 tomato root, plants pre-anthesis 77 1e-28
	emb AW394813 AW394813 sh35f08.yl Gm-c1017 Glycine max cDNA clone 81 1e-28
	emb AW233937 AW233937 sf32c05.yl Gm-c1028 Glycine max cDNA clone 92 2e-28
	emb AI441991 AI441991 sa82g05.y1 Gm-c1004 Glycine max cDNA clone 99 2e-28
50	emb AJ010448 AMY010448 Alopecurus myosuroides mRNA for glutathio 63 2e-28
	emb AJ010449 AMY010449 Alopecurus myosuroides mRNA for glutathio 64 2e-28
	emb AW687500 AW687500 NF010C06RT1F1049 Developing root Medicago 84 3e-28
	emb AB027501 AB027501 Daucus carota Dearg-1 mRNA, complete cds. 62 4e-28
	emb AW684848 AW684848 NF022C03NR1F1000 Nodulated root Medicago t 84 4e-28
55	emb AW684915 AW684915 NF023A04NR1F1000 Nodulated root Medicago t 75 4e-28
	emb AW830445 AW830445 sm27a05.y1 Gm-c1028 Glycine max cDNA clone 89 5e-28
	gb BE020437 BE020437 sm40g05.y1 Gm-c1028 Glycine max cDNA clone 89 5e-28
	emb AW677374 AW677374 DG1_6_A02.b1_A002 Dark Grown 1 (DG1) Sorgh 66 8e-28
	emb AW040981 AW040981 EST283845 tomato mixed elicitor, BTI Lycop 88 9e-28
50	
	1 DT104000DT104000 D00004004 D000 3 C 11
	gb/BE1240/9/BE1240/9 ES1394204 DSIL Medicago truncatula cDNA clo 75 3e-27

	emb X56268 NTAUX1 N.tabacum gene for an auxin-induced protein (p 79 4e-27 emb AW687359 AW687359 NF008G06RT1F1051 Developing root Medicago 84 4e-27 emb AW625637 AW625637 EST319544 tomato radicle, 5 d post-imbibit 60 7e-27
5	emb AW685686 AW685686 NF033F09NR1F1000 Nodulated root Medicago t 72 8e-27 emb AI778504 AI778504 EST259383 tomato susceptible, Cornell Lyco 72 1e-26 emb AW508224 AW508224 si51d09.yl Gm-r1030 Glycine max cDNA clone 86 1e-26 emb AI776426 AI776426 EST257526 tomato resistant, Cornell Lycope 77 2e-26
	emb[X56269]NTAUX35 N.tabacum gene for an auxin-induced protein (82 3e-26 gb[BE124113]BE124113 EST394238 DSIL Medicago truncatula cDNA clo 75 3e-26
10	emb AW774063 AW774063 EST333293 KV3 Medicago truncatula cDNA clo 79 4e-26
	emb AW775514 AW775514 EST334579 DSIL Medicago truncatula cDNA cl 72 6e-26 emb AW685579 AW685579 NF029C01NR1F1000 Nodulated root Medicago t 72 6e-26
	emb AW693566 AW693566 NF067F08ST1F1074 Developing stem Medicago 72 6e-26
15	emb AW776395 AW776395 EST335460 DSIL Medicago truncatula cDNA cl 72 6e-26
13	emb AW775759 AW775759 EST334824 DSIL Medicago truncatula cDNA cl 72 6e-26 emb AW775247 AW775247 EST331969 GVN Medicago truncatula cDNA clo 72 6e-26
*	emb AW684399 AW684399 NF016E04NR1F1000 Nodulated root Medicago t 72 6e-26
	emb AW559724 AW559724 EST314716 DSIR Medicago truncatula cDNA cl 72 6e-26 emb AW776111 AW776111 EST335176 DSIL Medicago truncatula cDNA cl 72 6e-26
20	emb AW775816 AW775816 EST334881 DSIL Medicago truncatula cDNA cl 72 6e-26
	emb AW684443 AW684443 NF017A06NR1F1000 Nodulated root Medicago t 72 6e-26
	emb AW573792 AW573792 EST316383 GVN Medicago truncatula cDNA clo 72 6e-26 emb AI778968 AI778968 EST259847 tomato susceptible, Cornell Lyco 78 1e-25
	emb AW031747 AW031747 EST275201 tomato callus, TAMU Lycopersicon 78 1e-25
25	emb AW127655 AW127655 M110397 DSLC Medicago truncatula cDNA clon 84 1e-25 emb AW559360 AW559360 EST314408 DSIR Medicago truncatula cDNA cl 72 2e-25
	emb AJ010450 AMY010450 Alopecurus myosuroides mRNA for glutathio 61 3e-25
	emb AI777263 AI777263 EST258228 tomato resistant, Cornell Lycope 75 5e-25
30	emb AW685702 AW685702 NF033B01NR1F1000 Nodulated root Medicago t 77 5e-25 emb AW443955 AW443955 EST308885 tomato mixed elicitor, BTI Lycop 75 5e-25
	emb AW040833 AW040833 EST283697 tomato mixed elicitor, BTI Lycop 75 5e-25
35	Query= AL050351.172_at 19664_at /id_source genbank /description "emb cab43638.1 (al050351) nad(p)h oxidoreductase, isoflavone
<i></i>	reductase-like protein [arabidopsis thaliana]" /blast_score 1.00e-177
	/ec_number /family reductase /chip nova /gb_link
	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb al050351 /ncgi
40	http://www.ncgr.org/cgi-bin/ff?al050351
	(927 letters)
	Database: plantfungal
45	661,018 sequences; 426,114,510 total letters
.5	Searchingdone
	Score E
50	Sequences producing significant alignments: (bits) Value
50	emb AF071477 AF071477 Pyrus communis isoflavone reductase relate 583 e-166
	emb AF202184 AF202184 Glycine max isoflavone reductase homolog 2 581 e-165
	emb X92075 STISOREDH S.tuberosum mRNA for isoflavone reductase h 542 e-153 emb AF135127 AF135127 Betula pendula isoflavone reductase homolo 534 e-151
55	emb AF242491 AF242491 Forsythia x intermedia clone 1 phenylcouma 527 e-149
	emb AF242492 AF242492 Forsythia x intermedia clone 2 phenylcouma 512 e-144 emb AJ005806 PTR5806 Populus trichocarpa mRNA for phenylcoumaran 497 e-140
	emb AJ005805 PTR5805 Populus trichocarpa mRNA for phenylcoumaran 497 e-140
6 0	emb AJ005804 PTR5804 Populus trichocarpa mRNA for phenylcoumaran 497 e-140
60	emb AJ005803 PTR5803 Populus trichocarpa mRNA for phenylcoumaran 495 e-139 emb AF201458 AF201458 Medicago sativa isoflavone reductase-like 294 e-136

	dbj[D28505[TOBA622A Tobacco mRNA for A622, complete cds. 462 e-129
	emb AF242498 AF242498 Tsuga heterophylla clone 6 phenylcoumaran 417 e-124
	emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1 403 e-124
	emb AF242497 AF242497 Tsuga heterophylla clone 5 phenylcoumaran 416 e-123
5	emb AW164323 AW164323 se71a03.yl Gm-c1023 Glycine max cDNA clone 426 e-118
	emb AF242494 AF242494 Tsuga heterophylla clone 2 phenylcoumaran 363 e-117
	emb AF242495 AF242495 Tsuga heterophylla clone 3 phenylcoumaran 363 e-117
	emb AI960922 AI960922 sc92f06.yl Gm-c1019 Glycine max cDNA clone 420 e-117
	emb AW560052 AW560052 EST315100 DSIR Medicago truncatula cDNA cl 369 e-114
10	emb AW560051 AW560051 EST315099 DSIR Medicago truncatula cDNA cl 410 e-113
	emb AI960719 AI960719 sc89e03.yl Gm-c1019 Glycine max cDNA clone 396 e-109
	emb AF242490 AF242490 Pinus taeda phenylcoumaran benzylic ether 358 e-106
	emb AF081678 AF081678 Pinus taeda phenylcoumaran benzylic ether 358 e-106
	emb AF242496 AF242496 Tsuga heterophylla clone 4 phenylcoumaran 356 e-105
15	emb AF242493 AF242493 Tsuga heterophylla clone 1 phenylcoumaran 356 e-105
	emb AF242499 AF242499 Tsuga heterophylla clone 7 phenylcoumaran 345 e-102
	emb[X58078]MSISREDMR M.sativa mRNA for isoflavone reductase. 308 e-100
	emb AJ003245 GMAJ3245 Glycine max mRNA for putative NADPH:isofla 311 2e-99
	emb AW306732 AW306732 sf47f07.yl Gm-c1009 Glycine max cDNA clone 222 2e-99
20	
20 .	gb S72472 S72472 isoflavone reductase [Pisum sativum=peas, seedl 300 2e-98
	emb AW277911 AW277911 sf89a12.yl Gm-c1019 Glycine max cDNA clone 357 7e-98
	emb AW423683 AW423683 sh50d08.yl Gm-c1017 Glycine max cDNA clone 258 2e-96
	emb AW560880 AW560880 EST315928 DSIR Medicago truncatula cDNA cl 335 3e-91
25	emb X60755 CANADPHIO C.arietinum mRNA for NADPH:isoflavone oxido 302 2e-90
23	emb AW308968 AW308968 sf92d11.yl Gm-c1019 Glycine max cDNA clone 331 5e-90
	gb BE020712 BE020712 sm52a04.yl Gm-c1028 Glycine max cDNA clone 191 2e-88
	emb AW508698 AW508698 si35d01.yl Gm-r1030 Glycine max cDNA clone 321 4e-87
	emb AI897693 AI897693 EST267136 tomato ovary, TAMU Lycopersicon 320 8e-87
20	gb BE022340 BE022340 sm73f05.yl Gm-c1028 Glycine max cDNA clone 289 3e-86
30	emb AI167005 AI167005 xylem.est.781 Poplar xylem Lambda ZAPII li 317 7e-86
	emb AW980520 AW980520 EST391673 GVN Medicago truncatula cDNA clo 316 2e-85
	emb AW568970 AW568970 si73g05.yl Gm-c1031 Glycine max cDNA clone 264 5e-85
	emb AW100852 AW100852 sd62c02.y1 Gm-c1008 Glycine max cDNA clone 310 8e-84
25	emb AW736641 AW736641 EST333133 KV3 Medicago truncatula cDNA clo 308 3e-83
35	emb AW980642 AW980642 EST391795 GVN Medicago truncatula cDNA clo 308 6e-83
	emb AW234069 AW234069 sf33h03.yl Gm-c1028 Glycine max cDNA clone 291 7e-78
	emb AI812729 AI812729 18D5 Pine Lambda Zap Xylem library Pinus t 291 7e-78
	emb AW687040 AW687040 NF005C11RT1F1085 Developing root Medicago 259 2e-77
40	emb AI901007 AI901007 sc18c12.yl Gm-c1013 Glycine max cDNA clone 288 3e-77
40	emb AW706449 AW706449 sj58e10.yl Gm-c1033 Glycine max cDNA clone 280 4e-77
	emb AF242506 AF242506 Thuja plicata clone 4 pinoresinol-laricire 166 4e-77
	emb AI899794 AI899794 sb92g12.yl Gm-c1017 Glycine max cDNA clone 286 1e-76
	emb AW278000 AW278000 sf89e04.yl Gm-c1019 Glycine max cDNA clone 286 2e-76
16	emb AW348609 AW348609 GM210002B22F12R Gm-r1021 Glycine max cDNA 263 5e-76
45	emb AF242504 AF242504 Thuja plicata clone 2 pinoresinol-laricire 160 7e-76
	emb AF242503 AF242503 Thuja plicata clone 1 pinoresinol-laricire 120 7e-76
	emb AW623613 AW623613 EST321558 tomato flower buds 3-8 mm, Corne 199 3e-75
	emb AW164589 AW164589 se73h03.yl Gm-c1023 Glycine max cDNA clone 281 6e-75
50	emb AW719567 AW719567 LjNEST6f2r Lotus japonicus nodule library, 281 8e-75
50	emb AI726822 AI726822 BNLGHi6647 Six-day Cotton fiber Gossypium 279 2e-74
	emb AW695822 AW695822 NF099E10ST1F1082 Developing stem Medicago 203 3e-74
	emb AI812838 AI812838 19H8 Pine Lambda Zap Xylem library Pinus t 243 9e-73
	emb AI730069 AI730069 BNLGHi6078 Six-day Cotton fiber Gossypium 273 le-72
۔ ہ	emb AW277687 AW277687 sf85c09.yl Gm-c1019 Glycine max cDNA clone 270 2e-72
55	emb AF242505 AF242505 Thuja plicata clone 3 pinoresinol-laricire 112 2e-72
	emb AF242500 AF242500 Thuja plicata phenylcoumaran benzylic ethe 112 2e-72
	emb AW559440 AW559440 EST314488 DSIR Medicago truncatula cDNA cl 269 3e-72
	emb AF242501 AF242501 Tsuga heterophylla clone 1 pinoresinol-lar 171 6e-72
C C	emb AW278307 AW278307 sf42d08.yl Gm-c1009 Glycine max cDNA clone 271 6e-72
60	emb AF242502 AF242502 Tsuga heterophylla clone 2 pinoresinol-lar 171 8e-72
	emb AW687008 AW687008 NF004H12RT1F1103 Developing root Medicago 255 1e-71

```
emb|AW310288|AW310288 sf33h03.x1 Gm-c1028 Glycine max cDNA clone... 263 2e-71
      gb|U81158|FXU81158 Forsythia x intermedia (+)-pinoresinol/(+)-la... 166 1e-70
      emb|AI488036|AI488036 EST246358 tomato ovary, TAMU Lycopersicon ... 265 4e-70
      emb|AW685137|AW685137 NF025H12NR1F1000 Nodulated root Medicago t... 262 2e-69
      emb|Y12689|CPIRLP C.paradisi mRNA isoflavone reductase-like prot... 123 1e-68
      emb|AI485705|AI485705 EST244026 tomato ovary, TAMU Lycopersicon ... 253 4e-68
      emb|AW348311|AW348311 GM210001B23E3R Gm-r1021 Glycine max cDNA 3... 257 8e-68
      gb|BE020979|BE020979 sm54c03.yl Gm-c1028 Glycine max cDNA clone ... 257 8e-68
      emb|AI162702|AI162702 A022P17U Hybrid aspen plasmid library Popu... 231 3e-66
10
      emb|AW774032|AW774032 EST333018 KV3 Medicago truncatula cDNA clo... 226 3e-66
      emb|AW775908|AW775908 EST334973 DSIL Medicago truncatula cDNA cl... 226 2e-65
      emb|AW684683|AW684683 NF019G01NR1F1000 Nodulated root Medicago t... 249 2e-65
      gb|U48590|LAU48590 Lupinus albus isoflavone reductase-like prote... 151 2e-65
      emb|AW038676|AW038676 EST280537 tomato mixed elicitor, BTI Lycop... 197 2e-65
15
      emb|AI443821|AI443821 sa30d07.y1 Gm-c1004 Glycine max cDNA clone... 248 3e-65
      emb|AW773814|AW773814 EST332800 KV3 Medicago truncatula cDNA clo... 223 4e-65
      emb|AI162699|AI162699 A022P13U Hybrid aspen plasmid library Popu... 243 4e-65
      emb|AI437725|AI437725 sa38g09.y1 Gm-c1004 Glycine max cDNA clone... 221 8e-65
      emb|AW985148|AW985148 NXNV_133_E11_F Nsf Xylem Normal wood Verti... 227 3e-64
      emb|AW696352|AW696352 NF107B01ST1F1011 Developing stem Medicago ... 216 7e-64
      emb|AJ132262|PBA132262 Populus balsamifera subsp. trichocarpa pc... 141 7e-64
      emb|AW736640|AW736640 EST333132 KV3 Medicago truncatula cDNA clo... 243 1e-63
      emb|AW278044|AW278044 sf89h09.y1 Gm-c1019 Glycine max cDNA clone... 242 3e-63
      emb|AW928288|AW928288 G200003e KV0 Medicago truncatula cDNA clon... 206 2e-62
25
      emb|AW776834|AW776834 EST335899 DSIL Medicago truncatula cDNA cl... 214 2e-62
      emb|AW775218|AW775218 EST331940 GVN Medicago truncatula cDNA clo... 214 2e-62
      emb|AW289885|AW289885 NXNV007E10F Nsf Xylem Normal wood Vertical... 238 4e-62
      emb|AI496272|AI496272 sb01f07.yl Gm-c1004 Glycine max cDNA clone... 236 2e-61
30
      Query= AC005687.19 at 19672 at /id source genbank /description
      gb|aac36019.1| (ac005687) rap2.6 [arabidopsis thaliana] /blast score
      1.00e-105/ec_number /family /chip nova/gb_link
      http://www3.ncbi.nlm.nih.gov/htbin-
35
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005687|/ncgi
      http://www.ncgr.org/cgi-bin/ff?ac005687
           (734 letters)
      Database: plantfungal
40
            661,018 sequences; 426,114,510 total letters
                                          Score
45
      Sequences producing significant alignments:
                                                         (bits) Value
      emb|AI488999|AI488999 EST247338 tomato ovary, TAMU Lycopersicon ... 123 2e-27
      emblAI483510|AI483510 EST249359 tomato ovary, TAMU Lycopersicon ... 122 2e-27
      emb|AI489709|AI489709 EST248048 tomato ovary, TAMU Lycopersicon ... 122 3e-27
50
      emb|AI771834|AI771834 EST252934 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI771755|AI771755 EST252855 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI490296|AI490296 EST248622 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI486929|AI486929 EST245251 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI899397|AI899397 EST268840 tomato ovary, TAMU Lycopersicon ... 122 4e-27
55
      emb|AI897787|AI897787 EST267230 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI483636|AI483636 EST249507 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI485460|AI485460 EST243781 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI771795|AI771795 EST252895 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI489199|AI489199 EST247538 tomato ovary, TAMU Lycopersicon ... 122 4e-27
60
      emb|AI483501|AI483501 EST249322 tomato ovary, TAMU Lycopersicon ... 122 4e-27
      emb|AI483741|AI483741 EST249612 tomato ovary, TAMU Lycopersicon ... 122 4e-27
```

```
emb[AI489919]AI489919 EST248258 tomato ovary, TAMU Lycopersicon ... 121 8e-27
      emb|AW033743|AW033743 EST277314 tomato callus, TAMU Lycopersicon... 120 1e-26
       emb|AI485175|AI485175 EST243479 tomato ovary, TAMU Lycopersicon ... 120 1e-26
      emb|AW685799|AW685799 NF030D09NR1F1000 Nodulated root Medicago t... 119 2e-26
 5
      emb|AW032669|AW032669 EST276228 tomato callus, TAMU Lycopersicon... 117 1e-25
      emb|AI484721|AI484721 EST242982 tomato ovary, TAMU Lycopersicon ... 117 1e-25
      emb|AI484063|AI484063 EST249934 tomato ovary, TAMU Lycopersicon ... 116 3e-25
      emb|AV428124|AV428124 AV428124 Lotus japonicus young plants (two... 115 4e-25
      emb|AI490297|AI490297 EST248623 tomato ovary, TAMU Lycopersicon ... 114 9e-25
10
      emb|AW782252|AW782252 sm03d11.y1 Gm-c1027 Glycine max cDNA clone... 113 1e-24
      emb|AW203601|AW203601 sf36b02.y1 Gm-c1028 Glycine max cDNA clone... 111 4e-24
      emb|AI898190|AI898190 EST267633 tomato ovary, TAMU Lycopersicon ... 111 8e-24
      emb|AI483545|AI483545 EST249394 tomato ovary, TAMU Lycopersicon ... 109 2e-23
      emb|AI485260|AI485260 EST243564 tomato ovary, TAMU Lycopersicon ... 108 6e-23
15
      emb|AF071893|AF071893 Prunus armeniaca AP2 domain containing pro... 108 6e-23
      emb|AI897176|AI897176 EST266715 tomato ovary, TAMU Lycopersicon ... 107 8e-23
      emb|AW560196|AW560196 EST315244 DSIR Medicago truncatula cDNA cl... 107 8e-23
      emb|AW560968|AW560968 EST316016 DSIR Medicago truncatula cDNA cl... 107 86-23
      emb|AW559374|AW559374 EST314422 DSIR Medicago truncatula cDNA cl... 105 3e-22
20 .
      emb|AW267756|AW267756 EST305884 DSIR Medicago truncatula cDNA cl... 105 5e-22
      emb|AW560135|AW560135 EST315183 DSIR Medicago truncatula cDNA cl... 105 5e-22
      emb|AW560134|AW560134 EST315182 DSIR Medicago truncatula cDNA cl... 105 5e-22
      emb|AW256448|AW256448 EST304585 KV2 Medicago truncatula cDNA clo... 105 5e-22
      emb|AW094484|AW094484 EST287664 tomato mixed elicitor, BTI Lycop... 105 5e-22
25
      gb|BE022152|BE022152 sm68b06.y1 Gm-c1028 Glycine max cDNA clone ... 104 1e-21
      emb|AW831226|AW831226 sm12d11.yl Gm-c1027 Glycine max cDNA clone... 104 1e-21
      emb|AW760676|AW760676 sl53e01.y1 Gm-c1027 Glycine max cDNA clone... 104 le-21
      gb|BE024062|BE024062 sm96c01.yl Gm-c1015 Glycine max cDNA clone ... 104 1e-21
      emb|AW568625|AW568625 si60b05.y1 Gm-r1030 Glycine max cDNA clone... 104 1e-21
30
      emb|AW458893|AW458893 sh16c04.yl Gm-c1016 Glycine max cDNA clone... 104 1e-21
      emb|AW156366|AW156366 se25b08.y1 Gm-c1015 Glycine max cDNA clone... 103 1e-21
      emb|AW185126|AW185126 se87b08.yl Gm-c1023 Glycine max cDNA clone... 103 2e-21
      emb|AW328989|AW328989 N200181e rootphos(-) Medicago truncatula c... 103 2e-21
      emb|AW152963|AW152963 se33c03.yl Gm-c1015 Glycine max cDNA clone... 98 2e-21
35
      emb|AW441775|AW441775 EST311171 tomato fruit red ripe, TAMU Lyco... 102 3e-21
      emb|AW221854|AW221854 EST298665 tomato fruit red ripe, TAMU Lyco... 102 3e-21
      emb|AW441715|AW441715 EST311111 tomato fruit red ripe, TAMU Lyco... 102 3e-21
      emb|AW219198|AW219198 EST301680 tomato root during/after fruit s... 102 3e-21
      emb|AV417624|AV417624 AV417624 Lotus japonicus young plants (two... 102 3e-21
40
      emb|AV407462|AV407462 AV407462 Lotus japonicus young plants (two... 102 3e-21
      emb|AI895742|AI895742 EST265185 tomato callus, TAMU Lycopersicon... 102 3e-21
      emb|AW931667|AW931667 EST357510 tomato fruit mature green, TAMU ... 101 4e-21
      emb|AW931028|AW931028 EST356871 tomato fruit mature green, TAMU ... 101 4e-21
      emb|AW040033|AW040033 EST282524 tomato mixed elicitor, BTI Lycop... 101 5e-21
45
      emb|AW040028|AW040028 EST282519 tomato mixed elicitor, BTI Lycop... 101 5e-21
      emb|AI487067|AI487067 EST245389 tomato ovary, TAMU Lycopersicon ... 101 5e-21
      emb|AW442735|AW442735 EST307665 tomato mixed elicitor, BTI Lycop... 101 5e-21
      emb|AW218830|AW218830 EST301310 tomato root during/after fruit s... 101 5e-21
      emb|AI483782|AI483782 EST249653 tomato ovary, TAMU Lycopersicon ... 101 5e-21
50
      emb|AW218836|AW218836 EST301316 tomato root during/after fruit s... 101 5e-21
      emb|AI483900|AI483900 EST249771 tomato ovary, TAMU Lycopersicon ... 101 5e-21
      emb|AI482665|AI482665 EST241988 tomato shoot, Cornell Lycopersic... 101 5e-21
      emb|AW760204|AW760204 sl59d04.yl Gm-c1027 Glycine max cDNA clone... 101 5e-21
      emb|AI496139|AI496139 sa95h06.y1 Gm-c1004 Glycine max cDNA clone... 101 5e-21
      emb|AW308962|AW308962 sf92d05.yl Gm-c1019 Glycine max cDNA clone... 101 7e-21
55
      emb|AW926284|AW926284 HVSMEg0006M23 Hordeum vulgare pre-anthesis... 101 7e-21
      emb|AI966369|AI966369 sc37h09.yl Gm-c1014 Glycine max cDNA clone... 101 7e-21
      emb|AI855585|AI855585 sc28b12.yl Gm-c1014 Glycine max cDNA clone... 101 7e-21
      emb|AW038227|AW038227 EST279884 tomato mixed elicitor, BTI Lycop... 101 7e-21
60
      emb|AI855661|AI855661 sc32e04.yl Gm-c1014 Glycine max cDNA clone... 101 7e-21
      emb|AW234175|AW234175 sf22b03.y1 Gm-c1028 Glycine max cDNA clone... 101 7e-21
```

```
emb|AW598575|AW598575 sj93c10.yl Gm-c1023 Glycine max cDNA clone... 101 7e-21
       emb|AW615838|AW615838 EST325336 tomato flower buds 0-3 mm, Corne... 100 9e-21
      gb|T14923|T14923 crs406 lambdaZAPST Ricinus communis cDNA clone ... 100 9e-21
      emb|AW093577|AW093577 EST286757 tomato mixed elicitor, BTI Lycop... 100 9e-21
      emb|AW621852|AW621852 EST312650 tomato root during/after fruit s... 100 9e-21
      emb|AI781904|AI781904 EST262783 tomato susceptible, Cornell Lyco... 100 9e-21
      emb|AW738052|AW738052 EST339479 tomato flower buds, anthesis, Co... 100 1e-20
      emb|AW726761|AW726761 GA_Ea0022K12 Gossypium arboreum 7-10 dpa ... 100 1e-20
      emb|AV422603|AV422603 AV422603 Lotus japonicus young plants (two... 100 1e-20
10
      emb|AW574073|AW574073 EST316664 GVN Medicago truncatula cDNA clo... 100 1e-20
      gb|BE057468|BE057468 sm58e08.y1 Gm-c1028 Glycine max cDNA clone ... 100 2e-20
      emb|AW755737|AW755737 sl08e02.yl Gm-c1036 Glycine max cDNA clone... 100 2e-20
      emb|AW747259|AW747259 WS1_67_A03.b1_A002 Water-stressed 1 (WS1) ... 100_2e-20
      emb|AI489450|AI489450 EST247789 tomato ovary, TAMU Lycopersicon ... 100 2e-20
      emb|AW037553|AW037553 EST278880 tomato mixed elicitor, BTI Lycop... 100 2e-20
15
      emb|AW745488|AW745488 WS1_35_E09.b1_A002 Water-stressed 1 (WS1) ... 100_2e-20
      emb|AI900301|AI900301 sc03g01.yl Gm-c1012 Glycine max cDNA clone... 99 4e-20
      emb|AI771801|AI771801 EST252901 tomato ovary, TAMU Lycopersicon ... 99 4e-20
      emb|AW329209|AW329209 N200421e rootphos(-) Medicago truncatula c... 98 6e-20
20
      emb|AI974084|AI974084 sd16c06.yl Gm-c1020 Glycine max cDNA clone... 98 6e-20
      emb|AW267914|AW267914 EST306256 DSIR Medicago truncatula cDNA cl... 98 6e-20
      emb|AI772393|AI772393 EST253493 tomato resistant, Cornell Lycope... 98 8e-20
      emb|AW397723|AW397723 sg83e11.yl Gm-c1026 Glycine max cDNA clone... 97 1e-19
      emb|AW034241|AW034241 EST277812 tomato callus, TAMU Lycopersicon... 97 2e-19
25
      Query= AC005770.30 at 19892 at /id source genbank /description
      gb|aac79626.1| (ac005770) putative protease inhibitor [arabidopsis
      thaliana] /blast score 2.00e-36 /ec number /family protease /chip
30
      nova/gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi
      http://www.ncgr.org/cgi-bin/ff?ac005770
           (378 letters)
35
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
      Searching......done
40
                                                  E
                                          Score
      Sequences producing significant alignments:
                                                          (bits) Value
      gb|BE057244|BE057244 sm99e04.y1 Gm-c1015 Glycine max cDNA clone ... 87 7e-17
45
      gb|BE057597|BE057597 sn04d12.yl Gm-c1015 Glycine max cDNA clone ... 87 7e-17
      gb|BE022905|BE022905 sm89a05.yl Gm-c1015 Glycine max cDNA clone ... 87 7e-17
      gb|BE022697|BE022697 sm87c09.yl Gm-c1015 Glycine max cDNA clone ... 87 7e-17
      emb|AW156430|AW156430 se26b01.yl Gm-c1015 Glycine max cDNA clone... 87 7e-17
      emb|AI938252|AI938252 sc41h01.y1 Gm-c1014 Glycine max cDNA clone... 87 7e-17
50
      emb|Z46949|SNPR6JT11 S.nigra mRNA for pathogenesis-related prote... 86 9e-17
      gb|BE024084|BE024084 sm96e02.yl Gm-c1015 Glycine max cDNA clone ... 85 2e-16
      emb|AI938085|AI938085 sc41h07.x1 Gm-c1014 Glycine max cDNA clone... 84 3e-16
      emb|AI930853|AI930853 sb43c07.yl Gm-c1015 Glycine max cDNA clone... 84 6e-16
      emb[AW156600]AW156600 se27e01.yl Gm-c1015 Glycine max cDNA clone... 83 1e-15
55
      emb|AI966712|AI966712 sc55h06.yl Gm-c1015 Glycine max cDNA clone... 80 6e-15
      gb|BE023986|BE023986 sm95a07.yl Gm-c1015 Glycine max cDNA clone ... 78 2e-14
      emb|AW433320|AW433320 sh55e08.y1 Gm-c1015 Glycine max cDNA clone... 78 2e-14
      gb|BE057243|BE057243 sm99e03.yl Gm-c1015 Glycine max cDNA clone ... 78 2e-14
      emb|AI522988|AI522988 sb07e02.yl Gm-c1004 Glycine max cDNA clone... 78 2e-14
60
      emb|AI937952|AI937952 sc06b01.yl Gm-c1012 Glycine max cDNA clone...
                                                                          78 2e-14
      emb|AI966518|AI966518 sc51b12.y1 Gm-c1015 Glycine max cDNA clone... 78 3e-14
```

```
emb|AI938255|AI938255 sc41h04.yl Gm-c1014 Glycine max cDNA clone... 78 3e-14
       emb|AI966697|AI966697 sc55e03.yl Gm-c1015 Glycine max cDNA clone... 78 3e-14
       emb|AW433162|AW433162 sh53b01.yl Gm-c1015 Glycine max cDNA clone... 77 5e-14
       emb|AW432522|AW432522 sh75d04.yl Gm-c1015 Glycine max cDNA clone...
 5
       emb|AW432580|AW432580 sh76c09.yl Gm-c1015 Glycine max cDNA clone... 75 3e-13
       emb|AJ132473|AHY132473 Amaranthus hypochondriacus mRNA for tryps... 75 3e-13
       emb|AW309047|AW309047 sf94c03.yl Gm-c1019 Glycine max cDNA clone... 74 4e-13
       emb|AW432514|AW432514 sh75c07.yl Gm-c1015 Glycine max cDNA clone... 72 2e-12
       emb|AI966650|AI966650 sc54d10.yl Gm-c1015 Glycine max cDNA clone... 71 3e-12
       emb|AW460209|AW460209 sh56d11.yl Gm-c1015 Glycine max cDNA clone... 70 6e-12
10
       emb|AI966675|AI966675 sc54h10.yl Gm-c1015 Glycine max cDNA clone... 68 2e-11
       emb|AI488671|AI488671 EST247010 tomato ovary, TAMU Lycopersicon ... 68 3e-11
       emb|AW033471|AW033471 EST277042 tomato callus, TAMU Lycopersicon... 52 4e-11
       emblAW041367|AW041367 EST284231 tomato mixed elicitor, BTI Lycop... 52 4e-11
15
       gb|J04099|TOMERIPII Tomato fruit-ripening protein (ethylene resp... 52 4e-11
       emb|AI930895|AI930895 sb44a05.yl Gm-c1015 Glycine max cDNA clone... 68 4e-11
       emb|AW041591|AW041591 EST284455 tomato mixed elicitor, BTI Lycop... 67 8e-11
       emb|AW929951|AW929951 EST354221 tomato flower buds 8 mm to pre-a... 50 9e-11
       emb|AI483878|AI483878 EST249749 tomato ovary, TAMU Lycopersicon ... 50 9e-11
20
       emb|AW944751|AW944751 EST336801 tomato flower buds 3-8 mm, Corne... 50 1e-10
       gb|M59427|TOMTRYINHI L.peruvianum proteinase inhibitor I gene, c... 50 2e-10
       gb|J05094|TOMPII L.peruvianum proteinase inhibitor I mRNA, compl... 50 2e-10
       emb|AW010812|AW010812 ST14C10 Pine TriplEx shoot tip library Pin... 64 4e-10
       emb|AI485251|AI485251 EST243555 tomato ovary, TAMU Lycopersicon ... 47 4e-10
25
       dbj|D26455|TOBTID44 Nicotiana glauca X Nicotiana langsdorffii mR... 51 5e-10
       emb|Z12623|NTPII3PI N.tabacum pre-pro-PI-Ib gene encoding pre-pr... 50 8e-10
       emb|Z12619|NTPII4PI N.tabacum PI-Ia gene encoding pre-pro-protei... 50 8e-10
       emb|X67075|NTTIMPB N.tabacum TIMPb mRNA for inhibitor of microbi... 50 8e-10
       emb|X67076|NTTIMPA N.tabacum TIMPa mRNA for inhibitor of microbi...
30
       emb|AW929928|AW929928 EST354198 tomato flower buds 8 mm to pre-a... 46 2e-09
       emb|AW616209|AW616209 EST307248 L. hirsutum trichome, Cornell Un... 48 3e-09
       emb|AW432477|AW432477 sh74f01.yl Gm-c1015 Glycine max cDNA clone... 61 4e-09
       emb|AW092750|AW092750 EST285930 tomato mixed elicitor, BTI Lycop... 45 4e-09
       gb]M74102|TOBCPII Nicotiana sylvestris serine proteinase inhibit... 52 6e-09
35
      emb|AW622766|AW622766 EST306752 tomato flower buds 3-8 mm, Corne... 46 1e-08
       emblAI563053|AI563053 EST00177 watermelon lambda zap library Cit... 58 3e-08
       emb|AI563140|AI563140 EST00264 watermelon lambda zap library Cit... 58 3e-08
       emb|AI723907|AI723907 RHIZ1_32_B07.y1_A001 Rhizome1 Sorghum hale... 57 5e-08
       emb|AI724626|AI724626 RHIZ1_11_A01.y1_A001 Rhizome1 Sorghum hale... 57 5e-08
40
      emblAJ250663|HVU250663 Hordeum vulgare partial mRNA for putative... 57 5e-08
      emb|AI724485|AI724485 RHIZ1_10_F03.y1_A001 Rhizomel Sorghum hale... 57 5e-08
       dbj|D13662|TOBGTI Nicotiana glauca X Nicotiana langsdorffii mRNA... 51 7e-08
      gb|L06137|POTINH1X Solanum tuberosum proteinase inhibitor 1 (pin... 44 1e-07
      gb|L06985|POTPIN1A Solanum tuberosum proteinase inhibitor I mRNA... 43 1e-07
45
      gb[M13938|TOMWIPIG Tomato (L.esculentum) wound-inducible protein... 42 2e-07
      emb|AI771798|AI771798 EST252898 tomato ovary, TAMU Lycopersicon ... 42 2e-07
      emb|AI490242|AI490242 EST248568 tomato ovary, TAMU Lycopersicon ... 42 2e-07
      emb|AI486930|AI486930 EST245252 tomato ovary, TAMU Lycopersicon ... 42 2e-07
      gb|BE049671|BE049671 NXNV_140 C03 F Nsf Xylem Normal wood Vertic... 55 2e-07
50
      gb|K03290|TOMWIPI Tomato leaf wound-induced proteinase inhibitor... 42 2e-07
      emb|X67950|STPIN1MR S.tuberosum pin1 mRNA for proteinase inhibit... 41 5e-07
      emb|X67675|STPIN1 S.tuberosum mRNA for proteinase inhibitor I.
                                                                      41 5e-07
      emb|AW443358|AW443358 EST308288 tomato mixed elicitor, BTI Lycop... 42 5e-07
      emb|X57035|HVICA2 H.vulgare chymotryposin inhibitor-2 gene.
                                                                      53 8e-07
55
      emb|AI899242|AI899242 EST268685 tomato ovary, TAMU Lycopersicon ...
      emb|AI487831|AI487831 EST246153 tomato ovary, TAMU Lycopersicon ...
      emb|Z12611|STPROINI S.tuberosum proteinase inhibitor I.
      emblAW944847|AW944847 EST336897 tomato flower buds 3-8 mm, Corne... 41 1e-06
      emb|AW443908|AW443908 EST308838 tomato mixed elicitor, BTI Lycop... 41 1e-06
60
      emb|AW040832|AW040832 EST283696 tomato mixed elicitor, BTI Lycop... 41 1e-06
      emb|AI485812|AI485812 EST244133 tomato ovary, TAMU Lycopersicon ... 41 1e-06
```

```
emb|AW442733|AW442733 EST307663 tomato mixed elicitor, BTI Lycop... 41 1e-06
       emb|X05404|HVCI2A Barley mRNA or chymotrypsin inhibitor-2 (CI-2A). 53 1e-06
       gb|C95416|C95416 C95416 Citrus unshiu Miyagawa-wase maturation s... 52 2e-06
      emb|AW746262|AW746262 WS1 40 H09.b1 A002 Water-stressed 1 (WS1) ... 52 2e-06
      emb|AW746284|AW746284 WS1_40_H09.g1_A002 Water-stressed 1 (WS1) ... 52_2e-06
      emb|AW437904|AW437904 ST78A12 Pine TriplEx shoot tip library Pin... 52 2e-06
      emb|AW093975|AW093975 EST287155 tomato mixed elicitor, BTI Lycop... 35 4e-06
      emb|AI781668|AI781668 EST262547 tomato susceptible, Cornell Lyco... 35 4e-06
      emb|AW092485|AW092485 EST285665 tomato mixed elicitor, BTI Lycop...
                                                                            35 4e-06
10
      emb|AI772725|AI772725 EST253825 tomato resistant, Cornell Lycope... 35 5e-06
      emb|AI778944|AI778944 EST259823 tomato susceptible, Cornell Lyco... 35 5e-06
      emb|AI774403|AI774403 EST255503 tomato resistant, Cornell Lycope... 35 5e-06
      emb|AI772154|AI772154 EST253254 tomato resistant, Cornell Lycope... 35 5e-06
      emb|AW094311|AW094311 EST287491 tomato mixed elicitor, BTI Lycop...
                                                                            35 5e-06
15
      emb|AW092125|AW092125 EST285221 tomato mixed elicitor, BTI Lycop...
                                                                            35 5e-06
      emb|AW039975|AW039975 EST282466 tomato mixed elicitor, BTI Lycop...
                                                                            35 5e-06
      emb|AW039971|AW039971 EST282462 tomato mixed elicitor, BTI Lycop...
                                                                            35 5e-06
      emb[AW040872]AW040872 EST283736 tomato mixed elicitor, BTI Lycop...
                                                                            35 5e-06
      emb|AW093509|AW093509 EST286689 tomato mixed elicitor, BTI Lycop...
                                                                            35 5e-06
20
      emb|AI938012|AI938012 sc40a06.x1 Gm-c1014 Glycine max cDNA clone...
                                                                            51 5e-06
      emb|AW039063|AW039063 EST281036 tomato mixed elicitor, BTI Lycop...
                                                                            38 8e-06
      Query= AJ001809.1 at 19894 at /id source genbank /description
25
      emb|caa05025.1| (aj001809) succinate dehydrogenase flavoprotein alpha
      subunit [arabidopsis thaliana] /blast score 0 /ec_number /family
      dehydrogenase /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|aj001809| /ncgi
30
      http://www.ncgr.org/cgi-bin/ff?aj001809
           (2247 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
35
                                           Score
      Sequences producing significant alignments:
                                                          (bits) Value
40
      emb|AL132984|SPAC1556 S.pombe chromosome I cosmid c1556.
      emb|Z26877|SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro... 408 0.0
      emb|Z49320|SCYJL045W S.cerevisiae chromosome X reading frame ORF... 403 0.0
      gb]M86909|YSCSDH1A Saccharomyces cerevisiae succinate dehydrogen... 408 0.0
45
      gb M94874 YSCSDH1B Saccharomyces cerevisiae succinate dehydrogen... 408 0.0
      emb|Z28148|SCYKL148C S.cerevisiae chromosome XI reading frame OR... 408 0.0
      gb|M86746|YSCSDHA Saccharomyces cerevisiae succinate dehydrogena... 408 0.0
      dbj D86573 D86573 Plasmodium falciparum DNA for flavoprotein sub... 676 0.0
      emb|AB031741|AB031741 Trypanosoma cruzi mRNA for succinate dehyd... 456 0.0
50
      dbj|D89263|D89263 Schizosaccharomyces pombe mRNA, partial cds, c... 637 0.0
      emb[Y10377]CATOP2 C.albicans TOP2 gene.
      emb|AI771965|AI771965 EST253065 tomato resistant, Cornell Lycope... 495 e-139
      emb|AW720194|AW720194 LjNEST16f8r Lotus japonicus nodule library... 440 e-122
      emb|AI898950|AI898950 EST268393 tomato ovary, TAMU Lycopersicon ... 434 e-121
55
      emb|AI727777|AI727777 BNLGHi9047 Six-day Cotton fiber Gossypium ... 391 e-114
      emb|AW775119|AW775119 EST334270 KV3 Medicago truncatula cDNA clo... 407 e-112
      emb|AL110721|CNS018RU Botrytis cinerea strain T4 cDNA library un... 323 e-110
      emb|AW729362|AW729362 GA_Ea0024M24 Gossypium arboreum 7-10 dpa ... 314 4e-94
      emb|AW687411|AW687411 NF009C11RT1F1085 Developing root Medicago ... 208 2e-85
60
      emb|AW180257|AW180257 MgA0347f MgA Library Mycosphaerella gramin... 309 4e-83
      emb|AA660851|AA660851 00746 MtRHE Medicago truncatula cDNA 5' si... 163 3e-82
```

--- WO 02/22675 ---- PCT/US01/28506

emblAW760184|AW760184 sl59b01.yl Gm-c1027 Glycine max cDNA clone... 304 1e-81 emb|AI676411|AI676411 etmEST0165 EtH1 Eimeria tenella cDNA clone... 261 7e-81 emb|AW278355|AW278355 sf43a10.y1 Gm-c1009 Glycine max cDNA clone... 301 le-80 emb|AW703689|AW703689 sk23b10.y1 Gm-c1028 Glycine max cDNA clone... 298 1e-79 5 emb|AW350842|AW350842 GM210009B10E8R Gm-r1021 Glycine max cDNA 3... 293 3e-78 emblAW350838|AW350838 GM210009B10E7R Gm-r1021 Glycine max cDNA 3... 276 4e-73 emb|AW563308|AW563308 LG1 228 B12.g1_A002 Light Grown 1 (LG1) So... 274 2e-72 emb|AW398787|AW398787 EST309287 L. pennellii trichome, Cornell U... 246 4e-67 emb|AW688181|AW688181 NF004D03ST1F1000 Developing stem Medicago ... 204 5e-67 10 emb|AW685660|AW685660 NF033C09NR1F1000 Nodulated root Medicago t... 235 4e-65 emblAQ873013|AQ873013 V57F7 mTn-3xHA/lacZ Insertion Library, str... 170 2e-63 emb[X54702]LPPLB08M L.polyphyllus pPLB08 mRNA. emb|AW180015|AW180015 MgA0071f MgA Library Mycosphaerella gramin... 233 4e-60 15 emb|AI495497|AI495497 sa98g08.yl Gm-c1004 Glycine max cDNA clone... 219 8e-56 emb|AQ659505|AQ659505 Sheared DNA-5G1.TR Sheared DNA Trypanosoma... 212 1e-53 emb|AI391973|AI391973 NCC1F7T3 Conidial Neurospora crassa cDNA c... 162 4e-50 emb|AW774144|AW774144 EST333227 KV3 Medicago truncatula cDNA clo... 184 2e-48 emb|AI055409|AI055409 coau0003O20 Cotton Boll Abscission Zone cD... 177 le-47 20 emb|AQ659508|AQ659508 Sheared DNA-5G3.TF Sheared DNA Trypanosoma... 140 2e-46 emb|AW922507|AW922507 DG1 20 E07.g1 A002 Dark Grown 1 (DG1) Sorg... 184 3e-45 emb|AW218470|AW218470 EST303653 tomato radicle, 5 d post-imbibit... 168 2e-40 emb|AW180288|AW180288 MgA0381f MgA Library Mycosphaerella gramin... 167 2e-40 25 emb|AW334279|AW334279 S32G2 AGS-1 Pneumocystis carinii f. sp. ca... 158 5e-39 gb|T15234|T15234 crs828 lambdaZAPST Ricinus communis cDNA clone ... 161 2e-38 emb|AQ873266|AQ873266 V62G2 mTn-3xHA/lacZ Insertion Library, str... 129 5e-37 emb|AW736632|AW736632 EST333124 KV3 Medicago truncatula cDNA clo... 136 4e-34 emb|AW287458|AW287458 LG1 228 B12.b1 A002 Light Grown 1 (LG1) So... 145 1e-33 30 emb|AV409739|AV409739 AV409739 Lotus japonicus young plants (two... 138 6e-33 emb|AW255532|AW255532 ML565 peppermint glandular trichome Mentha... 87 9e-33 emb|AQ646390|AQ646390 RPCI93-DpnII-29L18.TJ RPCI93-DpnII Trypano... 120 2e-32 emb|AW350507|AW350507 GM210008B20H12R Gm-r1021 Glycine max cDNA ... 140 4e-35 emb|AW736633|AW736633 EST333125 KV3 Medicago truncatula cDNA clo... 128 6e-32 emb|AA051852|AA051852 Cn0030-5 Cryptococcus neoformans, Stratage... 117 3e-31 emblAW759819|AW759819 sl54d12.yl Gm-c1027 Glycine max cDNA clone... 131 2e-29 gb|BE020875|BE020875 sm53d08.yl Gm-c1028 Glycine max cDNA clone ... 127 2e-28 emb|AW703733|AW703733 sk23g01.yl Gm-c1028 Glycine max cDNA clone... 127 2e-28 40 emb|AW991033|AW991033 SsS0224 Suaeda salsa ZAP cDNA library Suae... 95 9e-28 gb|BE057332|BE057332 sn01g03.y1 Gm-c1015 Glycine max cDNA clone ... 117 3e-25 emb|AW180944|AW180944 MgA0071r MgA Library Mycosphaerella gramin... 108 1e-22 emb|AI496172|AI496172 sa96c04.yl Gm-c1004 Glycine max cDNA clone... 98 3e-19 gb|BE024378|BE024378 894002F01.yl C. reinhardtii CC-1690, normal... 96 8e-19 45 emb|AW830714|AW830714 sm35c05.yl Gm-c1028 Glycine max cDNA clone... 81 3e-18 emb|AW568440|AW568440 si70g12.yl Gm-c1031 Glycine max cDNA clone... 88 2e-16 emb|AQ873304|AQ873304 V63D7 mTn-3xHA/lacZ Insertion Library, str... 57 3e-16 gb|BE125576|BE125576 DG1_28_E07.b1_A002 Dark Grown 1 (DG1) Sorgh... 76 1e-12 gb|BE034538|BE034538 MK01A06 MK Mesembryanthemum crystallinum cD... 74 3e-12 50 emb|AW773033|AW773033 925002H09.yl C. reinhardtii CC-2290, norma... 52 4e-12 gb|BE122635|BE122635 Ljirnpest30-425-h1 Ljirnp Lambda HybriZap t... 53 5e-12 emb|AQ872933|AQ872933 V55G2 mTn-3xHA/lacZ Insertion Library, str... 49 2e-10 emb|AU006770|AU006770 AU006770 Schizosaccharomyces pombe late lo... 65 2e-09 gb|L46545|L46545 BNAF1848 Mustard flower buds Brassica rapa cDNA... 61 4e-08 55 gb|L36344|YSCTGGMS Saccharomyces cerevisiae tRNA-Met, tRNA-Ser, ... 47 1e-06 gb|L26347|YSCSEQA Saccharomyces cerevisiae COR gene cluster, iso... 47 1e-06 emb|Z49551|SCYJR051W S.cerevisiae chromosome X reading frame ORF... 47 1e-06 emb|AQ502406|AQ502406 V17H2 mTn-3xHA/lacZ Insertion Library Sacc... 55 3e-06 gb|U18779|SCE8199 Saccharomyces cerevisiae chromosome V cosmid 8... 46 1e-05 60 emb|AC011017|AC011017 Leishmania major chromosome 35 clone L3184... 45 1e-05 emb|AL356456|LMFLUNK01 Leishmania major Friedlin cosmid clones L... 45 2e-05

emb|AL110853|CNS018VI Botrytis cinerea strain T4 cDNA library un... 38 1e-04 emb|AC022284|AC022284 Leishmania major chromosome 35 clone L3377... 43 2e-04 emb|AQ912027|AQ912027 LMAJFV1 ln10g05.yl Leishmania major FV1 ra... 37 2e-04 emb|Z99292|SPAC17A2 S.pombe chromosome I cosmid c17A2. 44 7e-04 emb|AI897849|AI897849 EST267292 tomato ovary, TAMU Lycopersicon ... 46 0.002 emblAZ218322|AZ218322 Sheared DNA-81H6.TF Sheared DNA Trypanosom... 46 0.002 emb|AQ652406|AQ652406 Sheared DNA-22G19.TR Sheared DNA Trypanoso... 40 0.003 emb|AW401245|AW401245 LamdiGest417est L.digitata gametophyte Lam... 38 0.009 emb|AQ948036|AQ948036 Sheared DNA-45P20.TF Sheared DNA Trypanoso... 42 0.020 10 emb|AA785876|AA785876 h8g02a1.rl Aspergillus nidulans 24hr asexu... 40 0.053 gb[BE036039]BE036039 MO18H07 MO Mesembryanthemum crystallinum cD... 40 0.099 emb|AQ850793|AQ850793 LMAJFV1_lm31g07.x1 Leishmania major FV1 ra... 39 0.14 emb|AF163958|AF163958 Saccharomyces cerevisiae isolate wt-13 tel... 29 0.19 emb|AW649153|AW649153 EST327607 tomato germinating seedlings, TA... 34 0.46 15 emb|AW618015|AW618015 EST313981 L. pennellii trichome, Cornell U... 37 0.49 emb|AW398425|AW398425 EST298272 L. pennellii trichome, Cornell U... 37 0.49 emb|AW678775|AW678775 WS1 1 B06.b2 A002 Water-stressed 1 (WS1) S... 37 0.67 emb|AW678627|AW678627 WS1 1 B06.b1 A002 Water-stressed 1 (WS1) S... 37 0.67 emb|AF136006|AF136006 Triticum aestivum eukaryotic initiation fa... 37 0.67 20 Query= AC005727.175 at 19914 at /id source genbank /description gb|aac79593.1| (ac005727) unknown protein [arabidopsis thaliana] /blast score 0 /ec number /family /chip nova /gb link 25 http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005727| /ncgi http://www.ncgr.org/cgi-bin/ff?ac005727 (2008 letters). 30 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 35 Score Sequences producing significant alignments: (bits) Value emb|AW234376|AW234376 sf24e02.yl Gm-c1028 Glycine max cDNA clone... 315 7e-85 emb|AW234848|AW234848 sf19h05.y1 Gm-c1028 Glycine max cDNA clone... 240 2e-62 40 emb|AI782064|AI782064 EST262943 tomato susceptible, Cornell Lyco... 220 4e-56 emb|AW290802|AW290802 NXNV047A02F Nsf Xylem Normal wood Vertical... 204 2e-51 emb|AA856223|AA856223 L30-246T3 Ice plant Lambda Uni-Zap XR expr... 182 1e-45 gb|BE058219|BE058219 sn13b08.yl Gm-c1016 Glycine max cDNA clone ... 184 2e-45 emb|AW458125|AW458125 sh78e12.yl Gm-c1016 Glycine max cDNA clone... 183 5e-45 45 emb|AW030539|AW030539 EST273794 tomato callus, TAMU Lycopersicon... 163 2e-43 emb|AW565896|AW565896 LG1_353_C06.g1_A002 Light Grown 1 (LG1) So... 156 5e-37 emb|AW569925|AW569925 si83d03.yl Gm-c1031 Glycine max cDNA clone... 153 4e-36 emb|AT000567|AT000567 AT000567 Brassica rapa guard cell Brassica... 106 4e-33 emb|AW648540|AW648540 EST326994 tomato germinating seedlings, TA... 69 2e-24 50 emb|AW033885|AW033885 EST277456 tomato callus, TAMU Lycopersicon... 108 1e-22 emb|AW284143|AW284143 LG1 262 C03.g1 A002 Light Grown 1 (LG1) So... 101 1e-20 emblAW676943|AW676943 DG1 2 E04.b1 A002 Dark Grown 1 (DG1) Sorgh... 101 2e-20 emb|AW277624|AW277624 sf84e05.yl Gm-c1019 Glycine max cDNA clone... 95 2e-18

emb|AW698260|AW698260 NXNV_070_G09_F Nsf Xylem Normal wood Verti... 81 3e-14 emb|AW560258|AW560258 EST315306 DSIR Medicago truncatula cDNA cl... 51 6e-14

emb|AV428005|AV428005 AV428005 Lotus japonicus young plants (two... 91 2e-17

emb|AW399438|AW399438 EST309938 L. pennellii trichome, Cornell U... 64 2e-16 emb|AF097667|AF097667 Mesembryanthemum crystallinum protein phos... 52 4e-15 emb|AW617510|AW617510 EST323921 L. hirsutum trichome, Cornell Un... 64 6e-15 emb|AW698259|AW698259 NXNV_070_G08_F Nsf Xylem Normal wood Verti... 83 6e-15 emb|AW560259|AW560259 EST315307 DSIR Medicago truncatula cDNA cl... 53 2e-14

55

60

```
emb|AW626583|AW626583 NXNV067A10 Nsf Xylem Normal wood Vertical ... 70 6e-14
      emb|AW163982|AW163982 Ljimpest18-406-a10 Ljimp Lambda HybriZap... 73 6e-14
      emb|AW698258|AW698258 NXNV 070 G07 F Nsf Xylem Normal wood Verti... 79 1e-13
      gb|BE058708|BE058708 sn19g01.yl Gm-c1016 Glycine max cDNA clone ... 51 5e-13
 5
      emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 49 7e-13
      emb|AF079355|AF079355 Mesembryanthemum crystallinum protein phos... 51 2e-12
      emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 50 2e-12
      emb|Z74998|SCYOR090C S.cerevisiae chromosome XV reading frame OR... 50 2e-12
      emb|AJ277744|FSY277744 Fagus sylvatica mRNA for ABA and calcium ... 56 2e-12
      emb|AI485178|AI485178 EST243482 tomato ovary, TAMU Lycopersicon ... 51 3e-12
10
      emb|AW932792|AW932792 EST358635 tomato fruit mature green, TAMU ... 51 8e-12
      emb|AW676913|AW676913 DG1_2_G04.b1_A002 Dark Grown 1 (DG1) Sorgh... 72_2e-11
      emb|AW164418|AW164418 se72c06.y1 Gm-c1023 Glycine max cDNA clone... 47 3e-11
      emb|AI726381|AI726381 BNLGHi5700 Six-day Cotton fiber Gossypium ... 44 7e-11
15
      emb|AW348221|AW348221 GM210001B12B8R Gm-r1021 Glycine max cDNA 3... 48 5e-10
      emb|AW650300|AW650300 EST328754 tomato germinating seedlings, TA... 46 6e-10
      gb|BE053500|BE053500 GA Ea0001P09f Gossypium arboreum 7-10 dpa ... 53 1e-09
      gb|C23895|C23895 C23895 Miyagawa-wase satsuma mandarin orange (M... 65 2e-09'
      emb|AI896264|AI896264 EST265707 tomato callus, TAMU Lycopersicon... 53 2e-09
      emb|AW687126|AW687126 NF006C06RT1F1049 Developing root Medicago ... 53 7e-09
      emb|AI897957|AI897957 EST267400 tomato ovary, TAMU Lycopersicon ... 48 1e-08
      emb|AW030242|AW030242 EST273497 tomato callus, TAMU Lycopersicon... 38 2e-08
      emb|AV420315|AV420315 AV420315 Lotus japonicus young plants (two... 52 3e-08
      emb|AW729643|AW729643 GA_Ea0025K03 Gossypium arboreum 7-10 dpa ... 59 8e-08
25
      emb|AI897759|AI897759 EST267202 tomato ovary, TAMU Lycopersicon ... 54 6e-07
      emb|AI897074|AI897074 EST266517 tomato ovary, TAMU Lycopersicon ... 56 1e-06
      emb|AI899132|AI899132 EST268575 tomato ovary, TAMU Lycopersicon ... 56 1e-06
      emb|AW256742|AW256742 EST304879 KV2 Medicago truncatula cDNA clo... 55 2e-06
      emb|AI489557|AI489557 EST247896 tomato ovary, TAMU Lycopersicon ... 54 3e-06
30
      emb|AI898184|AI898184 EST267627 tomato ovary, TAMU Lycopersicon ... 54 3e-06
      emb|AI895459|AI895459 EST264902 tomato callus, TAMU Lycopersicon... 54 4e-06
      emb|AW398099|AW398099 EST297982 L. pennellii trichome, Cornell U... 54 5e-06
      emb|AW207933|AW207933 M111162e DSIR Medicago truncatula cDNA clo... 54 5e-06
      emb|AV427908|AV427908 AV427908 Lotus japonicus young plants (two... 54 5e-06
35
      emb|AL355926|NCB17C10 Neurospora crassa DNA linkage group II BAC... 42 7e-06
      emb|AI486082|AI486082 EST244403 tomato ovary, TAMU Lycopersicon ... 53 7e-06
      emb|AW093348|AW093348 EST286528 tomato mixed elicitor, BTI Lycop... 53 1e-05
      emb|AW746773|AW746773 WS1 55 B12.b1 A002 Water-stressed 1 (WS1) ... 53 1e-05
      emb|AW666538|AW666538 GA_Ea0005H20 Gossypium arboreum 7-10 dpa ... 53 1e-05
40
      emb|AW309762|AW309762 sf24e02.x1 Gm-c1028 Glycine max cDNA clone... 52 1e-05
      emblAW624350lAW624350 EST322295 tomato flower buds 3-8 mm, Corne... 51 3e-05
      emb|AV417021|AV417021 AV417021 Lotus japonicus young plants (two... 51 3e-05
      emb|AW290215|AW290215 NXNV015C12F Nsf Xylem Normal wood Vertical... 51 4e-05
      emb|AI484987|AI484987 EST243250 tomato ovary, TAMU Lycopersicon ... 51 4e-05
45
      emb|AI728047|AI728047 BNLGHi9685 Six-day Cotton fiber Gossypium ... 51 4e-05
      emb|AI771145|AI771145 EST252341 tomato ovary, TAMU Lycopersicon ... 51 4e-05
      emb|AI939275|AI939275 sc69f06.yl Gm-c1016 Glycine max cDNA clone... 50 5e-05
      emb|AI052977|AI052977 Mpc4 Ice plant seedlings, RT-PCR, pCRII M... 50 5e-05
      emb|AW349802|AW349802 GM210006A20E6R Gm-r1021 Glycine max cDNA 3... 49 9e-05
50
      emblAW349791|AW349791 GM210006A20E12R Gm-r1021 Glycine max cDNA ... 49 9e-05
      emb|AW933759|AW933759 EST359602 tomato fruit mature green, TAMU ... 49 9e-05
      emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 43 1e-04
      emb|AW598662|AW598662 sj94c01.yl Gm-c1023 Glycine max cDNA clone... 49 2e-04
      emb|AW037487|AW037487 EST275994 tomato mixed elicitor, BTI Lycop... 49 2e-04
55
      emb|AW328948|AW328948 N200140e rootphos(-) Medicago truncatula c... 48 2e-04
      emb|AI442775|AI442775 sa26c12.x1 Gm-c1004 Glycine max cDNA clone... 48 2e-04
      emb|AW399213|AW399213 EST309713 L. pennellii trichome, Cornell U... 48 3e-04
      emb|AI779659|AI779659 EST260538 tomato susceptible, Cornell Lyco... 48 3e-04
      emb|AI486266|AI486266 EST244587 tomato ovary, TAMU Lycopersicon ... 41 4e-04
60
      emb|AW677101|AW677101 DG1_4_D08.b1_A002 Dark Grown 1 (DG1) Sorgh... 47 5e-04
      emb|AB029099|AB029099 AB029099 Cucumis sativus library (Chono M)... 47 5e-04
```

emb|AI897604|AI897604 EST267047 tomato ovary, TAMU Lycopersicon ... 47 6e-04 emb|AI898276|AI898276 EST267719 tomato ovary, TAMU Lycopersicon ... 47 6e-04 emb|AW101984|AW101984 sd81e10.y1 Gm-c1009 Glycine max cDNA clone... 46 9e-04 emb|AW696975|AW696975 NF111A04ST1F1024 Developing stem Medicago ... 46 0.001 5 emb|AL035475|PFMAL4P2 Plasmodium falciparum MAL4P2, complete seq... 46 0.001 emb|AW396281|AW396281 sh26f02.yl Gm-c1016 Glycine max cDNA clone... 38 0.002 emb|AW926387|AW926387 HVSMEg0007B08 Hordeum vulgare pre-anthesis... 38 0.002 emb|AF075581|AF075581 Mesembryanthemum crystallinum clone Mpc6 p... 42 0.002 emb|AI900423|AI900423 sc05e10.yl Gm-c1012 Glycine max cDNA clone... 45 0.002 10 emb|AI060327|AI060327 Mpc6 Ice plant seedlings, RT-PCR, pCRII M... 42 0.002 emb|AI897958|AI897958 EST267401 tomato ovary, TAMU Lycopersicon ... 40 0.003 emb|AW982223|AW982223 HVSMEg0002G04f Hordeum vulgare pre-anthesi... 44 0.003 gb|BE124122|BE124122 EST394247 DSIL Medicago truncatula cDNA clo... 35 0.004 emb|AW126333|AW126333 N100440e rootphos(-) Medicago truncatula c... 44 0.004 15 emb|AI461042|AI461042 sa73c01.yl Gm-c1004 Glycine max cDNA clone... 44 0.006

Query= AC005395.47_at 19951_at /id_source genbank /description gb|aac42241.1| (ac005395) unknown protein [arabidopsis thaliana]

/blast_score 1.00e-157 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005395| /ncgi http://www.ncgr.org/cgi-bin/ff?ac005395

(938 letters)

25

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E

Sequences producing significant alignments:

(bits) Value

gb|BE036593|BE036593 MP01G10 MP Mesembryanthemum crystallinum cD... 387 e-119 35 emb|AW329378|AW329378 N200608e rootphos(-) Medicago truncatula c... 386 e-107 emb|AW725467|AW725467 GA_Ea0018B18 Gossypium arboreum 7-10 dpa ... 275 e-105 emb|AI966343|AI966343 sc37e08.yl Gm-c1014 Glycine max cDNA clone... 260 6e-97 40 emb|AW442228|AW442228 EST311624 tomato fruit red ripe, TAMU Lyco... 308 5e-95 emb|AW255529|AW255529 ML562 peppermint glandular trichome Mentha... 319 3e-93 emb|AW221896|AW221896 EST298707 tomato fruit red ripe, TAMU Lyco... 215 2e-78 emb|AW678275|AW678275 WS1 14 A02.b1 A002 Water-stressed 1 (WS1) ... 157 1e-77 45 emb|AI730573|AI730573 BNLGHi7295 Six-day Cotton fiber Gossypium ... 272 3e-72 emb|AW219191|AW219191 EST301673 tomato root during/after fruit s... 211 5e-54 emb|AV409540|AV409540 AV409540 Lotus japonicus young plants (two... 211 7e-54 emb|AV423705|AV423705 AV423705 Lotus japonicus young plants (two... 207 1e-52 emb|AA231842|AA231842 CDO920.R cDNA from oat Avena sativa cDNA c... 175 9e-46 50 emb|AW695662|AW695662 NF097C11ST1F1085 Developing stem Medicago ... 166 4e-45 emb|AI960056|AI960056 sc37e08.x1 Gm-c1014 Glycine max cDNA clone... 98 2e-44 emb|AI759880|AI759880 sb65e12.yl Gm-c1017 Glycine max cDNA clone... 152 3e-41 emb|AW677045|AW677045 DG1_4_G06.b1_A002 Dark Grown 1 (DG1) Sorgh... 135 4e-31 emb|AW598595|AW598595 sj93f10.yl Gm-c1023 Glycine max cDNA clone... 118 5e-26 55 emb|AW684174|AW684174 NF013F01NR1F1000 Nodulated root Medicago t... 112 3e-24 emb|AW677664|AW677664 WS1 10 G12.b1 A002 Water-stressed 1 (WS1) ... 100 1e-20 emb|AW677709|AW677709 WS1_10_G12.g1_A002 Water-stressed 1 (WS1) ... 100 1e-20 emb|AW757178|AW757178 sl30b05.yl Gm-c1027 Glycine max cDNA clone... 95 4e-20 emb|AA231890|AA231890 CDO920.F cDNA from oat Avena sativa cDNA c... 82 8e-15 60 emb|AE001381|AE001381 Plasmodium falciparum chromosome 2, sectio... 57 2e-07

emb|AW734973|AW734973 sk92g05.y1 Gm-c1035 Glycine max cDNA clone... 56 4e-07

	emb AI612519 AI612519 TENGO335 T. Cruzi epimastigote normalised 47 2e-04 emb AA926384 AA926384 TENS1006 T. cruzi epimastigote normalized 38 0.13 emb AA555388 AA555388 CpEST.617 uniZAPCpIOWAsporoLib3 Cryptospor 37 0.25
5	emb AW666632 AW666632 GA_Ea0005D10 Gossypium arboreum 7-10 dpa 37 0.25 emb AW695873 AW695873 NF100C01ST1F1004 Developing stem Medicago 36 0.48
	emb AW685637 AW685637 NF032F04NR1F1000 Nodulated root Medicago t 35 0.66 emb AW930970 AW930970 EST356813 tomato fruit mature green, TAMU 35 0.91
	emb AW930458 AW930458 EST340831 tomato fruit mature green, TAMU 35 0.91
10	emb AW035833 AW035833 EST281987 tomato callus, TAMU Lycopersicon 35 0.91 emb AI211536 AI211536 p0h06a1.rl Aspergillus nidulans 24hr asexu 35 0.91
	emb AQ640157 AQ640157 927P1-18A7.TP 927P1 Trypanosoma brucei gen 35 1.2
	emb AW349276 AW349276 GM210004B21H2R Gm-r1021 Glycine max cDNA 3 34 2.4 emb AQ324698 AQ324698 mgxb0019F05r CUGI Rice Blast BAC Library P 34 2.4
	emb AA550044 AA550044 1130m3 gmbPfHB3.1, G. Roman Reddy Plasmodi 34 2.4
15	gb U19028 YSCL8300 Saccharomyces cerevisiae chromosome XII cosmi 34 2.4
	emb X06689 PCLIGH8 Phanerochaete chrysosporium gene for ligninas 29 2.5 gb M27401 PHALIGH8 Phanerochaete chrysosporium ligninase isozyme 29 2.5
	emb[X51590]PCGLG3 P. chrysosporium GLG3 (LIP) gene for lignin pe 29 2.5
20	gb M27884 PHALPIA P.chrysoporium lignin peroxidase isozyme H8 ge 29 2.5
20	emb AW693181 AW693181 NF061C03ST1F1000 Developing stem Medicago 33 3.2 emb AW761196 AW761196 s164d11.y1 Gm-c1027 Glycine max cDNA clone 33 4.4
•	emb AQ502162 AQ502162 V8A9 mTn-3xHA/lacZ Insertion Library Sacch 33 4.4
	gb M37701 PHALPO P.chrysosporium lignin peroxidase genes, comple 28 5.7
25	emb Z75009 SCYOR101W S.cerevisiae chromosome XV reading frame OR 32 6.1 gb U32307 SCU32307 Saccharomyces cerevisiae oligosaccharyltransf 32 6.1
	emb AW201959 AW201959 sf09d01.y1 Gm-c1027 Glycine max cDNA clone 32 6.1
	emb Z70690 SPAC1F3 S.pombe chromosome I cosmid c1F3. 32 6.1 emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo 32 6.1
	emb AL022070 SPBC3B9 S.pombe chromosome II cosmid c3B9. 32 6.1
30	emb AI416552 AI416552 sa10f05.yl Gm-c1003 Glycine max cDNA clone 32 6.1
	gb M33139 YSPRPA3 S.pombe ribosomal protein A3 (rpa2+) gene, com 32 6.1 gb BE056330 BE056330 00241 leafy spurge Lambda HybriZAP 2.1 two 32 8.4
	emb AF136004 AF136004 Triticum aestivum eukaryotic initiation fa 32 8.4
35	emb AW395197 AW395197 sh45b04.y1 Gm-c1017 Glycine max cDNA clone 32 8.4 emb AW671822 AW671822 LG1_351_G04.g1_A002 Light Grown 1 (LG1) So 32 8.4
55	emb AW671822 AW671822 LG1_351_G04.g1_A002 Light Grown 1 (LG1) So 32 8.4 emb AQ648854 AQ648854 Sheared DNA-18A21.TR Sheared DNA Trypanoso 32 8.4
	gb BE059776 BE059776 sn37a01.yl Gm-c1016 Glycine max cDNA clone 32 8.4
	emb X12698 PCLIGNINA P. chrysosporium mRNA for ligninase (rLDM(T 29 8.5
40	
	Query= AC002986.28_at 19982_at /id_source genbank /description "gb aac17040.1 (ac002986) similarity to a. thaliana gene product
	f21m12.20, gb ac000132. est gb z25651 comes from this gene.
45	[arabidopsis thaliana]" /blast_score 0 /ec_number /family /chip nova
73	/gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac002986 /ncgi
	http://www.ncgr.org/cgi-bin/ff?ac002986
	(1593 letters)
50	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
55	Score E
	Sequences producing significant alignments: (bits) Value
	gb BE053277 BE053277 GA_Ea0035A14f Gossypium arboreum 7-10 dpa 205 1e-78
60	emb AW831229 AW831229 sm12g02.yl Gm-c1027 Glycine max cDNA clone 207 3e-78 emb AW678776 AW678776 WS1_1_A04.b2_A002 Water-stressed 1 (WS1) S 224 1e-77
	emb AW678614 AW678614 WS1_1_A04.b1_A002 Water-stressed 1 (WS1) S 224 1e-77

emb|AW688577|AW688577 NF009B11ST1F1000 Developing stem Medicago ... 214 5e-75 emb|AW757260|AW757260 sl32a03.yl Gm-c1027 Glycine max cDNA clone... 194 le-74 emblAW684123|AW684123 NF012F07NR1F1000 Nodulated root Medicago t... 179 7e-70 emb|AW933688|AW933688 EST359531 tomato fruit mature green, TAMU ... 261 1e-68 emb|AW035607|AW035607 EST281345 tomato callus, TAMU Lycopersicon... 255 8e-67 emb|AW508601|AW508601 si34b06.yl Gm-r1030 Glycine max cDNA clone... 166 8e-66 emb|AW680760|AW680760 WS1_7_B05.b1_A002 Water-stressed 1 (WS1) S... 168 1e-65 emb|AW564408|AW564408 LG1 292 D08.b1 A002 Light Grown 1 (LG1) So... 251 1e-65 emb|AV411756|AV411756 AV411756 Lotus japonicus young plants (two... 186 3e-65 10 emb|AW926737|AW926737 HVSMEg0008A08 Hordeum vulgare pre-anthesis... 210 6e-64 emb|AW443003|AW443003 EST307933 tomato mixed elicitor, BTI Lycop... 160 8e-64 emb|AW928933|AW928933 EST337817 tomato flower buds 8 mm to pre-a... 244 1e-63 emb|AW684792|AW684792 NF021B07NR1F1000 Nodulated root Medicago t... 221 1e-63 emb|AW508690|AW508690 si35c03.yl Gm-r1030 Glycine max cDNA clone... 159 3e-62 15 emb|AI731330|AI731330 BNLGHi9231 Six-day Cotton fiber Gossypium ... 236 4e-61 emb|AW759875|AW759875 sl55c03.yl Gm-c1027 Glycine max cDNA clone... 216 3e-60 emb|AW508088|AW508088 si50f10.y1 Gm-r1030 Glycine max cDNA clone... 156 4e-60 emb|AW737936|AW737936 EST339363 tomato flower buds, anthesis, Co... 230 2e-59 emb|AW983534|AW983534 HVSMEg0010P13f Hordeum vulgare pre-anthesi... 144 3e-58 20 emb|AW208258|AW208258 M110914e GVSN Medicago truncatula cDNA clo... 201 2e-57 emb|AI899909|AI899909 sb96a05.yl Gm-c1012 Glycine max cDNA clone... 216 3è-55 emb|AW746930|AW746930 WS1 56 B01.b1 A002 Water-stressed 1 (WS1) ... 132 7e-55 emb|AW127622|AW127622 M110358 DSLC Medicago truncatula cDNA clon... 208 1e-52 emb|AW094255|AW094255 EST287435 tomato mixed elicitor, BTI Lycop... 195 1e-48 25 emb|AV424875|AV424875 AV424875 Lotus japonicus young plants (two... 159 3e-48 emb|AW216607|AW216607 EST295321 tomato callus, TAMU Lycopersicon... 191 2e-47 emb|AW622247|AW622247 EST313045 tomato root during/after fruit s... 190 2e-47 emb|AW761408|AW761408 sl67b04.yl Gm-c1027 Glycine max cDNA clone... 185 7e-46 emb|AW441544|AW441544 EST310940 tomato fruit red ripe, TAMU Lyco... 184 1e-45 30 emb[AW203607]AW203607 sf36b08.y1 Gm-c1028 Glycine max cDNA clone... 174 2e-42 emb|AW746061|AW746061 WS1_39_D07.b1_A002 Water-stressed 1 (WS1) ... 168 1e-40 emb|AI794979|AI794979 sb74e06.yl Gm-c1010 Glycine max cDNA clone... 108 1e-40 emb|AW755419|AW755419 sl03g08.yl Gm-c1036 Glycine max cDNA clone... 104 3e-40 emb|AW329571|AW329571 N200823e rootphos(-) Medicago truncatula c... 97 1e-37 emb|AW774738|AW774738 EST333889 KV3 Medicago truncatula cDNA clo... 157 1e-37 35 emb|AW201668|AW201668 sf05h05.yl Gm-c1027 Glycine max cDNA clone... 155 7e-37 emb|AW781444|AW781444 sl78f03.yl Gm-c1037 Glycine max cDNA clone... 154 2e-36 emb|AW037635|AW037635 EST279093 tomato mixed elicitor, BTI Lycop... 148 1e-34 emb|AI823132|AI823132 L30-1015T3 Ice plant Lambda Uni-Zap XR exp... 142 6e-33 40 emb|AW595996|AW595996 si96e10.y1 Gm-c1032 Glycine max cDNA clone... 138 1e-31 emb|AI896179|AI896179 EST265622 tomato callus, TAMU Lycopersicon... 135 1e-30 emb|AW756882|AW756882 sk82d02.yl Gm-c1016 Glycine max cDNA clone... 131 2e-29 emb[AW756279]AW756279 s118d04.y1 Gm-c1036 Glycine max cDNA clone... 130 2e-29 emb|AW621046|AW621046 sj95c02.y1 Gm-c1023 Glycine max cDNA clone... 123 3e-27 45 gb[U28373]YSCD9481 Saccharomyces cerevisiae chromosome IV cosmid... 64 2e-25 emb|AW924277|AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ... 109 7e-23 emb|AI960559|AI960559 sc86a02.y1 Gm-c1018 Glycine max cDNA clone... 109 7e-23 gb|BE060234|BE060234 HVSMEg0011K15f Hordeum vulgare pre-anthesis... 107 3e-22 emb|AW736643|AW736643 EST333135 KV3 Medicago truncatula cDNA clo... 104 2e-21 50 emb|AA231652|AA231652 BCD98.F cDNA from barley Hordeum vulgare c... 99 1e-19 emb|AW736642|AW736642 EST333134 KV3 Medicago truncatula cDNA clo... 92 8e-18 emb|AW568172|AW568172 si57d03.yl Gm-r1030 Glycine max cDNA clone... 84 2e-15 emb[AW256616]AW256616 EST304753 KV2 Medicago truncatula cDNA clo... 84 3e-15 emb|AI960723|AI960723 sc89e07.yl Gm-c1019 Glycine max cDNA clone... 78 2e-13 55 emb|AI728294|AI728294 BNLGHi10384 Six-day Cotton fiber Gossypium... 76 6e-13 emb|AI822771|AI822771 L30-604T3 Ice plant Lambda Uni-Zap XR expr... 76 9e-13 emb|AW564841|AW564841 LG1_310_B02.b1_A002 Light Grown 1 (LG1) So... 74 3e-12 emb|AW278636|AW278636 sf63b11.yl Gm-c1013 Glycine max cDNA clone... 70 5e-11 emb[AW350463]AW350463 GM210008A20F3R Gm-r1021 Glycine max cDNA 3... 64 4e-09 60 emb|AW563245|AW563245 LG1 204_C07.g1_A002 Light Grown 1 (LG1) So... 61 2e-08 emb|AW760716|AW760716 sl36b09.yl Gm-c1027 Glycine max cDNA clone... 45 2e-07

	emb AW318040 AW318040 sg60d08.yl Gm-c1007 Glycine max cDNA clone 56 6e-07
	- 1 · · · · · · · · · · · · · · · · · ·
	emb AW704696 AW704696 sk39d04.y1 Gm-c1028 Glycine max cDNA clone 45 1e-05
_	emb AW350967 AW350967 GM210010B10H7R Gm-r1021 Glycine max cDNA 3 51 2e-05
5	emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque 38 2e-04
	emb AW981040 AW981040 EST392193 GVN Medicago truncatula cDNA clo 45 0.002
	gb L44100 BLYFQ Hordeum vulgare (clone CD98) STS mRNA, sequence 43 0.006
*	emb AW618476 AW618476 EST320462 L. pennellii trichome, Cornell U 42 0.014
	emb AW678071 AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) 41 0.026
10	emb AB024989 AB024989 Cicer arietinum mRNA for chalcone reductas 40 0.036
10	* * * * * * * * * * * * * * * * * * *
	emb AW684697 AW684697 NF019H04NR1F1000 Nodulated root Medicago t 40 0.050
	emb AW256585 AW256585 EST304722 KV2 Medicago truncatula cDNA clo 40 0.050
	emb AW309364 AW309364 sf16d12.x1 Gm-c1028 Glycine max cDNA clone 38 0.24
15	emb AW348632 AW348632 GM210002B22H5R Gm-r1021 Glycine max cDNA 3 38 0.24
	emb AW348958 AW348958 GM210004A12C5R Gm-r1021 Glycine max cDNA 3 38 0.24
	emb AW309230 AW309230 sf29a01.x1 Gm-c1028 Glycine max cDNA clone 38 0.24
	emb AW101404 AW101404 sd79e02.yl Gm-c1009 Glycine max cDNA clone 37 0.44
	emb Z36281 TBI17RN T.brucei I17 mRNA for flagellar antigen. 36 0.45
20	emb[X82366]MSCHR1A M.sativa mRNA for chalcone reductase (1202 bp). 36 0.61
20	
	emb AW650600 AW650600 EST329054 tomato germinating seedlings, TA 36 0.61
	emb AW649434 AW649434 EST327888 tomato germinating seedlings, TA 36 0.61
	emb AW329584 AW329584 N200836e rootphos(-) Medicago truncatula c 36 0.83
25	gb BE059817 BE059817 sn37e05.yl Gm-c1016 Glycine max cDNA clone 35 1.2
	emb AW760667 AW760667 sl53d03.yl Gm-c1027 Glycine max cDNA clone 35 1.2
	emb AW782226 AW782226 sm03b02.y1 Gm-c1027 Glycine max cDNA clone 35 1.2
	emb AW760912 AW760912 sl60e10.yl Gm-c1027 Glycine max cDNA clone 35 1.2
	gb BE023356 BE023356 sm70h01.yl Gm-c1028 Glycine max cDNA clone 35 1.2
30	emb AW200818 AW200818 se93h05.yl Gm-c1027 Glycine max cDNA clone 35 1.2
-	emb AI210832 AI210832 10f05a1.fl Aspergillus nidulans 24hr asexu 29 1.4
	dbj D83718 GYCPKR Glycyrrhiza echinata mRNA for polyketide reduc 35 1.6
	emb AW472504 AW472504 si26b06.yl Gm-r1030 Glycine max cDNA clone 35 1.6
25	emb Z99173 NTCYSTPRO Nicotiana tabacum mRNA for cysteine protein 35 1.6
35	dbj D86558 D86558 Glycyrrhiza glabra mRNA for polyketide reducta 35 1.6
	Query= AC007017.124_at 19991_at /id_source genbank /description
	gb aad21459.1 (ac007017) similar to harpin-induced protein hin1 from
40	tobacco [arabidopsis thaliana] /blast score 1.00e-112 /ec number
	/family /chip nova /gb link
	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac007017 /ncgi
•	http://www.ncgr.org/cgi-bin/ff?ac007017
45	
43	(713 letters)
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
50	Searchingdone
•	Score E
	Sequences producing significant alignments: (bits) Value
	ocquences producing significant angiments. (this) value
55	
33	emb AF212183 AF212183 Nicotiana tabacum harpin inducing protein 221 3e-62
	emb AW216692 AW216692 EST295406 tomato callus, TAMU Lycopersicon 215 6e-61
	emb Y07563 NTHIN1 N.tabacum mRNA for hin1 gene. 212 2e-59
	emb AW621495 AW621495 EST312293 tomato root during/after fruit s 215 2e-59
	emb AW032166 AW032166 EST275620 tomato callus, TAMU Lycopersicon 212 1e-58
60	emb AW032166 AW032166 EST275620 tomato callus, TAMU Lycopersicon 212 1e-58 emb AI484933 AI484933 EST243196 tomato ovary, TAMU Lycopersicon 214 8e-55
60	emb AW032166 AW032166 EST275620 tomato callus, TAMU Lycopersicon 212 1e-58 emb AI484933 AI484933 EST243196 tomato ovary, TAMU Lycopersicon 214 8e-55 emb AI779911 AI779911 EST260790 tomato susceptible, Cornell Lyco 209 2e-53

```
emb[AW216459[AW216459 EST295089 tomato callus, TAMU Lycopersicon... 189 3e-53
      emb|AW596126|AW596126 si98d02.y1 Gm-c1032 Glycine max cDNA clone... 126 1e-49
      emb|AW034324|AW034324 EST277895 tomato callus, TAMU Lycopersicon... 182 2e-49
      emblAI895898|AI895898 EST265341 tomato callus, TAMU Lycopersicon... 180 5e-49
      emb|AW096867|AW096867 EST20D16 potato shoot cDNA library Solanum... 193 9e-49
      emb|AI896063|AI896063 EST265506 tomato callus, TAMU Lycopersicon... 179 1e-48
      emb|AW030430|AW030430 EST273685 tomato callus, TAMU Lycopersicon... 171 6e-48
      emb|AW033033|AW033033 EST276592 tomato callus, TAMU Lycopersicon... 170 1e-47
      emb|AW030771|AW030771 EST274026 tomato callus, TAMU Lycopersicon... 170 1e-47
10
      emb|AW032046|AW032046 EST275500 tomato callus, TAMU Lycopersicon... 170 1e-47
      emb|AW032073|AW032073 EST275527 tomato callus, TAMU Lycopersicon... 168 5e-47
      emb|AW030260|AW030260 EST273515 tomato callus, TAMU Lycopersicon... 166 2e-46
      emb|AI489927|AI489927 EST248266 tomato ovary, TAMU Lycopersicon ... 165 5e-46
      emb|AI488082|AI488082 EST246404 tomato ovary, TAMU Lycopersicon ... 184 5e-46
15
      emb|AI486820|AI486820 EST245142 tomato ovary, TAMU Lycopersicon ... 184 7e-46
      emb[AW034205]AW034205 EST277776 tomato callus, TAMU Lycopersicon... 163 1e-45
      emblAW030158|AW030158 EST273413 tomato callus, TAMU Lycopersicon... 163 2e-45
      emb[AW034505]AW034505 EST278121 tomato callus, TAMU Lycopersicon... 180 6e-45
      emb|AW036026|AW036026 EST276742 tomato callus, TAMU Lycopersicon... 166 8e-45
20
      emb|AW032069|AW032069 EST275523 tomato callus, TAMU Lycopersicon... 158 5e-44
      emb|AW032994|AW032994 EST276553 tomato callus, TAMU Lycopersicon... 160 7e-43
      emb|AW216803|AW216803 EST295517 tomato callus, TAMU Lycopersicon... 160 7e-43
      emb|AW033731|AW033731 EST277302 tomato callus, TAMU Lycopersicon... 159 1e-42
      emb|AW685851|AW685851 NF035H03NR1F1000 Nodulated root Medicago t... 112 2e-41
25
      emb|AI776989|AI776989 EST252081 tomato callus, TAMU Lycopersicon... 166 1e-40
      emb[AW035944]AW035944 EST282803 tomato callus, TAMU Lycopersicon... 144 7e-40
      emb|AW034103|AW034103 EST277598 tomato callus, TAMU Lycopersicon... 144 7e-40
      emb|AW032974|AW032974 EST276533 tomato callus, TAMU Lycopersicon... 144 7e-40
      emb|AI896142|AI896142 EST265585 tomato callus, TAMU Lycopersicon... 144 7e-40
30
      gb|BE022800|BE022800 sm88f04.y1 Gm-c1015 Glycine max cDNA clone ... 117 1e-38
      emb|AI777033|AI777033 EST252000 tomato callus, TAMU Lycopersicon... 148 2e-38
      emblAW423417|AW423417 sh66e06.yl Gm-c1015 Glycine max cDNA clone... 105 3e-37
      emb|AW099273|AW099273 sd37e04.yl Gm-c1016 Glycine max cDNA clone... 89 5e-37
      emb|AW220190|AW220190 EST302673 tomato root during/after fruit s... 138 1e-36
35
      emb|AI896428|AI896428 EST265859 tomato callus, TAMU Lycopersicon... 132 2e-36
      emb|AW033867|AW033867 EST277438 tomato callus, TAMU Lycopersicon... 127 1e-34
      emb|AI896215|AI896215 EST265658 tomato callus, TAMU Lycopersicon... 126 le-34
      emb|AW423696|AW423696 sh50e10.yl Gm-c1017 Glycine max cDNA clone... 117 4e-34
      emb|AW706093|AW706093 sj51g03.y1 Gm-c1033 Glycine max cDNA clone... 144 1e-33
40
      emblAI780237|AI780237 EST261116 tomato susceptible, Cornell Lyco... 139 2e-32
      emb|AI352735|AI352735 MB56-1G PZ204.BNlib Brassica napus cDNA cl... 138 3e-32
      emb|AW217026|AW217026 EST295740 tomato callus, TAMU Lycopersicon... 123 6e-32
      emb[AW570043]AW570043 sj17a02.yl Gm-c1032 Glycine max cDNA clone... 135 3e-31
      emb|AW099281|AW099281 sd37f04.yl Gm-c1016 Glycine max cDNA clone... 72 7e-31
45
      emb|AW573938|AW573938 EST316529 GVN Medicago truncatula cDNA clo... 77 7e-31
      emb|AW032507|AW032507 EST276066 tomato callus, TAMU Lycopersicon... 113 9e-31
      emb|AW032075|AW032075 EST275529 tomato callus, TAMU Lycopersicon... 112 2e-30
      emb|AW033024|AW033024 EST276583 tomato callus, TAMU Lycopersicon... 111 3e-30
      emb|AW216908|AW216908 EST295622 tomato callus, TAMU Lycopersicon... 108 4e-29
50
      emb|AW311014|AW311014 sg31e08.x1 Gm-c1024 Glycine max cDNA clone... 127 6e-29
      emb|AV427017|AV427017 AV427017 Lotus japonicus young plants (two... 66 3e-28
      emb|AI440724|AI440724 sa62g06.y1 Gm-c1004 Glycine max cDNA clone... 74 3e-28
      emb|AV417820|AV417820 AV417820 Lotus japonicus young plants (two... 74 8e-28
      emb|AW432916|AW432916 sh99g05.y1 Gm-c1016 Glycine max cDNA clone... 113 2e-27
55
      emb|AV415500|AV415500 AV415500 Lotus japonicus young plants (two... 74 2e-27
      emb|AI896041|AI896041 EST265484 tomato callus, TAMU Lycopersicon... 102 2e-27
      emb|AV426857|AV426857 AV426857 Lotus japonicus young plants (two... 74 5e-27
      emb|AW596730|AW596730 sj16a08.yl Gm-c1032 Glycine max cDNA clone... 120 1e-26
      emb|AW776958|AW776958 EST336023 DSIL Medicago truncatula cDNA cl... 117 7e-26
60
      emb|AW573973|AW573973 EST316564 GVN Medicago truncatula cDNA clo... 67 3e-24
      emblAW216899lAW216899 EST295613 tomato callus, TAMU Lycopersicon... 86 3e-23
```

	emb AV414410 AV414410 AV414410 Lotus japonicus young plants (two 62 2e-22 emb AI776990 AI776990 EST252082 tomato callus, TAMU Lycopersicon 105 4e-22 emb AW032747 AW032747 EST276306 tomato callus, TAMU Lycopersicon 82 3e-21
_	emb AW349817 AW349817 GM210005B12D5R Gm-r1021 Glycine max cDNA 3 100 9
5	21 amble W21624014 W216240 EGT205002 4 mass on the TANGUL mass in 100.0. 20
	emb AW216349 AW216349 EST295093 tomato callus, TAMU Lycopersicon 100 2e-20 emb AI960775 AI960775 sc90c07.yl Gm-c1019 Glycine max cDNA clone 63 3e-20
	emb AW686891 AW686891 NF003F09RT1F1000 Developing root Medicago 62 1e-19
	emb AI055043 AI055043 coau0002O01 Cotton Boll Abscission Zone cD 68 8e-19
10	emb AW687417 AW687417 NF009D05RT1F1045 Developing root Medicago 93 2e-18
10	emb AV426494 AV426494 AV426494 Lotus japonicus young plants (two 63 2e-18
	emb AW102192 AW102192 sd84e05.yl Gm-c1009 Glycine max cDNA clone 93 3e-18
	emb AV419918 AV419918 AV419918 Lotus japonicus young plants (two 63 4e-18
	emb AV426405 AV426405 AV426405 Lotus japonicus young plants (two 63 1e-17
15	emb AT000898 AT000898 AT000898 Brassica rapa guard cell Brassica 90 2e-17
	emb AW101413 AW101413 sd79f01.yl Gm-c1009 Glycine max cDNA clone 55 2e-17
	emb AW035459 AW035459 EST281197 tomato callus, TAMU Lycopersicon 73 5e-17
	emb AW102127 AW102127 sd83e05.yl Gm-c1009 Glycine max cDNA clone 88 9e-17
	emb AV427127 AV427127 AV427127 Lotus japonicus young plants (two 63 1e-16
20	emb AW738963 AW738963 gb16h01.yl Moss EST library PPN Physcomitr 85 3e-16
	-emb AV420136 AV420136 AV420136 Lotus japonicus young plants (two 63 4e-16
	emb AV423861 AV423861 AV423861 Lotus japonicus young plants (two 63 4e-16
	emb AI960004 AI960004 sc36e08.x1 Gm-c1014 Glycine max cDNA clone 83 2e-15
25	emb AW065130 AW065130 ST40A06 Pine TriplEx shoot tip library Pin 72 2e-15
25	emb AW207915 AW207915 M111138e DSIR Medicago truncatula cDNA clo 65 1e-14
	gb C96147 C96147 C96147 Marchantia polymorpha immature sex organ 46 3e-14
	emb AV426062 AV426062 AV426062 Lotus japonicus young plants (two 62 4e-14 emb AW133380 AW133380 se18b08.yl Gm-c1015 Glycine max cDNA clone 77 2e-13
30	emb AV408625 AV408625 AV408625 Lotus japonicus young plants (two 60 2e-13 emb AI725475 AI725475 BNLGHi12255 Six-day Cotton fiber Gossypium 54 4e-13
50	emb AI487763 AI487763 EST246085 tomato ovary, TAMU Lycopersicon 73 3e-12
	emb AW573972 AW573972 EST316563 GVN Medicago truncatula cDNA clo 54 6e-12
	emb AW625608 AW625608 EST319515 tomato radicle, 5 d post-imbibit 54 7e-12
35	
	Query= AC005489.2_at 20189_at /id_source genbank /description
	gb aad32864.1 ac005489_2 (ac005489) f14n23.2 [arabidopsis thaliana]
	/blast_score 2.00e-57 /ec_number /family /chip nova /gb_link
40	http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005489 /ncgi
40	http://www.ncgr.org/cgi-bin/ff?ac005489
	(504 letters)
	(304 1011013)
•	Database: plantfungal
45	661,018 sequences; 426,114,510 total letters
,	Searchingdone
	Score E
50	Sequences producing significant alignments: (bits) Value
	emb AW703956 AW703956 sk14d08.yl Gm-c1023 Glycine max cDNA clone 64 4e-18
	emb AW102211 AW102211 sd84g10.y1 Gm-c1009 Glycine max cDNA clone 64 8e-18
55	emb AW102144 AW102144 sd83g10.y1 Gm-c1009 Glycine max cDNA clone 64 1e-16
<i>)</i>	emb AW687497 AW687497 NF010C03RT1F1020 Developing root Medicago 53 6e-12
	emb AW255241 AW255241 ML241 peppermint glandular trichome Mentha 50 1e-10
	emb AV425186 AV425186 AV425186 Lotus japonicus young plants (two 55 le-10 emb AW597737 AW597737 sj97d03.yl Gm-c1023 Glycine max cDNA clone 39 le-09
	- VILLE IN 22 1 12 1 RES REST 1 2 1 STEP 1 COURT OF THE C
60	emb AW472079 AW472079 si19f11.yl Gm-c1029 Glycine max cDNA clone 46 9e-09
60	

```
emb|AW040753|AW040753 EST283617 tomato mixed elicitor, BTI Lycop...
      emblAW040757|AW040757 EST283621 tomato mixed elicitor, BTI Lycop... 37 8e-07
      emb|AV420178|AV420178 AV420178 Lotus japonicus young plants (two... 41 0.007
      emb|AI812313|AI812313 10G1 Pine Lambda Zap Xylem library Pinus t... 33 0.026
      emb|AW985454|AW985454 NXNV_136_G09_F Nsf Xylem Normal wood Verti... 33 0.026
      emb|AW985465|AW985465 NXNV_136_H10_F Nsf Xylem Normal wood Verti... 37_0.084
      emb|AW216679|AW216679 EST295393 tomato callus, TAMU Lycopersicon... 37 0.084
      emb|AW324783|AW324783 NXNV026E10F Nsf Xylem Normal wood Vertical... 28 0.71
      emb|AW754722|AW754722 PC07A05 Pine TriplEx pollen cone library P... 26 1.5
10
      emb|AW094476|AW094476 EST287656 tomato mixed elicitor, BTI Lycop... 33 2.0
      gb|U71016|DGU71016 Dactylis glomerata NADH dehydrogenase subunit... 32 2.8
      gb|U71028|HBU71028 Hordeum brevisubulatum NADH dehydrogenase sub... 32 2.8
      emb|AF056181|AF056181 Hordeum bogdanii NADH dehydrogenase subuni... 32 2.8
      gb|U22260|NTU22260 Nicotiana tabacum UMP synthase (pyr5-6) mRNA,... 32 3.8
15
      emb|AF236867|AF236867 Poa secunda NADH dehydrogenase subunit F (... 31 5.2
      gb U21924 ORU21924 Oryzopsis racemosa NADH dehydrogenase F (ndhF... 31 5.2
      gb|U71025|TAU71025 Triticum aestivum NADH dehydrogenase subunit ... 31 5.2
      gb|U71047|ORU71047 Oryzopsis racemosa NADH dehydrogenase subunit... 31 5.2
      gb|U71049|MCU71049 Melica ciliata NADH dehydrogenase subunit F (... 31 5.2
20
      gb|U71023|SMU71023 Secale montanum NADH dehydrogenase subunit F ... 31 5.2
      gb U71015 FRU71015 Festuca rubra NADH dehydrogenase subunit F (n... 31 5.2
      gb|U71027|ERU71027 Elytrigia repens NADH dehydrogenase subunit F... 31 5.2
      gb|U71033|BEU71033 Bromopsis erecta NADH dehydrogenase subunit F... 31 5.2
      emblAW287747|AW287747 LG1 271_H07.b1 A002 Light Grown 1 (LG1) So... 31 5.2
25
      emb|AF108029|AF108029 Elymus elymoides NADH dehydrogenase subuni... 31 5.2
      emb|AF108028|AF108028 Elymus elymoides x Leymus salinus subsp. s... 31 5.2
      emb|AF056180|AF056180 Pseudoroegneria spicata NADH dehydrogenase... 31 5.2
      emb|AF056179|AF056179 Leymus cinereus NADH dehydrogenase subunit... 31 5.2
      emb|AF056178|AF056178 Pascopyrum smithii cultivar Atkins142 NADH... 31 5.2
30
      emb|AF056177|AF056177 Pascopyrum smithii cultivar Walsh NADH deh... 31 5.2
      emb|AF056176|AF056176 Pascopyrum smithii cultivar Epc-8 NADH deh... 31 5.2
      emb|AF056175|AF056175 Pascopyrum smithii cultivar Rosanna NADH d... 31 5.2
      emb|AF056174|AF056174 Pascopyrum smithii cultivar Barton NADH de... 31 5.2
      emb|AF056173|AF056173 Pascopyrum smithii cultivar Atkins172 NADH... 31 5.2
35
      emb|AF056172|AF056172 Pascopyrum smithii cultivar Arriba NADH de... 31 5.2
      emb|AF056171|AF056171 Pascopyrum smithii cultivar R-9-1-5 NADH ... 31 5.2
      emb|AF056170|AF056170 Pascopyrum smithii cultivar Rodan NADH deh... 31 5.2
      emb|AF056169|AF056169 Pascopyrum smithii cultivar Flintlock NADH... 31 5.2
      emb|AF056168|AF056168 Elymus lanceolatus subsp. wawawaiensis NAD... 31 5.2
40
      emb|AF056167|AF056167 Psathyrostachys juncea NADH dehydrogenase ... 31 5.2
      emblAF056166|AF056166 Elymus lanceolatus subsp. lanceolatus NADH... 31 5.2
      emb|AF056165|AF056165 Leymus triticoides NADH dehydrogenase subu... 31 5.2
      gb|U22003|HVU22003 Hordeum vulgare NADH dehydrogenase F (ndhF) g... 31 5.2
      gb[U21999]DOU21999 Diarrhena obovata NADH dehydrogenase F (ndhF)... 31 5.2
45
      gb[U71011|SAU71011 Sesleria argentea NADH dehydrogenase subunit ... 31 7.1
      gb[U22006|PGU22006 Phaenosperma globosa NADH dehydrogenase F (nd... 31 7.1
      gb|U22000|ASU22000 Avena sativa NADH dehydrogenase F (ndhF) gene... 31 7.1
      emb|AZ214488|AZ214488 Sheared DNA-78B7.TF Sheared DNA Trypanosom... 31 7.1
      emb|AI736210|AI736210 sb24h08.yl Gm-c1008 Glycine max cDNA clone... 31 7.1
50
      gb|U71048|GDU71048 Glyceria declinata NADH dehydrogenase subunit... 31 7.1
      gb[U71018|AFU71018 Avena fatua NADH dehydrogenase subunit F (ndh... 31 7.1
      gb|M31615|TRBESAGF T.brucei metacyclic expression site-associate... 31 7.1
      emb|AQ944873|AQ944873 Sheared DNA-36B24.TF Sheared DNA Trypanoso... 31 7.1
      emb|AF108030|AF108030 Leymus salinus subsp. salmonis NADH dehydr... 31 7.1
55
      emb|AI856529|AI856529 sb40e03.yl Gm-c1014 Glycine max cDNA clone... 31 7.1
      gb[U71041]BPU71041 Brachypodium pinnatum NADH dehydrogenase subu... 30 9.8
      gb|U71042|BAU71042 Brachypodium arbuscula NADH dehydrogenase sub... 30 9.8
      emb|AQ640138|AQ640138 927P1-18A6.TP 927P1 Trypanosoma brucei gen... 30 9.8
      emb|AQ655335|AQ655335 Sheared DNA-25B9.TF Sheared DNA Trypanosom... 30 9.8
60
```

....WO.02/22675PCT/US01/28506

emb|caa18469.1| (al022347) serine/threonine kinase-like protein [arabidopsis thaliana] /blast score 0 /ec number /family kinase /chip nova/gb link http://www3.ncbi.nlm.nih.gov/htbin-5 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi http://www.ncgr.org/cgi-bin/ff?al022347 (2703 letters) Database: plantfungal 10 661,018 sequences; 426,114,510 total letters E Score 15 Sequences producing significant alignments: (bits) Value emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 318 e-148 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 289 3e-96 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 280 8e-93 20 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 281 3e-92 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 280 1e-91 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 268 le-91 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 278 3e-91 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 271 8e-90 25 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 221 5e-88 gb[M76647]BNASKR6A Brassica oleracea receptor protein kinase (SK... 277 9e-88 gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 272 9e-88 emb|Y12530|BOARLKGEN B.oleraceae gene encoding serine/threonine ... 133 1e-85 30 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 277 2e-85 emb|AW620957|AW620957 sj98a07.yl Gm-c1023 Glycine max cDNA clone... 252 5e-84 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 272 5e-84 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 224 6e-84 emb[Y14286]BOY14286 Brassica oleracea SFR3 gene, partial. 35 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 275 2e-82 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 129 6e-82 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 266 4e-81 emblAF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 258 1e-80 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 265 2e-80 gb[M97667]BNASTKR Brassica napus ssp. oleifera serine/threonine ... 273 1e-79 gb|BE057261|BE057261 sm99f12.yl Gm-c1015 Glycine max cDNA clone ... 297 3e-79 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 115 3e-78 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 262 9e-77 dbi|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 264 2e-76 45 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 279 2e-76 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 126 3e-76 emb[Y12531]BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 128 2e-75 emb|AW760240|AW760240 sl59g07.yl Gm-c1027 Glycine max cDNA clone... 280 3e-74

- emb|X79432|BOSRK3 B.oleracea SRK3 gene. 117 4e-74

 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 266 5e-70

 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 200 5e-68

 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 122 2e-67

 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 122 1e-65

 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 113 6e-65
- 55 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 108 7e-65 emb|AW831390|AW831390 sm22a06.yl Gm-c1028 Glycine max cDNA clone... 184 9e-65 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 216 4e-64 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 120 2e-63 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 108 1e-62
- 60 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 106 3e-62 emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 235 8e-62

emblAW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 227 7e-61 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 164 1e-60 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 174 1e-58 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 221 4e-58 5 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 225 1e-57 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 158 1e-56 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 158 2e-55 emb[Y16999[TCA16999 Theobroma cacao microsatellite DNA, clone mT... 133 3e-55 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 179 1e-54 10 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 133 5e-54 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 192 1e-53 emb|AI967314|AI967314 Ljirnpest00-017 Ljirnp Lambda HybriZap two... 119 2e-53 emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 183 4e-53 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 191 3e-50 15 emb|AW039406|AW039406 EST281663 tomato mixed elicitor, BTI Lycop... 111 9e-50 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 168 9e-50 emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 199 1e-49 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 111 2e-49 emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 181 6e-49 20 emblAI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 140 2e-47 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 77 2e-46 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 119 2e-46 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 136 3e-46 25 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 136 3e-46 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 128 3e-46 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 170 4e-46 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 126 6e-46 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 140 8e-46 30 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 140 8e-46 emb|Z18883|BOSRKRPB B.oleracea encoding S-receptor kinase relate... 183 2e-45 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 140 7e-45 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 117 2e-44 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 99 2e-44 35 emb|Z18862|BOSRKRPD B.oleracea encoding S-receptor kinase protein. 93 4e-44 emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 113 1e-43 emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycope... 142 3e-43 emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 79 9e-43 40 emb|AI822355|AI822355 LO-804T3 Ice plant Lambda Uni-Zap XR expre... 123 7e-42 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 123 7e-42 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 84 8e-42 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 73 1e-41 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 73 1e-41 45 emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 148 2e-41 emb|AW279355|AW279355 sf65g10.y1 Gm-c1013 Glycine max cDNA clone... 103 6e-41 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 169 8e-41 gb[U51330]TAU51330 Triticum aestivum leaf rust resistance kinase... 83 8e-41 emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 85 1e-40 50 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 69 1e-40 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 83 2e-40 gb|BE058691|BE058691 sn19e05.yl Gm-c1016 Glycine max cDNA clone ... 87 3e-40 emb|AW597214|AW597214 si71g06.y1 Gm-c1031 Glycine max cDNA clone... 91 1e-39 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 68 1e-39 55 gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 68 1e-39

Query= AL022347.12_s_at 20232_s_at /id_source genbank /description emb|caa18460.1| (al022347) protein kinase-like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link

(1953 letters)

```
Database: plantfungal
              661,018 sequences; 426,114,510 total letters
   5
        Searching.....
                                             Score
                                                    E
        Sequences producing significant alignments:
                                                            (bits) Value
 10
        emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 330 e-134
        gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 224 e-107
        gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 215 e-105
        gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 297 e-104
 15
        dbj[D30049]BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 285 e-103
        emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 287 e-103
        gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 304 e-102
        emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 289 e-102
        emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 292 e-102
       emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 291 e-101
        emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. -303 e-101
        emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 299 e-101
        gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 294 e-101
        emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 301 e-101
 25
       emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 302 e-101
        dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein... 287 e-100
       emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein.
        dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 288 e-100
       emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 303 e-100
 30
       gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 290 2e-99
       emb|AW620957|AW620957 sj98a07.yl Gm-c1023 Glycine max cDNA clone... 270 3e-93
       emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 264 3e-93
       gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 286 2e-92
       emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial.
                                                                      199 6e-92
       gb|BE057261|BE057261 sm99f12.yl Gm-c1015 Glycine max cDNA clone ... 310 3e-83
       emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 277 1e-80
       emb[Y12531]BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 127 7e-80
       emb[Y12530]BOARLKGEN B.oleraceae gene encoding serine/threonine ... 129 3e-76
       emb|AW760240|AW760240 sl59g07.yl Gm-c1027 Glycine max cDNA clone... 284 2e-75
· 40
       emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 126 3e-75
       emblAJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 126 4e-75
       emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 126 2e-74
       emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 119 3e-74
       emb|X79432|BOSRK3 B.oleracea SRK3 gene.
                                                                 118 8e-74
 45
       emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 117 1e-73
       emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 116 2e-73
       emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene.
       emblAI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 275 8e-73
       emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 116 1e-72
 50
       dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 124 1e-71
       emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 211 3e-71
       emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 109 3e-68
       emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 206 9e-67
       emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 254 1e-66
 55
       emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 179 3e-66
       gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 225 2e-65
       emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 186 4e-64
       emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 176 4e-63
       emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 176 1e-62
 60
       emb|AW203661|AW203661 sf36g06.yl Gm-c1028 Glycine max cDNA clone... 202 4e-61
       emb|AW666141|AW666141 sk32f11.yl Gm-c1028 Glycine max cDNA clone... 178 7e-61
```

```
emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 231 1e-59
      emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 231 2e-59
      emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 227 2e-58
      emb|AI901283|AI901283 sc31d08.yl Gm-c1014 Glycine max cDNA clone... 180 3e-57
      emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 124 8e-57
 5
      emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 194 2e-56
      emb|AW667985|AW667985 GA Ea0012C15 Gossypium arboreum 7-10 dpa ... 91 4e-56
      emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 127 1e-54
      emb[Y16999]TCA16999 Theobroma cacao microsatellite DNA, clone mT... 125 1e-53
      emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 129 2e-53
      emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 141 2e-53
      emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 184 3e-53
      emb|AI967314|AI967314 Ljirnpest00-017 Ljirnp Lambda HybriZap two... 143 6e-53
      emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 184 8e-53
      emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 161 4e-52
15
      emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 157 5e-51
      emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 157 5e-51
      emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 140 7e-51
      emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 161 1e-50
20
      emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 105 2e-50
      emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 112 5e-50
      emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 161 6e-50
      emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 112 1e-49
      emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 8e-49
25
      emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 128 2e-48
      emb[Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 78 2e-48
      emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 119 3e-48
      emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 166 1e-47
      emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 le-47
30
      emb|AW279355|AW279355 sf65g10.y1 Gm-c1013 Glycine max cDNA clone... 115 2e-47
      emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 112 2e-47
      emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 86 3e-47
      emb|Z18883|BOSRKRPB B.oleracea encoding S-receptor kinase relate... 176 3e-46
      emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 157 8e-46
35
      emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 107 1e-45
      emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 185 1e-45
      emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 86 1e-45
      gb|BE058691|BE058691 sn19e05.yl Gm-c1016 Glycine max cDNA clone ... 99 2e-45
      emb|AW278186|AW278186 sf40g07.yl Gm-c1009 Glycine max cDNA clone... 95 4e-45
40
      emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 72 8e-45
      gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 80 5e-44
      emb|Z18862|BOSRKRPD B.oleracea encoding S-receptor kinase protein. 89 1e-43
      emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 78 1e-43
      emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 89 2e-43
45
      gb[U28007|LEU28007 Lycopersicon esculentum Pto kinase interactor... 129 5e-43
      emblAW982539lAW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 82 5e-43
      emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 164 6e-43
      emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 175 9e-43
      emb|AW597214|AW597214 si71g06.yl Gm-c1031 Glycine max cDNA clone... 127 2e-42
50
```

Query= X74514.2_at 20238_at /id_source genbank /description emb|caa52619.1| (x74514) beta-fructofuranosidase [arabidopsis thaliana] /blast_score 0 /ec_number ec_3.2.1.26 /family hydrolase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x74514| /ncgi http://www.ncgr.org/cgi-bin/ff?x74514 (1947 letters)

60

55

Database: plantfungal

661,018 sequences; 426,114,510 total letters

	Searchingdone
5	Score E Sequences producing significant alignments: (bits) Value
10	emb AF000521 AF000521 Fragaria x ananassa cell wall invertase pr 413 0.0 emb Z35163 VFCWINV2 V.faba VFCWINV2 mRNA for cell wall invertase 418 0.0 gb M58362 DARBFRUC D.carota cell wall beta-fructosidase mRNA, co 239 0.0 emb X81792 CRCIN1 C.rubrum CIN1 mRNA for extracellular invertase. 181 0.0 emb X81834 NTMRNABDF N.tabacum mRNA for beta-fructosidase. 205 0.0 emb AF030420 AF030420 Triticum aestivum cell wall invertase (IVR 240 0.0
15	emb Y11176 CIFRUCTOS C.intybus mRNA for fructosidase. 144 0.0 emb Z21486 STBETFRUA S.tuberosum mRNA for invertase gene encodin 196 e-180 emb AJ272305 LPE272305 Lycopersicon pennellii mRNA for beta-fruc 190 e-170 emb X85327 PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169 emb AF063246 AF063246 Pisum sativum cell wall invertase (bfruct1 398 e-169
20	emb AJ272304 LES272304 Lycopersicon esculentum mRNA for beta-fru 190 e-169 emb Z22645 STBETFRCA S.tuberosum invertase gene encoding beta-fr 204 e-166 emb AF000520 AF000520 Fragaria x ananassa cell wall invertase (I 210 e-164 emb AB004558 AB004558 Lycopersicon esculentum mRNA for acid inve 200 e-164
25	emb X78424 DCINC1 D.carota (Queen Anne's Lace) Inv*Dc2 gene, 343 161 e-136 emb Z35162 VFCWINV1 V.faba VFCWINV1 mRNA for cell wall invertase I. 207 e-132 emb AF030421 AF030421 Triticum aestivum cell wall invertase (IVR 138 e-130 emb AJ133765 STU133765 Solanum tuberosum invGE and invGF genes. 148 e-128 gb U87849 CAU87849 Capsicum annuum acid beta-fructosidase mRNA, 200 e-126
30	emb AJ006067 ACE6067 Allium cepa mRNA for invertase. 210 e-126 emb A94218 A94218 Sequence 1 from Patent EP0952222. 176 e-122 emb AF002656 AF002656 Asparagus officinalis acid invertase mRNA, 198 e-120 gb U81520 CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl 173 e-120 emb X75351 DCRNABF D.carota (Nantaise) mRNA for soluble acid bet 202 e-120
35	emb X75353 DCRNASABF D.carota (Nantaise) mRNA for soluble acid b 203 e-120 emb AJ272307 LPE272307 Lycopersicon pennellii lin 5 gene for bet 145 e-119 emb X75352 DCRNAABF D.carota (Nantaise) mRNA for soluble acid be 203 e-119 emb X78423 DCINUC1 D.carota (Queen Anne's Lace) Inv*Dc3 gene, 44 160 e-118 emb A94222 A94222 Sequence 5 from Patent EP0952222. 173 e-117
40	emb Y09662 CSSS1FT C.scolymus mRNA for sucrose sucrose 1-fructos 170 e-117 emb A86530 A86530 Sequence 1 from Patent WO9839460. 170 e-117 emb AJ272306 LES272306 Lycopersicon esculentum lin 5 gene for be 145 e-116 emb AJ250634 TOF250634 Taraxacum officinale mRNA for sucrose:suc 169 e-116
45	gb U92438 PVU92438 Phaseolus vulgaris soluble acid invertase mRN 198 e-114 emb AW686881 AW686881 NF003E07RT1F1000 Developing root Medicago 413 e-114 dbj D10265 VIRINVA Vigna radiata mRNA for invertase, complete cds. 194 e-114 emb AJ009757 HTU9757 Helianthus tuberosus sst-1 gene. 171 e-113
50	emb A52468 A52468 Sequence 1 from Patent WO9621023. 171 e-113 emb X70368 STPAIN1A S.tuberosum PAIN-1 mRNA for beta-fructofuran 200 e-108 emb X67163 DCSBFRU D.carota mRNA for soluble beta-fructosidase. 140 e-107 gb L29099 POTBFRUASE Solanum tuberosum beta-fructosidase mRNA, c 198 e-107 dbj E07108 E07108 cDNA encoding acid invertase. 198 e-106
55	dbj D11350 TOMBFSD Tomato mRNA for beta-fructosidase, complete cds. 198 e-106 emb Z12026 LPBFRUCM L.pimpinellifolium beta-fructosidase mRNA fo 198 e-106 emb Z12025 LEBFRUCM L.esculentum beta-fructosidase mRNA for vacu 198 e-106 gb M81081 TOMACIN Tomato acid invertase (TIV1) mRNA, complete cds. 198 e-106 gb S70040 S70040 acid invertase [Lycopersicon esculentum=tomatoe 198 e-106
60	dbj E16293 E16293 cDNA encoding invertase. 198 e-106 dbj E08976 E08976 cDNA encoding tomato invertase. 198 e-106 emb AF017082 AF017082 Ipomoea batatas beta-fructofuranosidase (S 141 e-103 emb Y11124 CIPINVERT C.intybus mRNA for putative invertase. 138 e-102

60	
.	Score E Sequences producing significant alignments: (bits) Value
<i></i>	Searchingdone
55 ·	Database: plantfungal 661,018 sequences; 426,114,510 total letters
•	(1947 letters)
50	/ncgi
	thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
	emb caa52619.1 (x74514) beta-fructofuranosidase [arabidopsis
	emb AW441409 AW441409 EST310805 tomato fruit red ripe, TAMU Lyco 114 4e-62 Query= X74514.2 g at 20239 g at /id_source genbank /description
45	emb AI522941 AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone 201 le-63
A E	emb X91390 LELIN6 L.esculentum mRNA for invertase (LIN6). 133 5e-64
	emb AW738685 AW738685 EST340112 tomato flower buds, anthesis, Co 189 3e-64
	emb AW618261 AW618261 EST314311 L. pennellii trichome, Cornell U 248 1e-64
	emb AW350139 AW350139 GM210007B20F11R Gm-r1021 Glycine max cDNA 112 4e-66
40	emb[X83233]HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr 82 2e-68 emb[AF069309]AF069309 Triticum aestivum vacuolar invertase (WIVR 127 5e-67
	emb A48280 A48280 Sequence 1 from Patent WO9601904. 82 2e-68
	emb AW730389 AW730389 GA Ea0023K22 Gossypium arboreum 7-10 dpa 141 2e-68
	emb AW666614 AW666614 GA_Ea0005C10 Gossypium arboreum 7-10 dpa 207 3e-69
35	emb A48284 A48284 Sequence 5 from Patent WO9601904. 130 1e-69
	emb AF091546 AF091546 Hamamelis virginiana clone 6 beta-fructofu 193 3e-74 emb AV407850 AV407850 AV407850 Lotus japonicus young plants (two 267 2e-70
	emb Z83339 PSZ83339 P.sativum mRNA for cell wall invertase II. 280 2e-74
	emb AW685050 AW685050 NF024F09NR1F1000 Nodulated root Medicago t 248 5e-75
30	emb A48282 A48282 Sequence 3 from Patent WO9601904. 152 4e-75
	emb AF091545 AF091545 Hamamelis virginiana clone 4 beta-fructofu 196 2e-75
	emb AJ006066 ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc 132 2e-75
	emb AF014925 AF014925 Citrus unshiu acid invertase (CUAI1) gene, 138 4e-76
	emb[X81796]BVBIN44 B.vulgaris BIN44 mRNA for intracellular inver 149 5e-77
25	emb[X91391]LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78 emb[Y07838]ACY07838 A.cepa mRNA for fructan: fructan 6G-fructosyl 156 2e-77
	emb X91389 LELIN5 L.esculentum mRNA for invertase (LIN5). 129 1e-78 emb X91391 LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
	emb X81793 CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase. 135 2e-80
	emb AF091547 AF091547 Hamamelis virginiana clone 1 beta-fructofu 295 3e-81
20	emb X91392 LELIN8 L.esculentum mRNA for invertase (LIN8). 133 2e-82
••	gb BE055183 BE055183 GA_Ea0035H23f Gossypium arboreum 7-10 dpa 203 4e-83
	emb X81795 BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver 265 5e-86
	emb A52470 A52470 Sequence 3 from Patent WO9621023. 161 2e-87
10	emb AJ009756 HTU9756 Helianthus tuberosus fft-1 gene. 161 2e-87
15	emb Z12027 LEBFRUCG L.pimpineinfolium gene encooing vacuolar in 157 6e-88
	emb[Z12028]LPBFRUCG L.pimpinellifolium gene encoding vacuolar in 157 6e-88
	emb AF091548 AF091548 Hamamelis virginiana clone 3 beta-fructofu 327 1e-88 gb U84398 CIU84398 Cichorium intybus fructan-fructan 1-fructosyl 161 5e-88
	emb A94220 A94220 Sequence 3 from Patent EP0952222. 161 1e-88
10	emb AF091550 AF091550 Hamamelis virginiana clone C beta-fructofu 330 3e-89
1.0	emb AJ000481 CSFF1FRUC Cynara scolymus mRNA for fructan fructan 162 3e-89
	emb AF091549 AF091549 Hamamelis virginiana clone 7 beta-fructofu 331 9e-90
	emb AF062734 AF062734 Saccharum robustum soluble acid invertase 129 1e-91
	emb AF062735 AF062735 Saccharum officinarum soluble acid inverta 129 1e-91
5	emb[Y18707]DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge 161 2e-93
	emb[X97643]TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94 emb[Y18706]DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
	emb X95651 TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96 emb X97643 TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
	emb[X97642]TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97

	emb Z35163 VFCWINV2 V.faba VFCWINV2 mRNA for cell wall invertase 418 0.0
	gb[M58362]DARBFRUC D.carota cell wall beta-fructosidase mRNA, co 239 0.0
	emb[X81792]CRCIN1 C.rubrum CIN1 mRNA for extracellular invertase. 181 0.0
	emb[X81834]NTMRNABDF N.tabacum mRNA for beta-fructosidase. 205 0.0
5	
,	emb AF030420 AF030420 Triticum aestivum cell wall invertase (IVR 240 0.0
	emb Y11176 CIFRUCTOS C.intybus mRNA for fructosidase. 144 0.0
	emb Z21486 STBETFRUA S.tuberosum mRNA for invertase gene encodin 196 e-180
	emb AJ272305 LPE272305 Lycopersicon pennellii mRNA for beta-fruc 190 e-170
	emb X85327 PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169
10	emb AF063246 AF063246 Pisum sativum cell wall invertase (bfruct1 398 e-169
	emb AJ272304 LES272304 Lycopersicon esculentum mRNA for beta-fru 190 e-169
	emb Z22645 STBETFRCA S.tuberosum invertase gene encoding beta-fr 204 e-166
	emb AF000520 AF000520 Fragaria x ananassa cell wall invertase (I 210 e-164
	emb AB004558 AB004558 Lycopersicon esculentum mRNA for acid inve 200 e-164
15	
1,5	emb X69321 DCBFRUCT D.carota (Queen Anne's Lace) Inv*Dc1 gene. 178 e-145
	emb[X78424]DCINC1 D.carota (Queen Anne's Lace) Inv*Dc2 gene, 343 161 e-136
	emb Z35162 VFCWINV1 V.faba VFCWINV1 mRNA for cell wall invertase I. 207 e-132
	emb AF030421 AF030421 Triticum aestivum cell wall invertase (IVR 138 e-130
	emb AJ133765 STU133765 Solanum tuberosum invGE and invGF genes. 148 e-128
20 .	gb U87849 CAU87849 Capsicum annuum acid beta-fructosidase mRNA, 200 e-126
	emb AJ006067 ACE6067 Allium cepa mRNA for invertase. 210 e-126
	emb A94218 A94218 Sequence 1 from Patent EP0952222. 176 e-122
	emb AF002656 AF002656 Asparagus officinalis acid invertase mRNA, 198 e-120
	gb U81520 CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl 173 e-120
25	emb[X75351]DCRNABF D.carota (Nantaise) mRNA for soluble acid bet 202 e-120
	emb[X75353]DCRNASABF D.carota (Nantaise) mRNA for soluble acid bel 202 e-120
	emb AJ272307 LPE272307 Lycopersicon pennellii lin 5 gene for bet 145 e-119
	cmb/Y75250DCDNAADED comes Claritical washing and the city constitution of the constitu
	emb X75352 DCRNAABF D.carota (Nantaise) mRNA for soluble acid be 203 e-119
20	emb X78423 DCINUC1 D.carota (Queen Anne's Lace) Inv*Dc3 gene, 44 160 e-118
30	emb A94222 A94222 Sequence 5 from Patent EP0952222. 173 e-117
	emb[Y09662] CSSS1FT C.scolymus mRNA for sucrose sucrose 1-fructos 170 e-117
	emb A86530 A86530 Sequence 1 from Patent WO9839460. 170 e-117
	emb AJ272306 LES272306 Lycopersicon esculentum lin 5 gene for be 145 e-116
	emb AJ250634 TOF250634 Taraxacum officinale mRNA for sucrose:suc 169 e-116
35	emb Z49831 VFVCINVMR V.faba VFVCINV mRNA for invertase (beta-fru 199 e-115
	gb U92438 PVU92438 Phaseolus vulgaris soluble acid invertase mRN 198 e-114
	emb AW686881 AW686881 NF003E07RT1F1000 Developing root Medicago 413 e-114
	dbj D10265 VIRINVA Vigna radiata mRNA for invertase, complete cds. 194 e-114
	emb AJ009757 HTU9757 Helianthus tuberosus sst-1 gene. 171 e-113
40	emb A52468 A52468 Sequence 1 from Patent WO9621023. 171 e-113
	emb X70368 STPAIN1A S.tuberosum PAIN-1 mRNA for beta-fructofuran 200 e-108
	emb[X67163]DCSBFRU D.carota mRNA for soluble beta-fructosidase. 140 e-107
	gb L29099 POTBFRUASE Solanum tuberosum beta-fructosidase mRNA, c 198 e-107
	dbj[E07108]E07108 cDNA encoding acid invertase. 198 e-106
15	dbj[D11350 TOMBFSD Tomato mRNA for beta-fructosidase, complete cds. 198 e-106
15	ombi712026H DDEDLICAL minuminallifolium hate foresteid an under the control of th
	emb Z12026 LPBFRUCM L.pimpinellifolium beta-fructosidase mRNA fo 198 e-106
	emb Z12025 LEBFRUCM L.esculentum beta-fructosidase mRNA for vacu 198 e-106
	gb M81081 TOMACIN Tomato acid invertase (TIV1) mRNA, complete cds. 198 e-106
-^	gb S70040 S70040 acid invertase [Lycopersicon esculentum=tomatoe 198 e-106
50	dbj[E16293 E16293 cDNA encoding invertase. 198 e-106
	dbj E08976 E08976 cDNA encoding tomato invertase. 198 e-106
	emb AF017082 AF017082 Ipomoea batatas beta-fructofuranosidase (S 141 e-103
	emb Y11124 CIPINVERT C.intybus mRNA for putative invertase. 138 e-102
	emb X97642 TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
55	emb X95651 TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
	emb X97643 TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
	emb[Y18706]DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
	emb[Y18707[DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge 161 2e-93
	emb AF062735 AF062735 Saccharum officinarum soluble acid inverta 129 1e-91
50	embla F0627241A F062724 Seechamm rehigher self-ble self-brookers 129 16-91
,0	emb AF062734 AF062734 Saccharum robustum soluble acid invertase 129 1e-91

	emb AJ000481 CSFF1FRUC Cynara scolymus mRNA for fructan fructan 162 3e-89 emb AF091550 AF091550 Hamamelis virginiana clone C beta-fructofu 330 3e-89 emb A94220 A94220 Sequence 3 from Patent EP0952222. 161 1e-88
_	emb AF091548 AF091548 Hamamelis virginiana clone 3 beta-fructofu 327 1e-88
5	gb U84398 CIU84398 Cichorium intybus fructan-fructan 1-fructosyl 161 5e-88
٠.	emb Z12028 LPBFRUCG L.pimpinellifolium gene encoding vacuolar in 157 6e-88
	emb Z12027 LEBFRUCG L.esculentum gene for vacuolar invertase. 157 6e-88
	emb AJ009756 HTU9756 Helianthus tuberosus fft-1 gene. 161 2e-87
10	emb A52470 A52470 Sequence 3 from Patent WO9621023. 161 2e-87
10	emb[X81795]BVBIN35 B.vulgaris BIN35 mRNA for extracellular inver 265 5e-86
	gb BE055183 BE055183 GA_Ea0035H23f Gossypium arboreum 7-10 dpa 203 4e-83
	emb[X91392]LELIN8 L.esculentum mRNA for invertase (LIN8). 133 2e-82
	emb AF091547 AF091547 Hamamelis virginiana clone 1 beta-fructofu 295 3e-81
	emb[X81793]CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase. 135 2e-80
15	emb X91389 LELIN5 L. esculentum mRNA for invertase (LIN5). 129 1e-78
	emb X91391 LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
	emb Y07838 ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl 156 2e-77
	emb X81796 BVBIN44 B.vulgaris BIN44 mRNA for intracellular inver 149 5e-77
20	emb AF014925 AF014925 Citrus unshiu acid invertase (CUAI1) gene, 138 4e-76
20	emb AJ006066 ACE6066 Allium cepa mRNA for sucrose sucrose 1-fruc 132 2e-75
	emb AF091545 AF091545 Hamamelis virginiana clone 4 beta-fructofu 196 2e-75
	emb A48282 A48282 Sequence 3 from Patent WO9601904. 152 4e-75
	emb AW685050 AW685050 NF024F09NR1F1000 Nodulated root Medicago t 248 5e-75
25	emb Z83339 PSZ83339 P.sativum mRNA for cell wall invertase II. 280 2e-74
23	emb AF091546 AF091546 Hamamelis virginiana clone 6 beta-fructofiu 193 3e-74 emb AV407850 AV407850 AV407850 Lotus japonicus young plants (two 267 2e-70
	emb A48284 A48284 Sequence 5 from Patent WO9601904. 130 1e-69
	emb AW666614 AW666614 GA_Ea0005C10 Gossypium arboreum 7-10 dpa 207 3e-69
	emb AW730389 AW730389 GA_Ea0023K22 Gossypium arboreum 7-10 dpa 141 2e-68
30	emb A48280 A48280 Sequence 1 from Patent WO9601904. 82 2e-68
	emb X83233 HVSF6FT Hordeum vulgare mRNA for sucrose:fructan 6-fr 82 2e-68
	emb AF069309 AF069309 Triticum aestivum vacuolar invertase (WIVR 127 5e-67
	emb AW350139 AW350139 GM210007B20F11R Gm-r1021 Glycine max cDNA 112 4e-66
	emb AW618261 AW618261 EST314311 L. pennellii trichome, Cornell U 248 1e-64
35	emb AW738685 AW738685 EST340112 tomato flower buds, anthesis, Co 189 3e-64
	emb X91390 LELIN6 L.esculentum mRNA for invertase (LIN6). 133 5e-64
	emb AI522941 AI522941 sa92d01.yl Gm-c1004 Glycine max cDNA clone 201 le-63
	emb AW441409 AW441409 EST310805 tomato fruit red ripe, TAMU Lyco 114 4e-62
40	Query= AC005309.97_s_at 20245_s_at /id_source genbank /description
	emb caa05625.1 (aj002584) atmrp4 [arabidopsis thaliana] thaliana]
	/blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
	(4551 letters)
45	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
50	G E
JU	Score E Sequences producing significant alignments: (bits) Value
	Sequences producing significant anginients. (ons) value
	emb Z69369 SPAC3F10 S.pombe chromosome I cosmid c3F10. 314 e-119
	emb Z48179 SC9302X S.cerevisiae chromosome IV cosmid 9302. 185 e-114
55	gb L35237 YSCYCF1MRP Saccharomyces cerevisiae metal resistance p 184 e-114
	gb U33010 SPU33010 Schizosaccharomyces pombe cosmids 359, 1198 a 291 e-112
	emb AL356012 SPBC359 Schizosaccharomyces pombe cosmid c359. 291 e-112
	emb AW278374 AW278374 sf43c10.yl Gm-c1009 Glycine max cDNA clone 383 e-105
-0	dbj D89231 D89231 Schizosaccharomyces pombe mRNA, partial cds, c 308 e-105
60	emb AI781883 AI781883 EST262762 tomato susceptible, Cornell Lyco 370 e-101
	emb X91488 SCCEN12RG S.cerevisiae DNA from CEN12 region includin 159 1e-94

emb|X97560|SC32KBF S.cerevisiae 32kb DNA fragment of chromosome ... 159 1e-94 emb|Z73120|SCYLL015W S.cerevisiae chromosome XII reading frame O... 159 1e-94 emblAW031334|AW031334 EST274788 tomato callus, TAMU Lycopersicon... 315 1e-84 emb|AW441253|AW441253 EST310649 tomato fruit red ripe, TAMU Lyco... 308 2e-82 emb|AW686402|AW686402 NF037F01NR1F1000 Nodulated root Medicago t... 244 7e-78 emb|AW217265|AW217265 EST295979 tomato callus, TAMU Lycopersicon... 291 3e-77 emb|AW223995|AW223995 EST300806 tomato fruit red ripe, TAMU Lyco... 290 7e-77 emblAW222948|AW222948 EST299759 tomato fruit red ripe, TAMU Lyco... 285 2e-75 emb|AI437711|AI437711 sa38f05.y1 Gm-c1004 Glycine max cDNA clone... 276 7e-73 emb|AW476771|AW476771 ga37g03.yl Moss EST library PPU Physcomitr... 275 1e-72 10 emb|AW100468|AW100468 sd55e07.yl Gm-c1016 Glycine max cDNA clone... 272 2e-71 emb|AI487304|AI487304 EST245626 tomato ovary, TAMU Lycopersicon ... 268 2e-70 emblAI896472|AI896472 EST265903 tomato callus, TAMU Lycopersicon... 267 6e-70 emb|AW100453|AW100453 sd55c07.yl Gm-c1016 Glycine max cDNA clone... 266 1e-69 15 emb|AW034253|AW034253 EST277824 tomato callus, TAMU Lycopersicon... 265 2e-69 emb|AW216929|AW216929 EST295643 tomato callus, TAMU Lycopersicon... 259 1e-67 emb|AW759237|AW759237 sl38f09.yl Gm-c1027 Glycine max cDNA clone... 259 1e-67 emb|X94332|SCCHVIIRA S.cerevisiae DNA for fragment from chromoso... 171 2e-67 emb|Z73066|SCYGR281W S.cerevisiae chromosome VII reading frame O... 171 2e-67 dbj|E12376|E12376 Nucleotide sequence of scaur2 gene. 20 emb|AW092564|AW092564 EST285744 tomato mixed elicitor, BTI Lycop... 249 1e-64 emb|AF110027|AF110027 Candida albicans ATP-dependent transporter... 150 5e-64 emb|AI779714|AI779714 EST260593 tomato susceptible, Cornell Lyco... 246 9e-64 emb|AI900368|AI900368 sc04g04.yl Gm-c1012 Glycine max cDNA clone... 243 6e-63 25 emb|AW037624|AW037624 EST279082 tomato mixed elicitor, BTI Lycop... 242 1e-62 emb|AF110147|AF110147 Cryptosporidium parvum ATP-binding cassett... 242 2e-62 emb|Z73153|SCYLL048C S.cerevisiae chromosome XII reading frame O... 142 4e-62 emb|AL114698|CNS01BUA Botrytis cinerea strain T4 cDNA library un... 238 7e-62 emb|Z28329|SCYKR104W S.cerevisiae chromosome XI reading frame OR... 129 7e-61 30 emb|A1895676|A1895676 EST265119 tomato callus, TAMU Lycopersicon... 234 4e-60 emb|AL115672|CNS01CLC Botrytis cinerea strain T4 cDNA library un... 185 1e-58 emb|AW737284|AW737284 EST338711 tomato flower buds, anthesis, Co... 229 2e-58 emb|X17154|LTHCPG Leishmania tarentolae H circle borne ltpgpA ge... 197 2e-57 gb|L29484|LEIPGLYA Leishmania tarentolae P-glycoprotein related ... 181 2e-57 35 emb|AI729186|AI729186 BNLGHi12864 Six-day Cotton fiber Gossypium... 210 3e-57 gb|U11583|YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm... 136 6e-57 gb|L29485|LEIPGLYB Leishmania tarentolae P-glycoprotein related ... 171 6e-57 emb|AI489515|AI489515 EST247854 tomato ovary, TAMU Lycopersicon ... 222 2e-56 emb|AL135898|LMFL673 Leishmania major Friedlin chromosome 23 cos... 176 2e-56 emb|AW459613|AW459613 sh89d10.yl Gm-c1016 Glycine max cDNA clone... 219 1e-55 emb|AB009972|AB009972 Aspergillus oryzae gene for beta-1,4-xylos... 122 2e-53 emb|AW757110|AW757110 sl29c06.yl Gm-c1027 Glycine max cDNA clone... 208 3e-52 gb|BE021265|BE021265 sm56g10.yl Gm-c1028 Glycine max cDNA clone ... 206 9e-52 emb|AW761593|AW761593 sl69g02.yl Gm-c1027 Glycine max cDNA clone... 205 2e-51 45 emb|Z99262|SPAC9E9 S.pombe chromosome I cosmid c9E9. 129 2e-51 emb[Y09354]SPABC1 S.pombe ABC1 gene. 129 2e-51 emb|AL136538|SPAC30 S.pombe chromosome I cosmid c30. 144 le-48 emblAI974480|AI974480 T110430e KV0 Medicago truncatula cDNA clon... 196 1e-48 emb|AI495498|AI495498 sa98g09.y1 Gm-c1004 Glycine max cDNA clone... 194 4e-48 50 emb|AW736468|AW736468 EST332482 KV3 Medicago truncatula cDNA clo... 191 3e-47 emb|AW677202|AW677202 DG1_6_D10.b1_A002 Dark Grown 1 (DG1) Sorgh... 191_5e-47 gb|BE022474|BE022474 sm74d06.yl Gm-c1015 Glycine max cDNA clone ... 188 3e-46 emb|Z49222|TCPGP2 T.cruzi gene for P-glycoprotein. emb|AI437929|AI437929 sa41e03.y1 Gm-c1004 Glycine max cDNA clone... 153 2e-44 emblAI777095|AI777095 EST258060 tomato resistant, Cornell Lycope... 177 6e-43 55 emb|AQ935847|AQ935847 CpG2684B CpIOWAgDNA1 Cryptosporidium parvu... 175 3e-42 gb|U95956|TCU95956 Trypanosoma cruzi P-glycoprotein (tcpgp1A) ge... 130 9e-42 emb|AW830202|AW830202 sm24a04.yl Gm-c1028 Glycine max cDNA clone... 172 2e-41 emb|AL113101|CNS01ALX Botrytis cinerea strain T4 cDNA library un... 138 4e-41 60 emb|AW155943|AW155943 ga22b09.yl Moss EST library PPU Physcomitr... 167 7e-40

emb|AW202254|AW202254 sf12h06.yl Gm-c1027 Glycine max cDNA clone... 166 9e-40

emblAW759534|AW759534 sl44f02.yl Gm-c1027 Glycine max cDNA clone... 166 9e-40 emb|AW223508|AW223508 EST300319 tomato fruit red ripe, TAMU Lyco... 165 2e-39 emb|AW219577|AW219577 EST302059 tomato root during/after fruit s... 164 5e-39 emb|AW775340|AW775340 EST334405 DSIL Medicago truncatula cDNA cl... 161 3e-38 5 emb|Z28328|SCYKR103W S.cerevisiae chromosome XI reading frame OR... 122 6e-38 emb|AW039256|AW039256 EST281513 tomato mixed elicitor, BTI Lycop... 159 2e-37 emb|AJ388890|AJ388890 AJ388890 Medicago truncatula R108 Medicago... 159 2e-37 emb|AQ849029|AQ849029 LMAJFV1_lm45c02.x1 Leishmania major FV1 ra... 112 2e-37 gb[U55381]LTU55381 Leishmania tropica P-glycoprotein E gene, com... 114 4e-37 10 emb|AW350529|AW350529 GM210009A10F6R Gm-r1021 Glycine max cDNA 3... 157 7e-37 emb|AQ950989|AQ950989 Sheared DNA-52G21.TF Sheared DNA Trypanoso... 154 5e-36 emb|AF034608|AF034608 Candida albicans YOR1 homolog gene, partia... 153 9e-36 emb|AW775084|AW775084 EST334235 KV3 Medicago truncatula cDNA clo... 153 1e-35 emb|AQ911544|AQ911544 LMAJFV1_lm86e04.y1 Leishmania major FV1 ra... 127 1e-35 15 emb|AW781305|AW781305 sk68b06.yl Gm-c1016 Glycine max cDNA clone... 152 2e-35 emb|AW441948|AW441948 EST311344 tomato fruit red ripe, TAMU Lyco... 114 2e-35 emb|AW350905|AW350905 GM210009B10G8R Gm-r1021 Glycine max cDNA 3... 151 3e-35 emb|AQ849904|AQ849904 LMAJFV1 lm51d04.x1 Leishmania major FV1 ra... 118 3e-35 emb|AB013851|AB013851 Aspergillus oryzae gene for beta-xylosidas... 122 5e-35 emb|AW775168|AW775168 EST334319 KV3 Medicago truncatula cDNA clo... 150 6e-35 emb|AJ278038|BFU278038 Botryotinia fuckeliana BcatrG gene for MR... 148 4e-34 gb[U62929]FNU62929 Filobasidiella neoformans multidrug resistanc... 93 1e-32 emb|AQ946563|AQ946563 Sheared DNA-49C19.TR Sheared DNA Trypanoso... 142 2e-32 25 emb|AQ646228|AQ646228 RPCI93-DpnII-30J14.TV RPCI93-DpnII Trypano... 141 5e-32 gb|U62931|AFU62931 Aspergillus flavus multidrug resistance prote... 88 1e-31 emb|AW756083|AW756083 sl13f12.yl Gm-c1036 Glycine max cDNA clone... 135 2e-30 emb|AI676508|AI676508 etmEST0269 EtH1 Eimeria tenella cDNA clone... 135 2e-30 emb|AQ640396|AQ640396 927P1-5E2.TP 927P1 Trypanosoma brucei geno... 105 4e-30 30 emb|AI782195|AI782195 EST263074 tomato susceptible, Cornell Lyco... 134 4e-30 emb|AW033521|AW033521 EST277092 tomato callus, TAMU Lycopersicon... 134 6e-30 Query= AF084037.3 s at 20246 s at /id source genbank /description gb|aac95354.1| (af084037) receptor-like protein kinase [arabidopsis 35 thaliana] /blast score 0 /ec number /family /chip nova /gb link (2055 letters) Database: plantfungal 40 661,018 sequences; 426,114,510 total letters Searching.....done Score 45 Sequences producing significant alignments: (bits) Value emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 356 e-115 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. emb[X98520]BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 50 gb[M97667]BNASTKR Brassica napus ssp. oleifera serine/threonine ... 312 9e-99 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 313 1e-97 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 315 2e-97 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 323 3e-97 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 307 4e-95 55 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 308 1e-93 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 313 2e-93 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 312 1e-92 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 310 3e-92 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 309 7e-92 60 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 266 1e-90 emb[Y14286]BOY14286 Brassica oleracea SFR3 gene, partial.

dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 260 1e-89 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 286 2e-89 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 262 4e-89 dbi|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 258 3e-87 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 197 4e-84 emb[Y12530]BOARLKGEN B.oleraceae gene encoding serine/threonine ... 111 1e-83 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 268 4e-82 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 302 6e-81 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 302 8e-81 10 gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 232 1e-80 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 105 3e-80 gb|BE057261|BE057261 sm99f12.yl Gm-c1015 Glycine max cDNA clone ... 289 4e-77 emb[Y12531]BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 117 7e-75 emb|AW760240|AW760240 sl59g07.yl Gm-c1027 Glycine max cDNA clone... 261 1e-68 15 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 107 2e-68 emb[AB000970]AB000970 Brassica campestris gene for receptor kina... 109 2e-65 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 105 3e-65 dbi|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 104 1e-64 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 247 2e-64 20 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 105 5e-64 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 105 7e-64 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 190 1e-63 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 181 5e-63 emb|AW831390|AW831390 sm22a06.yl Gm-c1028 Glycine max cDNA clone... 183 6e-63 25 emb|AW620957|AW620957 sj98a07.yl Gm-c1023 Glycine max cDNA clone... 202 1e-62 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 109 2e-62 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 104 2e-62 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 239 7e-62 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 108 8e-62 30 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 99 7e-61 emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 158 3e-59 emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 187 1e-58 emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 227 2e-58 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 226 3e-58 35 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 215 7e-55 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 215 1e-54 emb|AI967314|AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two... 117 3e-54 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 212 9e-54 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 211 2e-53 40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 166 5e-53 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 119 1e-52 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 119 le-51 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 104 1e-51 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 119 4e-51 45 emb|AI899009|AI899009 EST268452 tomato ovary, TAMU Lycopersicon ... 161 7e-51 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 146 2e-50 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 157 9e-50 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 157 9e-50 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 84 2e-49 embly16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 106 2e-49 50 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 146 6e-49 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 152 8e-49 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 161 8e-49 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 119 2e-48 55 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 119 3e-48 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 161 4e-48 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 119 5e-48 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 141 1e-47 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 77 6e-47 60 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 118 8e-47 emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 106 4e-46

emb|X81833|BOSLR31 B.oleracea mRNA for SLR3-1 protein. 85 5e-46 emb|AI938169|AI938169 sc40d07.y1 Gm-c1014 Glycine max cDNA clone... 185 9e-46 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 109 1e-45 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 2e-45 5 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 99 2e-45 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 158 1e-44 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 77 3e-44 emb|AW039406|AW039406 EST281663 tomato mixed elicitor, BTI Lycop... 112 5e-44 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 65 7e-44 10 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 178 1e-43 emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 166 1e-42 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 62 2e-42 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 62 2e-42 emb|AW706972|AW706972 sk20a03.yl Gm-c1028 Glycine max cDNA clone... 174 2e-42 15 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 174 2e-42 emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 173 5e-42 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 170 3e-41 emb|AW775756|AW775756 EST334821 DSIL Medicago truncatula cDNA cl... 137 5e-41 emb|AF085168|AF085168 Triticum aestivum receptor-like protein ki... 68 6e-41 20 emb|AW597214|AW597214 si71g06.y1 Gm-c1031 Glycine max cDNA clone... 116 1e-40 emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycope... 127 2e-40 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 96 2e-40 gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 96 2e-40 emb[Y14600]SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 61 4e-40 25 Query= AC002387.237 at 20269 at /id source genbank /description gb|aab82640.1| (ac002387) putative pectinesterase [arabidopsis thaliana] /blast score 0 /ec number /family pectinesterase /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbin-30 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002387|/ncgi http://www.ncgr.org/cgi-bin/ff?ac002387 (1533 letters) Database: plantfungal 35 661,018 sequences; 426,114,510 total letters Searching..... E Score 40 Sequences producing significant alignments: (bits) Value gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 483 0.0 gb|U82976|CSU82976 Citrus sinensis pectinesterase mRNA, complete... 218 e-119 gb|U82975|CSU82975 Citrus sinensis pectinesterase (PECS-2.1) gen... 421 e-116 45 emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 208 e-111 emb|AF229849|AF229849 Vigna radiata pectin methylesterase isofor... 208 e-107 gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 205 e-106 emb|Z71752|NPPME2MR N.plumbaginifolia mRNA for pectin methyleste... 177 e-104 emb|Z71753|NPPME3MR N.plumbaginifolia mRNA for pectin methyleste... 177 e-103 50 emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. gb|U82973|CSU82973 Citrus sinensis pectinesterase (PECS-1.1) gen... 218 8e-97 emblAF056493|AF056493 Pisum sativum pectin methylesterase mRNA, ... 163 3e-95 emb|AF152171|AF152171 Solanum tuberosum cultivar Desiree pectin ... 190 2e-94

gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 190 8e-93 emb|X07910|LEPECES Tomato mRNA for pectin esterase. 190 1e-92

emb|A17010|A17010 tomato fruit pectin esterase seq ID no1.

emb|X74638|LEPEC1 L.esculentum mRNA for pectin esterase.

emb[X74639]LEPEC2 L.esculentum mRNA for pectin esterase clone.

55

emb|AJ249786|NTA249786 Nicotiana tabacum partial mRNA for pectin... 192 4e-94

gb|U50986|SLU50986 Solanum lycopersicum pectin methylesterase PM,... 188 6e-93

emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 190 5e-94

190 9e-94

190 9e-94

188 3e-93

emblA15983lA15983 L.esculentum mRNA for pectin esterase. 190 1e-92 gb U50985 SLU50985 Solanum lycopersicum pectin methylesterase PM... 185 2e-92 emb|Z71754|NPPME4MR N.plumbaginifolia mRNa for pectin methyleste... 177 2e-92 emb|X95991|PPPECESTR P.persica mRNA for pectin esterase. 161 3e-92 emb|A24196|A24196 L.esculentum pectin esterase clone pPE1. 5 188 7e-92 emb|AF081457|AF081457 Pisum sativum pectin methylesterase (rcpme... 136 4e-90 emb|X67425|PSPMEAG Pisum sativum pmeA gene for pectinesterase. emb|AW650699|AW650699 EST329153 tomato germinating seedlings, TA... 271 2e-86 emb[AW696177]AW696177 NF103C11ST1F1085 Developing stem Medicago ... 193 4e-83 10 emb|AB029461|AB029461 Salix gilgiana SgPME1 mRNA for pectin meth... 144 1e-82 emb|AW257370|AW257370 EST305507 KV2 Medicago truncatula cDNA clo... 232 7e-81 emb|AI166540|AI166540 xylem.est.362 Poplar xylem Lambda ZAPII li... 167 4e-79 emb[X85216]PVRNAPE P.vulgaris mRNA for pectinesterase. gb|U70676|LEU70676 Lycopersicon esculentum pection methylesteras... 188 1e-77 15 gb[U70677]LEU70677 Lycopersicon esculentum (LePME1) gene, partia... 188 4e-77 gb|U70675|LEU70675 Lycopersicon esculentum fruit-specific pectin... 189 1e-76 emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 187 1e-75 emb|AW429158|AW429158 EST306614 tomato flower buds 0-3 mm, Corne... 160 3e-74 emb|AW349192|AW349192 GM210004A21F6R Gm-r1021 Glycine max cDNA 3... 129 1e-72 emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 168 1e-70 emb|AW559494|AW559494 EST314542 DSIR Medicago truncatula cDNA cl... 141 2e-70 emb|AW774488|AW774488 EST333639 KV3 Medicago truncatula cDNA clo... 141 2e-70 emb|AW687047|AW687047 NF005D06RT1F1057 Developing root Medicago ... 132 6e-70 emb|AW784073|AW784073 NXNV 117 D06 F Nsf Xylem Normal wood Verti... 153 6e-70 25 gb|BE020131|BE020131 sm41e11.yl Gm-c1028 Glycine max cDNA clone ... 246 2e-69 emb|Y07899|CPSPE1 C.papaya mRNA for pectinesterase. emb|AI897776|AI897776 EST267219 tomato ovary, TAMU Lycopersicon ... 198 1e-68 emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 172 2e-68 30 emb|AW760550|AW760550 sl51g07.yl Gm-c1027 Glycine max cDNA clone... 155 2e-67 emb|AW329215|AW329215 N200427e rootphos(-) Medicago truncatula c... 149 3e-67 emb[X68029]PVVPE2 P.vulgaris PvVPE2 mRNA for pectin esterase. 149 2e-66 emb|AW774605|AW774605 EST333756 KV3 Medicago truncatula cDNA clo... 141 4e-66 emb|AW299038|AW299038 EST305712 KV2 Medicago truncatula cDNA clo... 141 4e-66 35 emb|AW649176|AW649176 EST327630 tomato germinating seedlings, TA... 180 7e-65 emb|AI782839|AI782839 EST263718 tomato susceptible, Cornell Lyco... 156 5e-64 gb|U28148|MSU28148 Medicago sativa putative pectinesterase mRNA,... 134 5e-64 emb[X97762]STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 165 1e-63 emb|AI440753|AI440753 sa53f07.yl Gm-c1004 Glycine max cDNA clone... 161 1e-63 40 emb|AW774519|AW774519 EST333670 KV3 Medicago truncatula cDNA clo... 137 3e-63 emb|AW706153|AW706153 sj52e04.yl Gm-c1033 Glycine max cDNA clone... 242 5e-63 emb|AW649290|AW649290 EST327744 tomato germinating seedlings, TA... 196 8e-63 emb|AW257345|AW257345 EST305482 KV2 Medicago truncatula cDNA clo... 167 9e-63 emb|AW616248|AW616248 EST307287 L. hirsutum trichome, Cornell Un... 173 1e-62 emb|AW758821|AW758821 NXNV_091_A04_F Nsf Xylem Normal wood Verti... 160 8e-62 45 emb|AW398150|AW398150 EST298033 L. pennellii trichome, Cornell U... 173 1e-61 gb|L27101|PETPPE1A Petunia inflata pectinesterase (PPE1) gene, c... 134 2e-61 emb|AI781139|AI781139 EST262018 tomato susceptible, Cornell Lyco... 205 2e-61 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 148 4e-61 50 gb|U82974|CSU82974 Citrus sinensis pectinesterase (PECS-1.2) gen... 216 6e-60 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 155 6e-60 emb|AW424141|AW424141 sh61d11.y1 Gm-c1015 Glycine max cDNA clone... 146 2e-59 emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 160 2e-59 emb[AW888107]AW888107 NXNV 129 C06 F Nsf Xylem Normal wood Verti... 141 6e-59 55 emb|AW620942|AW620942 sj95g05.yl Gm-c1023 Glycine max cDNA clone... 164 1e-58 emb|AW154926|AW154926 EST290291 tomato root deficiency, Cornell ... 190 2e-58 emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 135 2e-58 emb|AI780635|AI780635 EST261610 tomato susceptible, Cornell Lyco... 196 2e-58 emb|AW616681|AW616681 EST323092 L. hirsutum trichome, Cornell Un... 177 5e-58 60 emb|AW041247|AW041247 EST284111 tomato mixed elicitor, BTI Lycop... 135 7e-58 emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 190 1e-57

----WO 02/22675

25

emb|AW774676|AW774676 EST333827 KV3 Medicago truncatula cDNA clo... 113 1e-57 emb|AW287387|AW287387 LG1_303_C07.b1_A002 Light Grown 1 (LG1) So... 222 6e-57 emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 122 9e-57 emb|AW458218|AW458218 sh79h10.yl Gm-c1016 Glycine max cDNA clone... 120 1e-56 gb|L48178|BNAPECT Brassica campestris pectinesterase mRNA, 3' en... 110 1e-56 5 emb|AW616155|AW616155 EST296925 L. hirsutum trichome, Cornell Un... 177 3e-56 emb|AW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 155 3e-56 emblAW617508|AW617508 EST323919 L. hirsutum trichome, Cornell Un... 177 3e-56 emb|AW617079|AW617079 EST323490 L. hirsutum trichome, Cornell Un... 177 3e-56 10 emb|AW616977|AW616977 EST323388 L. hirsutum trichome, Cornell Un... 173 9e-56 emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 150 1e-55 emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 155 2e-55 emb|X68028|PVVPE3 P.vulgaris PvVPE3 mRNA for pectin esterase. emb|AW616290|AW616290 EST307330 L. hirsutum trichome, Cornell Un... 173 4e-55 15 emb|AW617047|AW617047 EST323458 L. hirsutum trichome, Cornell Un... 173 4e-55 emb|AW220280|AW220280 EST302763 tomato root during/after fruit s... 186 6e-55 emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 156 6e-55 emb|AI441604|AI441604 sa68e03.y1 Gm-c1004 Glycine max cDNA clone... 155 5e-54 emb|AI731654|AI731654 BNLGHi10367 Six-day Cotton fiber Gossypium... 152 1e-53 20

Query= Y14590.5_at 20287_at /id_source genbank /description emb|caa74930.1| (y14590) class iv chitinase [arabidopsis thaliana] /blast_score 1.00e-166 /ec_number /family chitinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14590| /ncgi http://www.ncgr.org/cgi-bin/ff?y14590 (825 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching......done

35 Score

Sequences producing significant alignments:

(bits) Value

Ε

emb[X57187]PVCHITIN P.vulgaris mRNA for chitinase. 238 e-123 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 248 e-112 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 201 e-107 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 247 1e-97 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 197 8e-96 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 136 6e-95 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 136 4e-94 45 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 227 5e-91 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 143 5e-91 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 164 1e-90 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 137 3e-90 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 142 4e-90 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 158 2e-89 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 133 4e-89 emb[X61488]BNCHITIN B.napus mRNA for chitinase. 181 5e-85 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 166 2e-84 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 164 2e-84 55 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 185 9e-83 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 127 8e-80 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 127 8e-80 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 126 2e-78 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 167 4e-78 60 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 131 5e-78

emb[AW030814]AW030814 EST274069 tomato callus, TAMU Lycopersicon... 126 1e-77

emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 126 2e-77 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 126 2e-77 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 170 3e-77 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 136 2e-76 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 215 1e-74 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 160 1e-74 emblAI776153|AI776153 EST257241 tomato resistant, Cornell Lycope... 164 1e-74 emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74 10 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74 gb|LA2467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71 emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70 15 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 154 1e-66 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66 20 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215_5e-65 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64 gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 208 6e-63 emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63 emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 121 1e-61 25 emb|AI055037|AI055037 coau0002N18 Cotton Boll Abscission Zone cD... 111 3e-60 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60 gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59 emb|AW924422|AW924422 WS1_69 C06.b1 A002 Water-stressed 1 (WS1) ... 171 4e-59 emb[X16939]NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58 30 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57 gb[BE034481 BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57 emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57 35 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57 emb|AW746018|AW746018 WS1 38 H11.gl A002 Water-stressed 1 (WS1) ... 221 4e-57 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56 emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56 40 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56 emb|AW924229|AW924229 WS1_51 H04.b1 A002 Water-stressed 1 (WS1) ... 215 3e-55 emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 215_3e-55 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55 emb[X76041]TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55 45 emb|AW745819|AW745819 WS1 _37_H11.g1_A002 Water-stressed 1 (WS1) ... 214 7e-55 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54 emblAF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54 emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54 50 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53 gb[U02605]STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53 emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53 55 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52 gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 205 3e-52 60 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51

emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51 emb|AF043248|AF043248 Solanum tuberosum class I chitinase (ChtC2... 100 3e-51 gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 112 4e-51 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50 emb[X88800[VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50 10 emb|X63899|PSCHITIN P.sativum mRNA for chitinase. 94 1e-49 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 15 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48 Query= Y14590.5_g_at 20288_g_at /id_source genbank /description emb|caa74930.1| (y14590) class iv chitinase [arabidopsis thaliana] 20 /blast_score 1.00e-166/ec_number /family /chip nova/gb link /ncgi (825 letters) Database: plantfungal 25 661,018 sequences; 426,114,510 total letters Score E 30 Sequences producing significant alignments: (bits) Value emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 238 e-123 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 248 e-112 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 201 e-107 35 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 247 1e-97 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 197 8e-96 dbi|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 136 6e-95 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 136 4e-94 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 227 5e-91 40 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 143 5e-91 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 164 1e-90 gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 137 3e-90 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 142 4e-90 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 158 2e-89 45 gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 133 4e-89 emb|X61488|BNCHITIN B.napus mRNA for chitinase. 181 5e-85 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 166 2e-84 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 164 2e-84 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 185 9e-83 50 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 127 8e-80 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 127 8e-80 emblAI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 126 2e-78 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 167 4e-78 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 131 5e-78 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 126 1e-77 emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 126 2e-77 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 126 2e-77 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 170 3e-77 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 136 2e-76 60 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 215 1e-74

gbBE034976BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 160 1e-74 emb|AI776153|AI776153 EST257241 tomato resistant, Cornell Lycope... 164 1e-74 emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 139 1e-74 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74 5 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72 emb[X74919]PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71 emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68 10 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 154 1e-66 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65 15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64 gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 208 6e-63 emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63 emb|AI729668|AI729668 BNLGHi13889 Six-day Cotton fiber Gossypium... 121 1e-61 emb|AI055037|AI055037 coau0002N18 Cotton Boll Abscission Zone cD... 111 3e-60 20 gbBE034616BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60 gbBE033502BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 100 4e-59 emb|AW924422|AW924422 WS1 69 C06.b1 A002 Water-stressed 1 (WS1) ... 171 4e-59 emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 108 2e-58 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58 25 emb|AW746695|AW746695 WS1 54 E02.gl A002 Water-stressed I (WS1) ... 224 6e-58 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57 gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57 emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57 30 emb|AW746018|AW746018 WS1 38 H11.gl A002 Water-stressed 1 (WS1) ... 221 4e-57 emb[X15494]STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 le-56 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56 emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56 35 emb|AW924229|AW924229 WS1 51 H04.b1 A002 Water-stressed 1 (WS1) ... 215 3e-55 emb|AW676775|AW676775 DG1 14_C09.g1 A002 Dark Grown 1 (DG1) Sorg... 215 3e-55 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 105 4e-55 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 109 6e-55 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 214_7e-55 40 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54 emblAF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54 emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 110 6e-54 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54 45 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53 emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 104 2e-53 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53 50 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53 emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52 gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 205 3e-52 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51 55 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51 emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51 emb|AF043248|AF043248 Solanum tuberosum class I chitinase (ChtC2... 100 3e-51 gb[U83592]MSU83592 Medicago sativa class I chitinase mRNA, compl... 112 4e-51 gb[U83591]MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51 60 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 102 7e-51 gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50

emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50 gb[U78888]GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50 emb|X63899|PSCHITIN P.sativum mRNA for chitinase. 94 le-49 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49 gbBE034450BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48 gb[U02287]HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). gb[M15173]TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48 10 Ouery= M92353.4 s at 20291 s at /id source genbank /description gb|aaa32738.1| (m92353) anthranilate synthase alpha subunit [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova 15 /gb link /ncgi (1788 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 20 Searching..... Score Sequences producing significant alignments: (bits) Value 25 gb|L34344|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 772 0.0 gb|L34343|RTAANTSYNA Ruta graveolens anthranilate synthase alpha... 467 0.0 emb|AF079168|AF079168 Nicotiana tabacum feedback-insensitive ant... 365 0.0 emb|AW931942|AW931942 EST357785 tomato fruit mature green, TAMU ... 356 3e-97 30 emb|AW218352|AW218352 EST303535 tomato radicle, 5 d post-imbibit... 210 1e-73 emb|AL031966|SPCC1442 S.pombe chromosome III cosmid c1442. 209 6e-69 emb|AW651095|AW651095 EST329549 tomato germinating seedlings, TA... 222 2e-64 dbj|D89256|D89256 Schizosaccharomyces pombe mRNA, partial cds, c... 205 5e-64 emb[AW982499]AW982499 HVSMEg0003G22f Hordeum vulgare pre-anthesi... 215 2e-58 35 emb|AW460005|AW460005 si07d11.yl Gm-c1029 Glycine max cDNA clone... 116 1e-57 gb[U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 123 4e-48 emb|X68327|SCTRP2 S.cerevisiae TRP2 gene for anthranilate syntha... 123 4e-48 emb|AW719463|AW719463 LjNEST5b1r Lotus japonicus nodule library,... 184 1e-45 emb|AI736775|AI736775 sb33d01.y1 Gm-c1012 Glycine max cDNA clone... 104 2e-40 gb|K01388|YSCTRP2 Yeast (S.cerevisiae) TRP2 gene coding for anth... 122 4e-38 emb|AL032684|SPBP8B7 S.pombe chromosome II p1 p8B7. 95 6e-25 emb|AW509018|AW509018 si39b01.y1 Gm-r1030 Glycine max cDNA clone... 113 5e-24 gb[T14852]T14852 crs299 lambdaZAPST Ricinus communis cDNA clone ... 107 2e-22 emb|AW223881|AW223881 EST300692 tomato fruit red ripe, TAMU Lyco... 103 4e-21 45 emb|AF119554|AF119554 Plasmodium falciparum para-aminobenzoic ac... 67 6e-10 emb|AL111470|CNS019CM Botrytis cinerea strain T4 cDNA library un... 45 2e-05 emb|AI329873|AI329873 b9g02ne.rl Neurospora crassa evening cDNA ... 48 3e-04 emb|AW224247|AW224247 EST300974 tomato fruit red ripe, TAMU Lyco... 46 7e-04 emb|AF149719|AF149719 Aspergillus fumigatus para aminobenzoic ac... 42 0.012 50 emb|AQ448372|AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P... 39 0.15 emb|AQ324360|AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P... 39 0.15 emb|AQ160089|AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P... 39 0.15 emb|AW599019|AW599019 gb01b03.y1 Moss EST library PPN Physcomitr... 37 0.38 emb|AW599000|AW599000 ga99h03.y1 Moss EST library PPN Physcomitr... 37 0.38 55 emb|AW678847|AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S... 35 0.88 emb|AW680390|AW680390 WS1_52 D12.g1_A002 Water-stressed 1 (WS1) ... 35 0.89 emb|AW678385|AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ... 35 0.89 emb|AW747146|AW747146 WS1_66_E07.b1_A002 Water-stressed 1 (WS1) ... 35 0.89 emb|AW678361|AW678361 WS1_15_H06.b1_A002 Water-stressed 1 (WS1) ... 35 0.90 60 emb|AW745749|AW745749 WS1_37_D12.b1_A002 Water-stressed 1 (WS1) ... 35 0.90

emb|AW747427|AW747427 WS1 68 B09.b1 A002 Water-stressed 1 (WS1) ... 35 0.90

```
emb|AW678071|AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
       emb|AW747468|AW747468 WS1_68_B09.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
       emb|AW672427|AW672427 LG1_359_A06.g1_A002 Light Grown 1 (LG1) So... 35 0.90
      emb|AW744836|AW744836 LG1 384_E07.g1 A002 Light Grown 1 (LG1) So... 35 0.90
 5
      emb|AW746170|AW746170 WS1 39 B05.g1 A002 Water-stressed 1 (WS1) ... 35 0.90
      emblAW922317|AW922317 DG1 17 E06.g1 A002 Dark Grown 1 (DG1) Sorg... 35 0.91
      emb|AQ648582|AQ648582 RPCI93-EcoRI-1M22.TP RPCI93-EcoRI Trypanos... 36 0.99
      emb|AQ643551|AQ643551 RPCI93-EcoRI-3124.TJ RPCI93-EcoRI Trypanos... 36 0.99
      emb|AI443370|AI443370 sa31b05.x1 Gm-c1004 Glycine max cDNA clone... 35 1.4
10
      emb|AW101313|AW101313 sd77d08.yl Gm-c1009 Glycine max cDNA clone... 35 1.4
      emb|AW678030|AW678030 WS1 12 B10.g1 A002 Water-stressed 1 (WS1) ... 35 1.4
      emb|AW349006|AW349006 GM210004A12H10R Gm-r1021 Glycine max cDNA ... 35 1.4
      emblAW309961|AW309961 sf27b12.x1 Gm-c1028 Glycine max cDNA clone... 35 1.4
      emb|AW678582|AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
15
      emb|AW317198|AW317198 sf38f03.x1 Gm-c1028 Glycine max cDNA clone... 35 1.4
      emb|AW678305|AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
      emb|AW680905|AW680905 WS1 8 A08.b1 A002 Water-stressed 1 (WS1) S... 35 1.4
      emblAW679666lAW679666 WS1 30 B11.g1 A002 Water-stressed 1 (WS1) ... 35 1.4
      emblAL031746|PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq... 35 1.9
20
      emb|AI959816|AI959816 sc94f02.y1 Gm-c1019 Glycine max cDNA clone... 35 1.9
      emb|AW924277|AW924277 WS1_52 D12.b1 A002 Water-stressed 1 (WS1) ...
      gb|J03998|PFAGAR Plasmodium falciparum glutamic acid-rich protei... 35 1.9
      emb|AW696796|AW696796 NF109A07ST1F1052 Developing stem Medicago ... 35 1.9
      emb|AW396753|AW396753 sf37c11.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
25
      gb|M98871|SOYCHS7A Glycine max chalcone synthase (chs7) gene, co... 35 2.6
      emb|AI460797|AI460797 sa69d02.yl Gm-c1004 Glycine max cDNA clone... 35 2.6
      emb|AW348617|AW348617 GM210002B22G1R Gm-r1021 Glycine max cDNA 3... 35 2.6
      emb|AW310362|AW310362 sf35a09.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
      emb|AI437832|AI437832 sa40c07.y1 Gm-c1004 Glycine max cDNA clone... 35 2.6
30
      gb|BE023927|BE023927 sm94c05.yl Gm-c1015 Glycine max cDNA clone ... 35 2.6
      emb|AW424189|AW424189 sh62b04.y1 Gm-c1015 Glycine max cDNA clone... 35 2.6
      emb|AW102370|AW102370 sd86h01.yl Gm-c1009 Glycine max cDNA clone... 35 2.6
      emb|AW101907|AW101907 sd72d01.yl Gm-c1008 Glycine max cDNA clone... 35 2.6
      emb|AW309356|AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
35
      emb|AL355932|NCB5O22 Neurospora crassa DNA linkage group II BAC ... 34 3.5
      emb|AQ652663|AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom... 34 3.5
      emb|Z98056|SPAC5D6 S.pombe chromosome I cosmid c5D6.
                                                                    34 3.5
      emb|AW348286|AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3... 34 4.9
      emb|AB018422|AB018422 Pisum sativum mRNA for DNA binding zinc fi... 34 4.9
40
      emb|AW734949|AW734949 sk93b10.yl Gm-c1035 Glycine max cDNA clone... 34 4.9
      emb|AW679089|AW679089 WS1 22 A07.g1 A002 Water-stressed I (WS1) ... 34 4.9
      emb|AW306776|AW306776 sf48c12.yl Gm-c1009 Glycine max cDNA clone... 34 4.9
      gb|M36941|BLYHORDCA Hordeum vulgare C-hordein gene, complete cds.
      gb|BE034677|BE034677 ML01H08 ML Mesembryanthemum crystallinum cD... 33 6.7
45
      emb|Z26877|SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro... 33 6.7
      emb|AW267708|AW267708 EST305836 DSIR Medicago truncatula cDNA cl... 33 6.7
      emb|Z28162|SCYKL162C S.cerevisiae chromosome XI reading frame OR... 33 6.7
      emb|AW980990|AW980990 EST392143 GVN Medicago truncatula cDNA clo... 33 6.7
      gb|BE037412|BE037412 MP20G03 MP Mesembryanthemum crystallinum cD... 33 6.7
50
      emb|Z28161|SCYKL161C S.cerevisiae chromosome XI reading frame OR... 33 6.7
      emb|AI726247|AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium ... 33 6.7
      emb|AE001401|AE001401 Plasmodium falciparum chromosome 2, sectio... 33 6.7
      emb|AW573801|AW573801 EST316392 GVN Medicago truncatula cDNA clo... 33 6.7
      emb|Z98547|PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque... 33 9.2
55
      emb|AQ659747|AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom... 33 9.2
      gb|BE021269|BE021269 sm56h04.yl Gm-c1028 Glycine max cDNA clone ... 33 9.2
      emb|AW222457|AW222457 EST299268 tomato fruit red ripe, TAMU Lyco... 33 9.2
      emb|AB012116|AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 33 9.2
      emb|AW725836|AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ... 33 9.2
60
      emb|AQ324451|AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P... 33 9.2
      gb|M73492|LEIHSP90 Leishmania donovani heat shock protein 90 mRN... 33 9.2
```

emb|AW132634|AW132634 se06h07.y1 Gm-c1013 Glycine max cDNA clone... 33 9.2 emb|AI166186|AI166186 a032p32u Hybrid aspen plasmid library Popu... 33 9.2 gb|BE053953|BE053953 GA_Ea0031D23f Gossypium arboreum 7-10 dpa ... 33 9.2

Query= AC007168.86_at 20331_at /id_source genbank /description gb|aad23617.1|ac007168_8 (ac007168) putative aspartate aminotransferase [arabidopsis thaliana] /blast_score 0 /ec_number /family aminotransferase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-

10 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac007168| /ncgi http://www.ncgr.org/cgi-bin/ff?ac007168 (1342 letters)

Database: plantfungal

15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score F

emb|AI729480|AI729480 BNLGHi13474 Six-day Cotton fiber Gossypium... 365 e-116

20 Sequences producing significant alignments:

(bits) Value

emb|AW032260|AW032260 EST275714 tomato callus, TAMU Lycopersicon... 336 2e-91 emb|AW719468|AW719468 LjNEST5c2r Lotus japonicus nodule library,... 297 2e-79 emb|AW729492|AW729492 GA_Ea0025C18 Gossypium arboreum 7-10 dpa ... 291 8e-78 emb|AW924000|AW924000 WS1_32_E10.b1_A002 Water-stressed 1 (WS1) ... 277 1e-73 emb|AW042762|AW042762 ST25B02 Pine TriplEx shoot tip library Pin... 268 2e-72 emb|AW755778|AW755778 sl09c05.y1 Gm-c1036 Glycine max cDNA clone... 248 1e-64 emb|AW737762|AW737762 EST339189 tomato flower buds, anthesis, Co... 169 1e-60 emb|AW621695|AW621695 EST312493 tomato root during/after fruit s... 206 3e-52 emb|AW350933|AW350933 GM210010B10D11R Gm-r1021 Glycine max cDNA ... 203 3e-51 emb|AI166669|AI166669 xylem.est.479 Poplar xylem Lambda ZAPII li... 144 3e-50

emb|AI496468|AI496468 sb08a12.yl Gm-c1004 Glycine max cDNA clone... 197 2e-49
emb|AI774565|AI774565 EST255665 tomato resistant, Cornell Lycope... 192 7e-48
emb|AW907026|AW907026 EST343253 potato stolon, Cornell Universit... 186 4e-46
emb|AW423906|AW423906 sh57f06.yl Gm-c1015 Glycine max cDNA clone... 173 2e-42
emb|AW458923|AW458923 sh16f03.yl Gm-c1016 Glycine max cDNA clone... 171 8e-42
gb|BE057095|BE057095 sm97d03.yl Gm-c1015 Glycine max cDNA clone ... 164 2e-39

40 emb|AW704991|AW704991 sk41b08.yl Gm-c1019 Glycine max cDNA clone... 161 8e-39 emb|AW034075|AW034075 EST277570 tomato callus, TAMU Lycopersicon... 150 2e-35 emb|AI166457|AI166457 xylem.est.288 Poplar xylem Lambda ZAPII li... 145 7e-35 emb|AW738611|AW738611 EST340038 tomato flower buds, anthesis, Co... 131 1e-29 emb|AW679816|AW679816 WS1_32_E10.gl_A002 Water-stressed 1 (WS1) ... 126 5e-28

45 emb|AW599717|AW599717 ga92a09.y1 Moss EST library PPN Physcomitr... 126 5e-28 emb|AW704716|AW704716 sk39f03.y1 Gm-c1028 Glycine max cDNA clone... 100 5e-20 emb|Z98531|SPAC6B12 S.pombe chromosome I cosmid c6B12. 50 1e-13 emb|AW268000|AW268000 EST306222 DSIR Medicago truncatula cDNA cl... 58 1e-13 emb|AW684914|AW684914 NF023A07NR1F1000 Nodulated root Medicago t... 58 1e-13

50 emb|AW191292|AW191292|T113595e KV2 Medicago truncatula cDNA clon... 58 1e-13 emb|AW040370|AW040370|EST283234 tomato mixed elicitor, BTI Lycop... 56 5e-13 emb|AI440588|AI440588 sa68b05.y1 Gm-c1004 Glycine max cDNA clone... 57 2e-12 emb|AW831752|AW831752 sm16f02.y1 Gm-c1027 Glycine max cDNA clone... 60 8e-12 emb|AW906615|AW906615|EST342737 potato stolon, Cornell Universit... 56 1e-11

55 gb|L00673|TRBANTA Trypanosoma cruzi antigen tyrosine aminotransf... 40 7e-10 emb|AI773775|AI773775 EST254875 tomato resistant, Cornell Lycope... 63 5e-09 emb|AW691076|AW691076 NF041A07ST1F1000 Developing stem Medicago ... 61 2e-08 emb|AW477177|AW477177 ga42h10.y1 Moss EST library PPU Physcomitr... 61 3e-08 emb|AI900082|AI900082 sb98f05.y1 Gm-c1012 Glycine max cDNA clone... 45 2e-07 gb|BE022324|BE022324 sm73d10.y1 Gm-c1028 Glycine max cDNA clone ... 45 2e-07

emb|AW690226|AW690226 NF030F01ST1F1000 Developing stem Medicago ... 40 3e-07

emb|AI736990|AI736990 sb36c06.yl Gm-c1013 Glycine max cDNA clone... 57 4e-07 emb|AV409052|AV409052 AV409052 Lotus japonicus young plants (two... 56 6e-07 gb|BE020537|BE020537 sm44h11.yl Gm-c1028 Glycine max cDNA clone ... 42 2e-06 emb[Z49335]SCYJL060W S.cerevisiae chromosome X reading frame ORF... 54 2e-06 5 emb|AF074932|AF074932 Sinapis arvensis 1-aminocyclopropane-1-car... 36 2e-05 emb|AI562691|AI562691 TENS2678 T. cruzi epimastigote normalized ... 37 3e-05 emb|AI460900|AI460900 sa70f07.yl Gm-c1004 Glycine max cDNA clone... 50 5e-05 emb|AB015494|AB015494 Passiflora edulis PE-ACS1 mRNA for ACC syn... 36 5e-05 10 emb|AI483496|AI483496 EST249317 tomato ovary, TAMU Lycopersicon ... 38 5e-05 gb[M34289]TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha... 36 1e-04 gb|L20634|POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb... 36 1e-04 emb|X62536|LEACC L.esculentum mRNA for ACC synthase. emb|AI487017|AI487017 EST245339 tomato ovary, TAMU Lycopersicon ... 36 1e-04 15 emb|X59145|LEACC2MR Lycopersicon esculentum LE-ASCC2 mRNA (ptACC... 35 2e-04 emb|AW568631|AW568631 si60b11.yl Gm-r1030 Glycine max cDNA clone... 47 3e-04 dbj|D88273|D88273 Hordeum vulgare naat-A mRNA for nicotianamine ... 36 8e-04 emb|AB005788|AB005788 Hordeum vulgare mRNA for nicotianamine ami... 35 0.001 emb|AV390505|AV390505 AV390505 Chlamydomonas reinhardtii C9 Chla... 35 0.002 20 emb|AV414385|AV414385 AV414385 Lotus japonicus young plants (two... 44 0.002 emb|AI054518|AI054518 coau0001D13 Cotton Boll Abscission Zone cD... 35 0.003 emb|Z18953|PHAMCRBSY P.hybrida mRNA for 1-aminocyclopropane 1-ca... 37 0.004 emb|AB007639|AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 33 0.007 emb|AI941267|AI941267 sb86g03.yl Gm-c1010 Glycine max cDNA clone... 31 0.007 25 emb|AB033502|AB033502 Populus euphratica peacs-1 mRNA for 1-amin... 42 0.008 gb|U73816|MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ... 32 0.009 emb|AI773174|AI773174 EST254274 tomato resistant, Cornell Lycope... 32 0.010 emb[X82273]BOACCS B.oleracea mRNA for ACC synthase. 42 0.012 emb|AJ012550|CSI012550 Citrus sinensis acs1 gene, exons 1-4. 41 0.016 30 emb|Z11613|VRACCSYNM V.radiata mRNA for ACC synthase. 41 0.016 emb|Z18952|DCAMCRBSY D.caryophyllus mRNA for 1-aminocyclopropane... 41 0.016 emb|Z11562|VRACCSYN V.radiata mRNA for 1-aminocyclopropane-1-car... 41 0.016 gb|U68216|CPU68216 Carica papaya ACC synthase mRNA, complete cds. emb|AF178076|AF178076 Carica papaya 1-aminocyclopropane-1-carbox... 41 0.022 35 emb|AF048753|AF048753 Citrus X paradisi 1-aminocyclopropane-1-ca... 41 0.022 emb|AW925529|AW925529 HVSMEg0002F12 Hordeum vulgare pre-anthesis... 41 0.022 emb|AW030650|AW030650 EST273905 tomato callus, TAMU Lycopersicon... 41 0.022 emb|AJ012577|CPA012577 Carica papaya mRNA for 1-aminocyclopropan... 41 0.022 emb|AJ012551|CSI012551 Citrus sinensis mRNA for ACC synthase. 40 emb|AI440609|AI440609 sa68d05.y1 Gm-c1004 Glycine max cDNA clone... 41 0.022 emb|AW928458|AW928458 EST337246 tomato flower buds 8 mm to pre-a... 41 0.022 emb|AJ276295|CSI276295 Citrus sinensis partial mRNA for ACC synt... 40 0.030 gb|U17231|PHU17231 Pelargonium hortorum clone pGAC-2 1-aminocycl... 40 0.030 emb|AF177769|AF177769 Carica papaya 1-aminocyclopropane-1-carbox... 40 0.030 45 gb|U88971|PHU88971 Pelargonium hortorum 1-aminocyclopropane-1-ca... 40 0.030 emb|AF170705|AF170705 Mangifera indica 1-aminocyclopropane-1-car... 40 0.041 gb|BE020529|BE020529 sm44h02.yl Gm-c1028 Glycine max cDNA clone ... 40 0.057 emb|AW100199|AW100199 sd26h06.yl Gm-c1012 Glycine max cDNA clone... 40 0.057 emb[X67100]GMCACCS1 G.max mRNA for ACC synthase. 50 emb|AI487927|AI487927 EST246249 tomato ovary, TAMU Lycopersicon ... 40 0.057 emb|AF239987|AF239987 Prunus persica ACC synthase ACS1 mRNA, par... 40 0.057 emb|AW221912|AW221912 EST298723 tomato fruit red ripe, TAMU Lyco... 40 0.057 emb|AW774036|AW774036 EST333022 KV3 Medicago truncatula cDNA clo... 40 0.057 emb|AI165890|AI165890 B003P14U Hybrid aspen plasmid library Popu... 40 0.057 emb|AJ277160|CPA277160 Carica papaya partial paccs1A gene for 1-... 39 0.078 55 emb|AW703931|AW703931 sk25h05.yl Gm-c1028 Glycine max cDNA clone... 39 0.078 emblAW928492|AW928492 EST337280 tomato flower buds 8 mm to pre-a... 39 0.078 emb|AW043088|AW043088 ST29B11 Pine TriplEx shoot tip library Pin... 39 0.078 emb|Y09204|NTHPA N.tabacum mRNA for histidinol-phosphate aminotr... 30 0.10 60 emb|AF083814|AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR... 39 0.11 gb[U17230]PHU17230 Pelargonium hortorum clone pGAC-2G 1-aminocyc... 39 0.11

```
Query= AC005850.19 s at 20365 s at /id_source genbank /description
      gb|aad25552.1|ac005850 9 (ac005850) highly similar to mlo proteins
      [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 5
      /gb link /ncgi
           (1752 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
10
      Searching......done
                                          Score
      Sequences producing significant alignments:
                                                          (bits) Value
15
      emb|A92838|A92838 Sequence 12 from Patent WO9804586.
                                                                    258 e-123
      emb|Z83834[HVMLO H.vulgare mRNA for Mlo protein.
                                                                   261 e-116
      emb|A92833|A92833 Sequence 7 from Patent WO9804586.
                                                                    261 e-116
      emblA92828|A92828 Sequence 2 from Patent WO9804586.
                                                                    261 e-116
20
      emb|AW216578|AW216578 EST295292 tomato callus, TAMU Lycopersicon... 165 6e-78
      emb|AJ005341|LUAJ5341 Linum usitatissimum mRNA for MLO-like prot... 287 2e-76
      emb|AW934153|AW934153 EST359996 tomato fruit mature green, TAMU ... 235 4e-74
      emb|AW132264|AW132264 sd98f11.yl Gm-c1013 Glycine max cDNA clone... 128 2e-60
      emb|AI779924|AI779924 EST260803 tomato susceptible, Cornell Lyco... 228 8e-59
25
      gb|BE020055|BE020055 sm38e01.yl Gm-c1028 Glycine max cDNA clone ... 199 2e-58
      emb|AW132268|AW132268 sd98g11.yl Gm-c1013 Glycine max cDNA clone... 124 5e-58
      emb|AI729603|AI729603 BNLGHi13760 Six-day Cotton fiber Gossypium... 202 8e-51
      emb|AI054629|AI054629 coau0001J02 Cotton Boll Abscission Zone cD... 133 2e-44
      emblAV426381|AV426381 AV426381 Lotus japonicus young plants (two... 145 3e-43
30
      emb|AI729043|AI729043 BNLGHi12416 Six-day Cotton fiber Gossypium... 142 6e-42
      emb[Y14573]HVCH4H Hordeum vulgare DNA for chromosome 4H.
                                                                         107 7e-41
      emb|A92831|A92831 Sequence 5 from Patent WO9804586.
                                                                    107 7e-41
      emb|AI731933|AI731933 BNLGHi11440 Six-day Cotton fiber Gossypium... 136 3e-40
      emb|AI440563|AI440563 sa84c07.y1 Gm-c1004 Glycine max cDNA clone... 155 1e-36
35
      emb|AI166945|AI166945 xylem.est.727 Poplar xylem Lambda ZAPII li... 149 4e-35
      emb|A92829|A92829 Sequence 3 from Patent WO9804586.
      gb|BE059771|BE059771 sn36h06.yl Gm-c1016 Glycine max cDNA clone ... 137 2e-31
      emb|AB011444|AB011444 Triticum aestivum WESR3 mRNA, partial cds.
      emb[AW350270]AW350270 GM210007B20B6R Gm-r1021 Glycine max cDNA 3... 127 7e-31
40
      emb|AI778500|AI778500 EST259379 tomato susceptible, Cornell Lyco... 76 3e-30
      emb|AW299018|AW299018 EST305692 KV2 Medicago truncatula cDNA clo... 125 1e-27
      emblAW442776|AW442776 EST307706 tomato mixed elicitor, BTI Lycop... 117 2e-25
      emb|AW719459|AW719459 LjNEST4h6r Lotus japonicus nodule library,... 85 4e-25
      emb|AW087034|AW087034 gal1d07.yl Moss EST library CPU Ceratodon ... 83 5e-25
      emb|AW672144|AW672144 LG1 357 A11.b1 A002 Light Grown 1 (LG1) So... 108 1e-22
      emb|AT000894|AT000894 AT000894 Brassica rapa guard cell Brassica... 108 2e-22
      emb|AW906979|AW906979 EST343206 potato stolon, Cornell Universit... 98 2e-19
      emb|Z95496|HVMLOH1 H.vulgare Mlo-h1 gene.
                                                                 98 2e-19
      emb|A92836|A92836 Sequence 10 from Patent WO9804586.
                                                                     98 2e-19
```

50 emb|A92832|A92832 Sequence 6 from Patent WO9804586. 98 2e-19 emb|AW570038|AW570038 si85h06.y1 Gm-c1031 Glycine max cDNA clone... 96 6e-19 emb|AA660856|AA660856 00751 MtRHE Medicago truncatula cDNA 5', m... 90 4e-17 emb|AT000630|AT000630 AT000630 Brassica rapa guard cell Brassica... 87 5e-16 gb|BE022484|BE022484 sm74e08.y1 Gm-c1015 Glycine max cDNA clone ... 84 3e-15

emb|AW672173|AW672173 LG1_357_A11.g1_A002 Light Grown 1 (LG1) So... 80 4e-14
 emb|AI443125|AI443125 sa84f05.y1 Gm-c1004 Glycine max cDNA clone... 78 3e-13
 emb|AW870276|AW870276 NXNV_128_G07_F Nsf Xylem Normal wood Verti... 77 4e-13
 emb|AW726816|AW726816 GA_Ea0022N04 Gossypium arboreum 7-10 dpa ... 50 6e-13
 emb|AI960937|AI960937 sc92h06.y1 Gm-c1019 Glycine max cDNA clone... 76 1e-12

60 emb|AW569990|AW569990 si85c05.yl Gm-c1031 Glycine max cDNA clone... 75 1e-12 emb|AI484886|AI484886 EST243149 tomato ovary, TAMU Lycopersicon ... 73 7e-12

	emb AW285009 AW285009 LG1_297_B09.g1_A002 Light Grown 1 (LG1) So 72 1e-11
	emb AW203816 AW203816 sf38e09.yl Gm-c1028 Glycine max cDNA clone 62 2e-08
	emb AW719871 AW719871 LjNEST11d10r Lotus japonicus nodule librar 51 8e-08
	emb AW757069 AW757069 sl02g02.yl Gm-c1036 Glycine max cDNA clone 59 9e-08
5	emb AW567653 AW567653 si77b05.yl Gm-c1031 Glycine max cDNA clone 55 2e-06
	emb AT000874 AT000874 AT000874 Brassica rapa guard cell Brassica 46 7e-04
•	emb AI563090 AI563090 EST00214 watermelon lambda zap library Cit 37 0.010
	emb Z74921 BOK8A2 B.oleracea mRNA (unknown). 31 0.26
•	emb AZ221382 AZ221382 Gm_UMb001_002_A13R UMN Soybean BAC Library 33 0.6
10	gb BE035329 BE035329 MM06C12 MM Mesembryanthemum crystallinum cD 36 0.71
~ ~	emb AW186503 AW186503 se68f07.yl Gm-c1019 Glycine max cDNA clone 36 0.97
	emb AW218260 AW218260 EST303441 tomato radicle, 5 d post-imbibit 35 1.3
	1 1 1 1 1 1 1 1 1 1
	embla W693662 A W693662 NF067A 11ST1F1084 Developing stem Medicago 35 1.3
15	emb AW688978 AW688978 NF014A05ST1F1000 Developing stem Medicago 35 1.3
13	emb AI374173 AI374173 T6346 MVAT4 bloodstream form of serodeme W 35 1.3
•	emb AW689953 AW689953 NF027B09ST1F1000 Developing stem Medicago 35 1.3
	emb AW218259 AW218259 EST303440 tomato radicle, 5 d post-imbibit 35 1.3
	emb X96770 SCLACHXVI S.cerevisiae chromosome XVI, left arm DNA. 35 1.8
20	emb X05498 SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA. 35 1.8
20	emb Z73500 SCYPL144W S.cerevisiae chromosome XVI reading frame O 35 1.8
	gb U43703 SCU43703 Saccharomyces cerevisiae chromosome XVI cosmi 35 1.8
	emb Z73499 SCYPL143W S.cerevisiae chromosome XVI reading frame O 35 1.8
	emb AJ242498 CCL242498 Candida cloacae mRNA for long chain fatty 35 1.8
25	emb AQ949106 AQ949106 Sheared DNA-49L9.TR Sheared DNA Trypanosom 35 2.5
25	emb AQ650344 AQ650344 Sheared DNA-28J12.TF Sheared DNA Trypanoso 35 2.5
	emb AQ657515 AQ657515 Sheared DNA-3K7.TR Sheared DNA Trypanosoma 35 2.5
	emb Z74965 SCYOR057W S.cerevisiae chromosome XV reading frame OR 34 3.5
	emb AC007061 AC007061 Leishmania major chromosome 3 clone L1559 34 3.5
20	emb AQ642037 AQ642037 RPCI93-DpnII-29K3.TJ RPCI93-DpnII Trypanos 34 3.5
30	emb AQ445280 AQ445280 GSSTc01558 Trypanosoma cruzi random genomi 34 3.5
	emb Z70678 SCXV55KB S.cerevisiae chromosome XV DNA, 54.7 kb region. 34 3.5
	emb AQ659145 AQ659145 Sheared DNA-16H2.TF Sheared DNA Trypanosom 34 3.5
	gb U88830 SCU88830 Saccharomyces cerevisiae Sgt1p (SGT1) gene, c 34 3.5
25	emb AC005927 AC005927 Leishmania major chromosome 3 clone L3561 34 3.5
35	emb AQ637975 AQ637975 927P1-6A12.TV 927P1 Trypanosoma brucei gen 34 3.5
	emb AL031744 PFMAL1P1 Plasmodium falciparum chromosome 1 strain 29 4.5
	emb AF091345 AF091345 Schizosaccharomyces pombe N-terminal serin.: 34 4.7
	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC 34 4.7
40	emb AQ948416 AQ948416 Sheared DNA-38M22.TR Sheared DNA Trypanoso 34 4.7
40	emb AW257222 AW257222 EST305359 KV2 Medicago truncatula cDNA clo 34 4.7
	emb Y13973 CACIP1 Candida sp. CIP1 gene. 34 4.7
	emb AL031263 SPBC17F3 S.pombe chromosome II cosmid c17F3. 34 4.7
	emb AF152552 AF152552 Sorghum bicolor chalcone synthase 5 (CHS5) 34 4.7
45	emb AQ655690 AQ655690 Sheared DNA-9G1.TR Sheared DNA Trypanosoma 34 4.7
43	emb AZ212373 AZ212373 Sheared DNA-101E1.TF Sheared DNA Trypanoso 34 4.7
	emb AJ250726 TBR250726 Trypanosoma brucei HSP100 gene, GPI-PLC g 34 4.7
•	gb M17420 YSTHEP Saccharomyces cerevisiae heptapeptide repeat re 33 6.5
	emb AI730517 AI730517 BNLGHi6942 Six-day Cotton fiber Gossypium 33 6.5
50	emb Z49511 SCYJR011C S.cerevisiae chromosome X reading frame ORF 33 6.5
50	gb U59312 HVU59312 Hordeum vulgare (1,4)-beta-xylan endohydrolas 33 6.5
	emb Z74188 SCYDL140C S.cerevisiae chromosome IV reading frame OR 33 6.5
	emb[X87611 SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 33 6.5
	emb AA003500 AA003500 T3189 MVAT4 bloodstream form of serodeme W 33 6.5
	emb AQ951709 AQ951709 Sheared DNA-51E22.TF Sheared DNA Trypanoso 33 6.5
55	
	Query= AC005314.38_at 20368_at /id_source genbank /description
	gb aac36163.1 (ac005314) putative serpin [arabidopsis thaliana]
	/blast_score 0 /ec_number /family /chip nova /gb_link
	http://www3.ncbi.nlm.nih.gov/htbin-
50	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005314 /ncgi
	http://www.ncgr.org/cgi-bin/ff?ac005314

(1125 letters)

```
Database: plantfungal
      661,018 sequences; 426,114,510 total letters
```

5 Searching......done Sequences producing significant alignments: (bits) Value 10 emb[Y11486]TASERPIN T.aestivum mRNA for serpin WZS3. 112 2e-68 emb|AJ245879|TAE245879 Triticum aestivum mRNA for serpin (WSZ2a ... 113 7e-66 emb|AJ245878|TAE245878 Triticum aestivum mRNA for serpin (WSZ1c ... 116 2e-65 emb|Y11485|TAESERPIN T.aestivum mRNA for serpin WZS2. 116 2e-62 15 emb|Z49890|TAWZCISPN T.aestivum WZCI mRNA for serpin. 109 3e-60 emb|X95277|HVSER H.vulgare mRNA for serpin. 98 6e-58 emb|AW458573|AW458573 sh10h03.yl Gm-c1016 Glycine max cDNA clone... 115 6e-55 emb|X97636|HVSERP H.vulgare mRNA for serpin. 96 2e-44 emb|AW598408|AW598408 sj91a11.yl Gm-c1023 Glycine max cDNA clone... 144 2e-43 20 gb/BE058355/BE058355 sn15a03.yl Gm-c1016 Glycine max cDNA clone ... 134 3e-40 emb|AW688254|AW688254 NF005C03ST1F1000 Developing stem Medicago ... 127 7e-38 emb|Z15116|HVPAZXG H.vulgare pazx gene encoding protein zx. emb|AF118560|AF118560 Avena fatua barley protein Z homolog mRNA,... 73 7e-32 emb|AW394511|AW394511 sh33b01.yl Gm-c1017 Glycine max cDNA clone... 81 2e-31 25 emb|AI730301|AI730301 BNLGHi6607 Six-day Cotton fiber Gossypium ... 77 8e-31 emb|AI725411|AI725411 BNLGHi11751 Six-day Cotton fiber Gossypium... 55 9e-30 emb|AV420945|AV420945 AV420945 Lotus japonicus young plants (two... 126 4e-28 emb|AI772215|AI772215 EST253315 tomato resistant, Cornell Lycope... 116 6e-27 emb|X51726|HVPAZ1 Barley Paz1 gene for protein Z. 30 emb|AW219573|AW219573 EST302055 tomato root during/after fruit s... 83 4e-26 emb|AI726323|AI726323 BNLGHi5614 Six-day Cotton fiber Gossypium ... 112 8e-26 emb|AW926241|AW926241 HVSMEg0006L04 Hordeum vulgare pre-anthesis... 117 2e-25 emb|AW729167|AW729167 GA_Ea0024E14 Gossypium arboreum 7-10 dpa ... 73 6e-24 emb|AW725528|AW725528 GA_Ea0018H14 Gossypium arboreum 7-10 dpa ... 73 6e-24 35 emb|AV408545|AV408545 AV408545 Lotus japonicus young plants (two... 68 9e-22 gb|BE036749|BE036749 MP04H03 MP Mesembryanthemum crystallinum cD... 48 1e-21 emb|AW983183|AW983183 HVSMEg0008J04f Hordeum vulgare pre-anthesi... 64 2e-21 emb|AW728267|AW728267 GA_Ea0016C18 Gossypium arboreum 7-10 dpa ... 102 4e-21 emb|AW099940|AW099940 sd18f07.y2 Gm-c1012 Glycine max cDNA clone... 57 5e-18 40 emb|AW720162|AW720162 LjNEST16a4r Lotus japonicus nodule library... 84 1e-15 emb|AW598800|AW598800 ga88d04.y1 Moss EST library PPU Physcomitr... 84 3e-15 gb|BE058596|BE058596 sn18b11.yl Gm-c1016 Glycine max cDNA clone ... 48 7e-14 gb|BE051905|BE051905 GA Ea0023M15f Gossypium arboreum 7-10 dpa ... 56 4e-13 emb|AV428665|AV428665 AV428665 Lotus japonicus young plants (two... 70 3e-11 45 emb|AV418072|AV418072 AV418072 Lotus japonicus young plants (two... 70 4e-11

emb|AW428704|AW428704 Ljirnpest22-785-g1 Ljirnp Lambda HybriZap ... 70 4e-11 emb|AW560154|AW560154 EST315202 DSIR Medicago truncatula cDNA cl... 69 5e-11 emb|AQ917127|AQ917127 T233156b Medicago truncatula BAC library M... 47 3e-09 emb|AW306929|AW306929 sf50e08.yl Gm-c1009 Glycine max cDNA clone... 56 4e-08

50 emb|AW010023|AW010023 ST01E04 Pine TriplEx shoot tip library Pin... 41 1e-07 emb[X51727]HVPAZPSE Barley DNA for pseudogene PAZ. 51 3e-07 gb|BE022668|BE022668 sm75h09.yl Gm-c1015 Glycine max cDNA clone ... 56 7e-07 emb[X05902]HVPROTZ Barley mRNA fragment for protein Z. 46 8e-07 emb|AW102228|AW102228 sd85a05.yl Gm-c1009 Glycine max cDNA clone... 48 7e-06

55 emb|AI779352|AI779352 EST260231 tomato susceptible, Cornell Lyco... 51 1e-05 emb|AI779351|AI779351 EST260230 tomato susceptible, Cornell Lyco... 51 1e-05 emb|AV420150|AV420150 AV420150 Lotus japonicus young plants (two... 50 3e-05 emb[AW599056]AW599056 gb01e09.yl Moss EST library PPN Physcomitr... 50 3e-05 emb|AV414917|AV414917 AV414917 Lotus japonicus young plants (two... 50 3e-05

emb|AW738877|AW738877 gb03f10.y1 Moss EST library PPN Physcomitr... 42 0.002 emb|AW693477|AW693477 NF065F09ST1F1000 Developing stem Medicago ...

	emb AW905918 AW905918 EST342091 potato stolon, Cornell Universit 35 0.81
	emb Z49939 SC9959 S.cerevisiae chromosome XIII cosmid 9959. 35 1.5
•	gb[BE059186[BE059186 sn27d04.yl Gm-c1016 Glycine max cDNA clone 35 1.5
	emb AW119311 AW119311 A57 Neospora caninum Lambda Zap cDNA libra 34 2.1
5	emb AL114606 CNS01BRQ Botrytis cinerea strain T4 cDNA library un 34 2.1
•	emb AL114185 CNS01BG1 Botrytis cinerea strain T4 cDNA library un 34 2.1
•	
	emb AQ367717 AQ367717 toxb0002L20r CUGI Tomato BAC Library Lycop 34 2.1
10	emb AL114160 CNS01BFC Botrytis cinerea strain T4 cDNA library un 34 2.1
10	emb AL115273 CNS01CA9 Botrytis cinerea strain T4 cDNA library un 34 2.1
	emb AL113815 CNS01B5R Botrytis cinerea strain T4 cDNA library un 34 2.1
	emb AI490380 AI490380 EST248706 tomato ovary, TAMU Lycopersicon 34 2.9
	emb AL116919 CNS01DJZ Botrytis cinerea strain T4 cDNA library un 34 2.9
	gb U68716 BFU68716 Botryotinia fuckeliana endopolygalacturonase 33 4.0
15	gb[L25681]HYBRG18S Hydnora africana Thunb. 18S ribosomal RNA (18 33 4.0
	emb[Al165169]Al165169 A077P18U Hybrid aspen plasmid library Popu 33 4.0
	gb[BE020501]BE020501 sm44e08.y1 Gm-c1028 Glycine max cDNA clone 33 5.5
	gb]M55639 AURRR16S Aureobasidium pullulans 16S-like ribosomal RN 33 5.5
20	emb AQ953266 AQ953266 Sheared DNA-39D4.TF Sheared DNA Trypanosom 33 5.5
20	emb AI494738 AI494738 sb14f02.yl Gm-c1004 Glycine max cDNA clone 33 5.5
• • •	gb M35065 BLYPROZ Barley protein Z mRNA, partial cds. 33.5.5
	emb AV409233 AV409233 AV409233 Lotus japonicus young plants (two 26 6.2
	emb AJ273043 AJ273043 AJ273043 Metarhizium anisopliae ARSEF 2575 32 7.5
	emb AF106529 AF106529 Monacrosporium leptosporum 18S small subun 32 7.5
25	emb AW569360 AW569360 si86a11.yl Gm-c1031 Glycine max cDNA clone 32 7.5
	emb X51599 NTCHN50 Tobacco CHN50 gene for endochitinase. 32 7.5
	emb AL356192 NCB24B19 Neurospora crassa DNA linkage group II BAC 32 7.5
	emb AF123288 AF123288 Lagynion scherffelii small subunit ribosom 32 7.5
	emb[AW180275]AW180275 MgA0367f MgA Library Mycosphaerella gramin 32 7.5
30	
30	emb AL356172 NCB23L21 Neurospora crassa DNA linkage group II BAC 32 7.5
	emb AI779615 AI779615 EST260494 tomato susceptible, Cornell Lyco 32 7.5
	emb[X64519]NTCHN50G N.tabacum chitinase gene 50 for class I chit 32 7.5
	emb AF123299 AF123299 Chrysosphaera parvula small subunit riboso 32 7.5
	emb AQ398442 AQ398442 mgxb0015C20f CUGI Rice Blast BAC Library P 32 7.5
35	
	Query= AL024486.131_at 20420_at /id_source genbank /description
	emb caa19698.1 (al024486) putative chitinase [arabidopsis thaliana]
	/blast score 0 /ec number /family chitinase /chip nova /gb link
	http://www3.ncbi.nlm.nih.gov/htbin-
40	post/entrez/query?db=n&form=6&dopt=g&uid=gb al024486 /ncgi
• -	http://www.ncgr.org/cgi-bin/ff?al024486
	(1140 letters)
	(11.10.104.010)
	Database: plantfungal
45	661,018 sequences; 426,114,510 total letters
43	001,016 sequences, 420,114,510 total fetters
	Searchingdone
	Searchingdone
	0 T
50	Score E
50	Sequences producing significant alignments: (bits) Value
	LINESCOND TO STATE OF
	emb[X78325]NTSNNPZ N.tabacum (Samsun NN) Pz mRNA. 317 e-139
	emb A72838 A72838 Sequence 1 from Patent WO9505467. 314 e-138
	emb X77110 NTCHIVR N.tabacum chi-V mRNA for chitinase class V. 312 e-137
55	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR 189 3e-84
	emb X77111 NTCHIVD N.tabacum chi-V gene. 204 1e-69
	emb A72844 A72844 Sequence 7 from Patent WO9505467. 204 7e-69
	emb AW690230 AW690230 NF030F05ST1F1000 Developing stem Medicago 139 4e-66
	emb AF108893 AF108893 AF108893 Capsicum annuum root 1st-branched 201 7e-51
60	emb AW032116 AW032116 EST275570 tomato callus, TAMU Lycopersicon 186 2e-46
-	omble Wiscouts AVISCOUTS ECT215462 DCTD Mediana towards aDNA at 160, 20 41

```
emb|AW351251|AW351251 GM210011A20A4R Gm-r1021 Glycine max cDNA 3... 145 6e-
      emb|AV423067|AV423067 AV423067 Lotus japonicus young plants (two... 129 2e-32
      emb|AV412385|AV412385 AV412385 Lotus japonicus young plants (two... 129 4e-29
      emb|AV411642|AV411642 AV411642 Lotus japonicus young plants (two... 84 3e-28
      emb|AI495953|AI495953 sb18c04.y1 Gm-c1004 Glycine max cDNA clone... 111 1e-23
      emb|AV422006|AV422006 AV422006 Lotus japonicus young plants (two... 75 3e-21
      emb|AF188932|AF188932 Hypocrea rufa strain Hy9 42 kDa endochitin... 68 1e-20
      emb|AF188921|AF188921 Trichoderma atroviride strain DAOM 165782 ... 70 3e-20
10
      gb[U49455]THU49455 Trichoderma harzianum endochitinase (chil) mR... 69 3e-20
      emblAF188918|AF188918 Hypocrea koningii 42 kDa endochitinase gen... 71 3e-20
      emblAF188930|AF188930 Trichoderma asperellum strain CBS 361.97, ... 68 6e-20
      emb|AF188926|AF188926 Trichoderma asperellum strain GJS 90-14 42... 68 6e-20
      emb|AF188923|AF188923 Hypocrea rufa strain GJS 89-142 42 kDa end... 68 8e-20
15
      emb|X79381|THECH42 T.harzianum (IMI 206040) ech-42 gene.
                                                                        68 9e-20
      gb|L14614|TRRENDOCHI Trichoderma harzianum endochitinase mRNA, c... 68 9e-20
      emb|AF188920|AF188920 Trichoderma atroviride strain DAOM 165779 ... 68 9e-20
      emb|AF188929|AF188929 Trichoderma asperellum strain CBS 433.97, ... 68 9e-20
      emb|AF188933|AF188933 Trichoderma asperellum strain BBA 68646R 4... 68 9e-20
20
      gb|$78423|$78423 chit42=endochitinase [Trichoderma harzianum, mR... 67 9e-20
      gb[U88560]THU88560-Trichoderma hamatum endochitinase-gene, compl... 68 1e-19
      emb|AF188931|AF188931 Hypocrea vinosa 42 kDa endochitinase gene,... 68 1e-19
      emb|AF188927|AF188927 Trichoderma viride strain GJS 90-20 42 kDa... 68 2e-19
      gb[U33265]CIU33265 Coccidioides immitis complement fixation/chit... 60 2e-19
25
      gb[U60807]CIU60807 Coccidioides immitis complement fixation-chit... 60 3e-19
      emb|AF188924|AF188924 Trichoderma viride strain ATCC 32630, syno... 68 4e-19
      emb|AF188928|AF188928 Trichoderma viride strain BBA 66069R 42 kD... 68 4e-19
      emb|AF188925|AF188925 Trichoderma viride strain Tr6 42 kDa endoc... 68 4e-19
      emb|AF188919|AF188919 Trichoderma viride strain ATCC 18652, syno... 66 2e-18
30
      emb|AF188922|AF188922 Hypocrea rufa strain GJS 89-127 42 kDa end... 66 3e-18
      emb|AF050098|AF050098 Trichoderma virens chitinase gene, complet... 65 2e-17
      emb|X64104|AACHI1A A.album chi1 gene for chitinase.
      emb|AJ243014|MFL243014 Metarhizium flavoviride mRNA for chitinas... 62 8e-17
      emb|AF027498|AF027498 Metarhizium anisopliae chitinase CHIT42 (C...
35
      emb|AF027497|AF027497 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
      emb|AI967677|AI967677 Ljirnpest08-687-g4 Ljirnp Lambda HybriZap ... 72 5e-14
      emb|AV421624|AV421624 AV421624 Lotus japonicus young plants (two... 63 2e-13
      emb|AI899627|AI899627 EST269070 tomato susceptible, Cornell Lyco... 75 1e-12
      dbj|D87894|D87894 Rhizopus oligosporus DNA for chitinase, comple... 59 2e-10
40
      emb|AV407063|AV407063 AV407063 Lotus japonicus young plants (two... 68 2e-10
      emb|AF009354|AF009354 Leishmania donovani chitinase (Chi-1) gene... 57 4e-09
      emb|AA786967|AA786967 m7dl lal.rl Aspergillus nidulans 24hr asexu... 54 5e-09
      emb|AA966331|AA966331 w4a12a1.rl Aspergillus nidulans 24hr asexu... 54 5e-09
      emb|AI212420|AI212420 x5f11a1.rl Aspergillus nidulans 24hr asexu... 43 6e-08
45
      emb|AI210660|AI210660 k0b03a1.rl Aspergillus nidulans 24hr asexu... 53 1e-07
      emb|AA785435|AA785435 g7d04a1.rl Aspergillus nidulans 24hr asexu... 54 2e-07
      emb|AA787768|AA787768 rld06al.rl Aspergillus nidulans 24hr asexu... 46 2e-06
      emb|AA784794|AA784794 g2d07a1.rl Aspergillus nidulans 24hr asexu... 43 2e-06
      gb|L41663|COICTS1CHI Coccidioides immitis chitinase (cts1) gene,... 44 5e-06
50
      gb U51271 CIU51271 Coccidioides immitis complement-fixation anti... 44 5e-06
      gb|U60806|CIU60806 Coccidioides immitis complement-fixation chit... 44 5e-06
      emb|AI213337|AI213337 zlb11a1.rl Aspergillus nidulans 24hr asexu... 50 7e-06
      emb|AI211269|AI211269 o0h07a1.rl Aspergillus nidulans 24hr asexu... 43 1e-05
      emb|AW334147|AW334147 S31A10 AGS-1 Pneumocystis carinii f. sp. c... 51 1e-05
      emb|Z71415|THENDOCHS T.hamatum endochitinase gene.
                                                                       50 3e-05
      emb|AA786295|AA786295 13d02a1.rl Aspergillus nidulans 24hr asexu... 31 6e-05
      emb|AI209456|AI209456 a0h06a1.rl Aspergillus nidulans 24hr asexu... 43 6e-05
      gb|M11815|YSKGKL1A Plasmid pGKL1 from killer yeast (K.lactis), c... 39 1e-04
      emb|X01095|KLKILL1L Yeast DNA killer plasmid pGKL1.
                                                                       39 1e-04
      emb[X00762]KLKILL05 Kluyveromyces lactis (killer strain) plasmid...
                                                                       39 1e-04
      emb|X07127|KLK1P Kluyveromyces lactis killer plasmid kl DNA.
                                                                        39 1e-04
```

	· · · · · · · · · · · · · · · · · · ·
•	emb[X89212]MADNACHIA M.anisopliae DNA for ChiA gene. 48 1e-04
	emb A86212 A86212 Sequence 871 from Patent EP0866129. 48 2e-04
	emb AA787160 AA787160 m8b03al.rl Aspergillus nidulans 24hr asexu 46 8e-04
_	gb[U28373]YSCD9481 Saccharomyces cerevisiae chromosome IV cosmid 45 0.001
5	emb AA966303 AA966303 v7h11a1.rl Aspergillus nidulans 24hr asexu 43 0.005
	emb AA788389 AA788389 r7f09a1.rl Aspergillus nidulans 24hr asexu 30 0.039
	emb AI210224 AI210224 h0g10a1.rl Aspergillus nidulans 24hr asexu 32 0.13
	dbj D87063 D87063 Aspergillus nidulans chiB gene for chitinase, 31 0.15
	emb AA787747 AA787747 r1b07a1.rl Aspergillus nidulans 24hr asexu 31 0.17
10	emb AA783278 AA783278 c3h07a1.rl Aspergillus nidulans 24hr asexu 31 0.17
	emb AA785323 AA785323 g6e04a1.rl Aspergillus nidulans 24hr asexu 31 0.17
	emb AW335048 AW335048 S42E2 AGS-1 Pneumocystis carinii f. sp. ca 37 0.23
	emb AW333489 AW333489 S22D2 AGS-1 Pneumocystis carinii f. sp. ca 36 0.44
1.5	emb AI210899 AI210899 m0b11a1.rl Aspergillus nidulans 24hr asexu 29 0.57
15	emb AW310633 AW310633 sg22d12.x1 Gm-c1024 Glycine max cDNA clone 36 0.60
•	emb AA785309 AA785309 g6d06a1.rl Aspergillus nidulans 24hr asexu 31 0.77
	gb L19093 PEARHOGTPP Pisum sativum rho (ras-related) GTP-binding 35 1.6
	gb BE053716 BE053716 GA_Ea0002M02f Gossypium arboreum 7-10 dpa 34 2.1
	emb AQ162416 AQ162416 mgxb0012N01r CUGI Rice Blast BAC Library P 34 2.1
20	emb AW108998 AW108998 gate0002M02f Gossypium arboreum 7-10 dpa f 34 2.1
	emb AI727383 AI727383-BNLGHi7901 Six-day Cotton fiber Gossypium 34 2.1
	emb AL353817 NC1A9 Neurospora crassa DNA linkage group V Cosmid 34 2.9
	emb AI730373 AI730373 BNLGHi6756 Six-day Cotton fiber Gossypium 34 2.9
25	emb AJ273533 AJ273533 AJ273533 Metarhizium anisopliae ARSEF 2575 33 4.0
25	gb BE054457 BE054457 GAEa0034I24f Gossypium arboreum 7-10 dpa 33 4.0
	emb AJ274366 AJ274366 AJ274366 Metarhizium anisopliae ARSEF 2575 33 4.0
	emb AJ274146 AJ274146 AJ274146 Metarhizium anisopliae ARSEF 2575 33 4.0
	emb AF006311 AF006311 Cookeina tricholoma 18S ribosomal RNA gene 32 4.2
30	emb AW625979 AW625979 EST319874 tomato radicle, 5 d post-imbibit 33 5.5
30	emb AB027528 AB027528 Physcomitrella patens ppCRY1 mRNA for blue 33 5.5
	Oners 707336 167 s at 20420 s at /id source conbank /description
	Query= Z97336.167_s_at 20429_s_at /id_source genbank /description
	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana]
35	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
35	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana]
35	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
35	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (2034 letters)
	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0/ec_number /family /chip nova/gb_link /ncgi (2034 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters
35 40	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (2034 letters) Database: plantfungal
	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	emb cab10219.1 (z97336) hypothetical protei [arabidopsis thaliana] /blast score 0 /ec_number /family /chip nova /gb_link /ncgi
40 45 50	emb cab10219.1 (297336) hypothetical protei [arabidopsis thaliana] /blast score 0 /ec_number /family /chip nova /gb_link /ncgi

	emb AI054990 AI054990 coau0002L09 Cotton Boll Abscission Zone cD 40 0.037
	emb AW929405 AW929405 EST338193 tomato flower buds 8 mm to pre-a 39 0.17
	emb AW649475 AW649475 EST327929 tomato newer odds 8 min to pre-a 39 0.17
٠,	emb AW222512 AW222512 EST299323 tomato fruit red ripe, TAMU Lyco 38 0.23
5	emb AW222518 AW222518 EST299329 tomato fruit red ripe, TAMU Lyco 38 0.23
	emb AI781303 AI781303 EST262182 tomato susceptible, Cornell Lyco 38 0.23
٠.	emb A1779448 A1779448 EST260327 tomato susceptible, Cornell Lyco 38 0.23
	emb AW053754 AW053754 L30-1647T3 Ice plant Lambda Uni-Zap XR exp 38 0.23
	emb AF141013 AF141013 Vigna unguiculata clone KINE12 disease res 32 0.32
10	emb AW164678 AW164678 se76b06.yl Gm-c1023 Glycine max cDNA clone 38 0.32
	emb AW736367 AW736367 EST332286 KV3 Medicago truncatula cDNA clo 37 0.42
	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb). 34 0.77
	emb AV420300 AV420300 AV420300 Lotus japonicus young plants (two 36 0.82
	emb AW424334 AW424334 sh64b12.yl Gm-c1015 Glycine max cDNA clone 36 0.82
15	
13	
	gb U34385 SCU34385 Saccharomyces cerevisiae ankyrin repeat prote 34 0.98
	emb AQ522032 AQ522032 CpG0990A CpIOWAgDNA1 Cryptosporidium parvu 36 1.
	emb AQ083671 AQ083671 CpG0567A CpIOWAgDNA1 Cryptosporidium parvu 36 1.
	emb AF141012 AF141012 Vigna unguiculata clone KIND12 disease res 30 1.4
20	emb AW283124 AW283124 LG1_224_H10.gl_A002 Light Grown 1 (LG1) So 35 1.6
	emb AI054715 AI054715 coau0001M19 Cotton Boll Abscission Zone cD 35 1.6
	emb[Y10579]VFPOTCHAN V.faba mRNA for potassium channel. 29 1.7
	emb AQ935638 AQ935638 CpG2573A CpIOWAgDNA1 Cryptosporidium parvu 35 2.
	emb AW040703 AW040703 EST283567 tomato mixed elicitor, BTI Lycop 35 2.1
25	emb X73850 BNPNL3 B.napus (pNL3) mRNA for acyl-ACP-thioesterase. 35 2.9
25	emb AL096797 SPBC146 S.pombe chromosome II cosmid c146. 35 2.9
	emb[X87842]BNDNAFATA B.napus FatA gene. 35 2.9
	emb AF073683 073693S155 Tinguarra sicula internal transcribed sp 35 2.9
20	dbj D30788 YSPCUT3B Schizosaccharomyces pombe gene for cut3 prot 35 2.9
30	gb BE035556 BE035556 MO09B06 MO Mesembryanthemum crystallinum cD 35 2.9
	gb[M21813]YSCELF2B S.cerevisiae SUI3 gene encoding translation i 35 2.9
	gb BE036920 BE036920 MP09B06 MP Mesembryanthemum crystallinum cD 35 2.9
	gb BE035567 BE035567 MO09C08 MO Mesembryanthemum crystallinum cD 27 3.2
	emb AW923857 AW923857 DG1_60_G12.g1_A002 Dark Grown 1 (DG1) Sorg 30 3.4
35	emb AA680502 AA680502 T3691 Bloodstream form of serodeme ILTat1 34 4.0
	emb AW691484 AW691484 NF041F05ST1F1000 Developing stem Medicago 34 4.0
	emb AI055156 AI055156 coau0003D05 Cotton Boll Abscission Zone cD 34 4.0
: .	emb AL356815 NCB24H17 Neurospora crassa DNA linkage group II BAC 30 4.2
	emb AF181702 AF181702 Leptosphaeria contecta 18S ribosomal RNA g 34 5.5
40	emb AW145916 AW145916 ga35g12.yl Moss EST library PPN Physcomitr 34 5.5
	emb AW617253 AW617253 EST323664 L. hirsutum trichome, Cornell Un 34 5.5
	emb AW615864 AW615864 EST325362 tomato flower buds 0-3 mm, Corne 34 5.5
	emb AW691785 AW691785 NF044B05ST1F1000 Developing stem Medicago 34 5.5
	dbj D38256 YSCSCT1 Yeast gene for suppressor of ctr mutation. 34 5.5
45	gb[U26175]LDU26175 Leishmania donovani lipophosphoglycan biosynt 34 5.5
10	emb AB029613 AB029613 Aspergillus terreus TOP2 gene for type II 34 5.5
	emb AW696259 AW696259 NF104F08ST1F1074 Developing stem Medicago 34 5.5
	emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S 33 7.6
5 0	emb AV421315 AV421315 AV421315 Lotus japonicus young plants (two 33 7.6
50	emb AW599293 AW599293 gb13a06.yl Moss EST library PPN Physcomitr 33 7.6
	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone 33 7.6
	gb U16862 PFU16862 Plasmodium falciparum HSP70-like protein gene 33 7.6
	emb AI213448 AI213448 z2allal.fl Aspergillus nidulans 24hr asexu 33 7.6
	emb X73849 BNPNL2 B.napus (pNL2) mRNA for acyl-ACP-thioesterase. 33 7.6
55	emb AW694856 AW694856 NF080G09ST1F1071 Developing stem Medicago 33 7.6
	emb AV408901 AV408901 AV408901 Lotus japonicus young plants (two 33 7.6
	emb AV412721 AV412721 AV412721 Lotus japonicus young plants (two 33 7.6
	emb AI759851 AI759851 sb65b08.y1 Gm-c1017 Glycine max cDNA clone 33 7.6
	emb AZ124240 AZ124240 T223104b Medicago truncatula BAC library M 33 7.6
60	emb[Y08926]PFAARP1PR P.falciparum mRNA for AARP1 protein, partial. 33 7.6
JJ	emb AV410224 AV410224 AV410224 Lotus japonicus voing plants (two 33 7.6
	OMORY TROCKTER VYROLLY BY VYROLLY LANGS ROOMICUS VOIME DRAMS RWO ?? / D

emb|AO849926|AO849926 LMAJFV1 lm51f05.x1 Leishmania major FV1 ra... 33 7.6 emblAL034557PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 27 8.3 emblAO944606|AO944606 Sheared DNA-48P15.TR Sheared DNA Trypanoso... 28 8.4 emb|AF099095|AF099095 Samanea saman pulvinus inward-rectifying c... 26 9.8 Query= AC005896.161_g_at 20620_g_at /id_source genbank /description gb|aac98070.1| (ac005896) putative c2h2-type zinc finger protein [arabidopsis thaliana] /blast score 8.00e-92 /ec number /family /chip nova /gb link /ncgi 10 (864 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 15 Score E Sequences producing significant alignments: (bits) Value 20 emb|AB006600|AB006600 Petunia x hybrida mRNA for ZPT2-13, comple... 86 1e-30 emb|AB000451|AB000451 Petunia hybrida mRNA for PEThy; ZPT2-5, com... 74 5e-29 emb|AW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 76 9e-29 emb|AB006599|AB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 77 1e-28 emb|AB006601|AB006601 Petunia x hybrida mRNA for ZPT2-14, comple... 72 2e-26 25 emb|AI898309|AI898309 EST267752 tomato ovary, TAMU Lycopersicon ... 68 3e-26 emb|AI485362|AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon... emb|AW030869|AW030869 EST274159 tomato callus, TAMU Lycopersicon... 68 5e-24 emb|AI966235|AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone... 72 3e-23 30 emb|AB006603|AB006603 Petunia x hybrida mRNA for ZPT2-8, complet... 65 1e-22 emb|AI486627|AI486627 EST244948 tomato ovary, TAMU Lycopersicon ... 61 1e-22 emb|AI485555|AI485555 EST243876 tomato ovary, TAMU Lycopersicon ... emb|AI488341|AI488341 EST246663 tomato ovary, TAMU Lycopersicon ... emb|AI486228|AI486228 EST244549 tomato ovary, TAMU Lycopersicon ... 35 emb|AI959966|AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone... emb|AI771123|AI771123 EST252223 tomato ovary, TAMU Lycopersicon ... emb|AI897376|AI897376 EST266819 tomato ovary, TAMU Lycopersicon ... 68 5e-22 emb|AI894711|AI894711 EST264154 tomato callus, TAMU Lycopersicon... 68 6e-22 emb|AV422177|AV422177 AV422177 Lotus japonicus young plants (two... 103 2e-21 emb|AB006602|AB006602 Petunia x hybrida mRNA for ZPT2-7, complet... 66 6e-21 emb|AI485123|AI485123 EST243427 tomato ovary, TAMU Lycopersicon ... 68 6e-21 emb|AW216442|AW216442 EST295072 tomato callus, TAMU Lycopersicon... 68 8e-21 emb|AW687462|AW687462 NF009H03RT1F1031 Developing root Medicago ... 70 2e-20 emb|AI771824|AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... 68 2e-20 45 emblAW034640lAW034640 EST278324 tomato callus, TAMU Lycopersicon... 68 7e-20 emb|AW033868|AW033868 EST277439 tomato callus, TAMU Lycopersicon... 72 1e-19 emb|AI487993|AI487993 EST246315 tomato ovary, TAMU Lycopersicon ... 68 le-18 emb|AW684455|AW684455 NF017B06NR1F1000 Nodulated root Medicago t... 68 2e-18 emb|X60700|PHEPF1 P.hybrida EPF1 gene for DNA-binding protein. 50 emb|AB006604|AB006604 Petunia x hybrida mRNA for ZPT2-9, complet... 59 5e-18 emb|AI489727|AI489727 EST248066 tomato ovary, TAMU Lycopersicon ... 50 1e-16 emb|AW034622|AW034622 EST278306 tomato callus, TAMU Lycopersicon... 87 2e-16 emb|AB035132|AB035132 Petunia x hybrida gene for C2H2 zinc-finge... 57 1e-15 emb|AB006597|AB006597 Petunia x hybrida mRNA for ZPT2-10, comple... 57 1e-15 55 emb|AB035133|AB035133 Petunia x hybrida gene for C2H2 zinc-finge... 56 2e-15 emb|AB006605|AB006605 Petunia x hybrida mRNA for ZPT3-3, complet... 56 2e-15 emb|AW777036|AW777036 M111167e DSIR Medicago truncatula cDNA clo... 74 2e-15 emb|AI488445|AI488445 EST246784 tomato ovary, TAMU Lycopersicon ... 50 4e-15 emb|AF119050|AF119050 Datisca glomerata zinc-finger protein 1 (z... 53 7e-15 60 emb|AB000455|AB000455 Petunia hybrida mRNA for PEThy;ZPT4-1, com... 55 9e-15 emb|AI988657|AI988657 sd06b03.yl Gm-c1020 Glycine max cDNA clone... 51 le-14

	emb AW781249 AW781249 sk67b08.yl Gm-c1016 Glycine max cDNA clone 51 1e-14
	gb LA6574 LA6574 BNAF1975 Mustard flower buds Brassica rapa cDNA 59 1e-14
	emb Y16131 Y16131 Y16131 young root nodules Medicago sativa subs 51 2e-14
	dbj D26085 PETZFDB3 Petunia zinc-finger DNA binding protein gene. 50 2e-14
5	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds. 53 2e-14
_	emb AB000453 AB000453 Petunia hybrida mRNA for PEThy;ZPT3-1, com 55 2e-14
	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds. 53 2e-14
•	dbj D26084 PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro 52 3e-14
	emb Y18788 MSY18788 Medicago sativa mRNA for putative TFIIIA (or 51 3e-14
10	emb AW560934 AW560934 EST315982 DSIR Medicago truncatula cDNA cl 51 3e-14
10	emb A1988290 A1988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone 52 3e-14
	emb AW706944 AW706944 sk08e10.yl Gm-c1023 Glycine max cDNA clone 50 5e-14
	dbj D26083 PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin 52 6e-14
	emb AF053077 AF053077 Nicotiana tabacum osmotic stress-induced z 51 6e-14
15	emb AW729218 AW729218 GA
15	emb AW102472 AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone 52 1e-13
	emb AW680050 AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S 50 2e-13
•	
	gb BE095284 BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two 53 2e-13
20	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon 49 2e-13
20	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA 52 2e-13
	_gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR 52 2e-13
	emb AW775559 AW775559 EST334624 DSIL Medicago truncatula cDNA cl 50 2e-13
	gb BE123920 BE123920 EST394045 DSIL Medicago truncatula cDNA clo 50 2e-13
25	gb U68763 GMU68763 Glycine max putative transcription factor SCO 48 3e-13
25	gb BE059872 BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone 48 3e-13
	emb AW153229 AW153229 se37f05.yl Gm-c1015 Glycine max cDNA clone 48 3e-13
	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon 48 4e-13
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon 48 4e-13
20	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon 48 4e-13
30	emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon 48 4e-13
	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon 48 4e-13
	emb AW279005 AW279005 sg04d04.yl Gm-c1019 Glycine max cDNA clone 48 6e-13
	emb AW164639 AW164639 se74f02.yl Gm-c1023 Glycine max cDNA clone 48 6e-13
25	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon 48 1e-12
35	emb AW278572 AW278572 sf46c03.yl Gm-c1009 Glycine max cDNA clone 48 1e-12
	dbj D26086 PETZFP4 Petunia zinc-finger protein gene. 49 3e-12
	emb AW616587 AW616587 EST322998 L. hirsutum trichome, Cornell Un 47 9e-12
-	emb AW924420 AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) 50 9e-12
40	emb AI778714 AI778714 EST259593 tomato susceptible, Cornell Lyco 46 1e-11
40	emb AI487287 AI487287 EST245609 tomato ovary, TAMU Lycopersicon 46 1e-11
	emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop 46 1e-11
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon 46 2e-11
	emb AB006606 AB006606 Petunia x hybrida mRNA for ZPT4-4, complet 53 2e-11
45	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon 48 2e-11
45	emb X87374 PSZINCFIN P.sativum putative zinc finger protein. 64 3e-11
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit 46 6e-11
	emb AI894812 AI894812 EST264255 tomato callus, TAMU Lycopersicon 68 7e-11
	emb AI966679 AI966679 sc55al1.yl Gm-c1015 Glycine max cDNA clone 52 1e-10
50	emb AW219517 AW219517 EST301915 tomato root during/after fruit s 46 2e-10
50	gb BE058334 BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone 48 3e-10
	emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon 46 3e-10
	emb AI771385 AI771385 EST252485 tomato ovary, TAMU Lycopersicon 66 3e-10
	emb AV426673 AV426673 AV426673 Lotus japonicus young plants (two 47 5e-10
c	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon 45 5e-10
55	emb AB006598 AB006598 Petunia x hybrida mRNA for ZPT2-11, comple 64 7e-10
	emb AW219736 AW219736 EST302218 tomato root during/after fruit s 46 7e-10
	emb AW924443 AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) 48 9e-10
	emb AB000452 AB000452 Petunia hybrida mRNA for PEThy;ZPT2-6, com 64 1e-09

Query= AL049658.102_at 20625_at /id_source genbank /description emb|cab41131.1| (al049658) hypothetical protein [arabidopsis thaliana]

5

/blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|al049658| /ncgi http://www.ncgr.org/cgi-bin/ff?al049658 (1890 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

10 Searching......done

Score (bits) Value Sequences producing significant alignments: 15 emb|AW559251|AW559251 EST306087 DSIR Medicago truncatula cDNA cl... 169 3e-49 emb[AW032676]AW032676 EST276235 tomato callus, TAMU Lycopersicon... 181 le-44 emb|AI778594|AI778594 EST259473 tomato susceptible, Cornell Lyco... 181 1e-44 emb|AW774727|AW774727 EST333878 KV3 Medicago truncatula cDNA clo... 169 6e-41 emb|AV423915|AV423915 AV423915 Lotus japonicus young plants (two... 163 3e-39' 20 emb|AW559836|AW559836 EST314884 DSIR Medicago truncatula cDNA cl... 131 6e-37 emb|AW349142|AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3... 107 3eemb|AW560074|AW560074 EST315122 DSIR Medicago truncatula cDNA cl... 84 6e-23 emb|AI855891|AI855891 sc30h08.y1 Gm-c1014 Glycine max cDNA clone... 100 4e-21 25 emblAW560073|AW560073 EST315121 DSIR Medicago truncatula cDNA cl... 77 5e-21 emb[AW225676]AW225676 ST70B12 Pine TriplEx shoot tip library Pin... 91 3e-17 emb|AW870069|AW870069 NXNV 123 G03 F Nsf Xylem Normal wood Verti... 68 3e-17 emb|AW587665|AW587665 ST63B10 Pine TriplEx shoot tip library Pin... 87 4e-17 emb|AW011208|AW011208 ST18A05 Pine TriplEx shoot tip library Pin... 89 1e-16 emb|AW438038|AW438038 ST83G07 Pine TriplEx shoot tip library Pin... 84 5e-15 30 emb|AV417662|AV417662 AV417662 Lotus japonicus young plants (two... 54 7e-15 emb[AI920196]AI920196 1726 Pine Lambda Zap Xylem library Pinus t... 54 2e-14 emb|AW981483|AW981483 EST392636 DSIL Medicago truncatula cDNA cl... 70 5e-13 emblAW689240|AW689240 NF017A06ST1F1000 Developing stem Medicago ... 76 8e-13 35 emb|AW684289|AW684289 NF015A11NR1F1000 Nodulated root Medicago t... 70 1e-12 emblAW933515lAW933515 EST359274 tomato fruit mature green, TAMU ... 48 3e-12 emb|AW685948|AW685948 NF036G07NR1F1000 Nodulated root Medicago t... 58 8e-12 emb|AW687095|AW687095 NF005H11RT1F1095 Developing root Medicago ... 72 1e-11 emb|AW686129|AW686129 NF033H12NR1F1000 Nodulated root Medicago t... 47 1e-11 40 emb|AI894750|AI894750 EST264193 tomato callus, TAMU Lycopersicon... 59 3e-11 emb|AW698315|AW698315 NXNV 071 G01 F Nsf Xylem Normal wood Verti... 71 3e-11 emb|AW290408|AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical... 67 4c-11 emblAW065112IAW065112 ST39G09 Pine TriplEx shoot tip library Pin... 51 5e-11 emblAW560897[AW560897 EST315945 DSIR Medicago truncatula cDNA cl... 55 7e-11 45 emb|AW257406|AW257406 EST305543 KV2 Medicago truncatula cDNA clo... 55 7e-11 emb|AW217058|AW217058 EST295772 tomato callus, TAMU Lycopersicon... 51 5e-10 emb|AV407304|AV407304 AV407304 Lotus japonicus young plants (two... 65 2e-09 gb|BE049795|BE049795 NXNV 144 C08 F Nsf Xylem Normal wood Vertic... 53 7e-09 emb|AW746848|AW746848 WS1 55 B02.g1 A002 Water-stressed 1 (WS1).... 57 5e-07 emb|AW888098|AW888098 NXNV 108 F09 F Nsf Xylem Normal wood Verti... 56 1e-06 50 emb|AW032082|AW032082 EST275536 tomato callus, TAMU Lycopersicon... 51 2e-06 emb|AW032864|AW032864 EST276423 tomato callus, TAMU Lycopersicon... 46 2e-06 emb|AW736866|AW736866 NXNV 083 H05_F Nsf Xylem Normal wood Verti... 52 2e-05 emb|AW775153|AW775153 EST334304 KV3 Medicago truncatula cDNA clo... 51 4e-05 55 emb|AV411498|AV411498 AV411498 Lotus japonicus young plants (two... 47 5e-04 emb|AW934555|AW934555 EST353447 tomato flower buds 0-3 mm, Corne... 36 9e-04 emb|AW010126|AW010126 ST02C06 Pine TriplEx shoot tip library Pin... 46 0.001 emb|AW031593|AW031593 EST275047 tomato callus, TAMU Lycopersicon... 31 0.001 emb|AW746715|AW746715 WS1 55 B02.b1 A002 Water-stressed 1 (WS1) ... 39 0.001 emb|AW720513|AW720513 LjNEST18e1r Lotus japonicus nodule library... 46 0.001 60 emb|AW773847|AW773847 EST332833 KV3 Medicago truncatula cDNA clo... 35 0.004

	emb AZ051219 AZ051219 Gm_UMb001_062_F16R UMN Soybean BAC Library 38 0.006
	emb AW684275 AW684275 NF014H05NR1F1000 Nodulated root Medicago t 43 0.007
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin 43 0.007
	emb AW687647 AW687647 NF011F10RT1F1090 Developing root Medicago 35 0.019
5	emb AW560122 AW560122 EST315170 DSIR Medicago truncatula cDNA cl 35 0.019
	emb AW687408 AW687408 NF009C08RT1F1065 Developing root Medicago 35 0.019
	emb AW560121 AW560121 EST315169 DSIR Medicago truncatula cDNA cl 35 0.019
10	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic 41 0.032
10	emb AI781175 AI781175 EST262054 tomato susceptible, Cornell Lyco 40 0.060
	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un 31 0.063
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso 40 0.083
	emb AW693887 AW693887 NF070B08ST1F1064 Developing stem Medicago 40 0.083
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso 38 0.22
15	emb AI487450 AI487450 EST245772 tomato ovary, TAMU Lycopersicon 37 0.41
•	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco 37 0.41
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon 37 0.41
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U 28 0.52
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso 35 0.53
20	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti 33_0.53
	emb AW690496 AW690496 NF035B12ST1F1000 Developing stem Medicago 37 0.56
	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago 37 0.56
	emb AW686233 AW686233 NF035E09NR1F1000 Nodulated root Medicago t 37 0.56
_	emb AW257090 AW257090 EST305227 KV2 Medicago truncatula cDNA clo 37 0.56
25	
23	
•	
	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c 36 0.77
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic 27 0.96
30	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo 36 1.1
30	emb AW317531 AW317531 sg51e11.yl Gm-c1025 Glycine max cDNA clone 33 1.3
	emb AC009259 AC009259 Trypanosoma brucei chromosome VI clone RPC 35 1.4
	emb AW702888 AW702888 TgESTzz91a12.y1 TgRH*-Tachyzoite cDNA Toxo 35 1.4
	emb AF013339 AF013339 Cucurbita moschata clone 3 internal transc 35 1.4
25	emb AW704685 AW704685 sk39c02.yl Gm-c1028 Glycine max cDNA clone 35 1.4
35	emb AQ650196 AQ650196 Sheared DNA-18B3.TF Sheared DNA Trypanosom 35 1.4
	emb AW685575 AW685575 NF029B05NR1F1000 Nodulated root Medicago t 35 2.0
	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo 35 2.0
	emb Z38060 SC5610 S.cerevisiae chromosome IX sequence derived fr 35 2.0
	emb AW033298 AW033298 EST276869 tomato callus, TAMU Lycopersicon 35 2.0
40	gb L36822 SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas 35 2.0
	emb AQ952285 AQ952285 Sheared DNA-39M20.TF Sheared DNA Trypanoso 35 2.0
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus 30 2.3
	emb AI441832 AI441832 sa47h09.y1 Gm-c1004 Glycine max cDNA clone 35 2.7
	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago 31 3.1
45	emb AW685287 AW685287 NF027B11NR1F1000 Nodulated root Medicago t 31 3.1
	emb AW932856 AW932856 EST358699 tomato fruit mature green, TAMU 34 3.8
	emb AF013320 AF013320 Cucurbita fraterna clone 2 internal transc 34 3.8
	emb AW719424 AW719424 LjNEST4dl1r Lotus japonicus nodule library 29 4.2
	emb[X90770]LEMSREPRG L.esculentum microsatellite repeat DNA region. 34 5.2
50	emb AW133354 AW133354 se17h02.y1 Gm-c1013 Glycine max cDNA clone 34 5.2
	emb AI967637 AI967637 Ljirnpest08-639-b9 Ljirnp Lambda HybriZap 34 5.2
	emb AW156054 AW156054 ga24c05.yl Moss EST library PPU Physcomitr 34 5.2
	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like 34 5.2
	emb AB000394 AB000394 Ipomoea purpurea DNA, LTR retrotransposon 34 5.2
55	
	Query= X91919.1_at 20641_at /id source genbank /description
	"emb caa63012.1 (x91919) lea76 homologue type1 [arabidopsis thaliana]
	arabidopsis thaliana. ests gb n97082, gb z27056 and gb z29902 come
60	from this gene." /blast_score 9.00e-78 /ec_number /family /chip nova
UU	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb x91919 /ncgi

---WO 02/22675 --- PCT/US01/28506

http://www.ncgr.org/cgi-bin/ff?x91919 (762 letters)

Database: plantfungal 5 661,018 sequences; 426,114,510 total letters Searching......done Score E 10 Sequences producing significant alignments: (bits) Value emb|AJ224519|CAR224519 Cicer arietinum mRNA for LEA protein (clo... 148 6e-35 emb[X15348]BNLEA76 Brassica napus LEA76 mRNA for late embryogene... 135 4e-31 emb|AF117884|AF117884 Glycine max seed maturation protein PM30 (... 88 1e-30 15 emb|AJ224518|CAR224518 Cicer arietinum mRNA for LEA protein (clo... 126 2e-28 emb|AW472097|AW472097 si20a05.yl Gm-c1029 Glycine max cDNA clone... 86 9e-27 emb|AW395529|AW395529 sg72c09.yl Gm-c1007 Glycine max cDNA clone... 88 7e-24 emb|AW507599|AW507599 si53h08.yl Gm-r1030 Glycine max cDNA clone... 88 7e-24 emb|AW318205|AW318205 sg62d04.yl Gm-c1007 Glycine max cDNA clone... 88 7e-24 20 emb|AW568476|AW568476 si59c06.yl Gm-r1030 Glycine max cDNA clone... 88 7e-24 emb|AW567816|AW567816-si66b10.yl-Gm-r1030 Glycine max cDNA clone... 88 7e-24 emb|AW706800|AW706800 sk03e03.y1 Gm-c1023 Glycine max cDNA clone... 88 1e-23 emb|AW509384|AW509384 si22d10.yl Gm-c1029 Glycine max cDNA clone... 86 2e-23 emb|AW746690|AW746690 WS1_54_F07.g1_A002 Water-stressed 1 (WS1) ... 106 2e-22 25 emb|AW096396|AW096396 EST289576 tomato mixed elicitor, BTI Lycop... 103 1e-21 emb[X78205]HVHVA1 H.vulgare (Himalaya) HVA1 gene. 77 1e-20 emb|X13498|HVABAIP Barley pHVA1 mRNA for an ABA-inducible protein. 77 1e-20 gb|M36000|BLYABA Barley abscisic acid (ABA) mRNA, complete cds. emb|AW680076|AW680076 WS1_3_C03.g1_A002 Water-stressed 1 (WS1) S... 100 2e-20 30 emb|AW397921|AW397921 sg69h06.y1 Gm-c1007 Glycine max cDNA clone... 57 3e-20 emb[AW747095]AW747095 WS1 65 C09.gl A002 Water-stressed 1 (WS1) ... gb|BE034388|BE034388 MH04B06 MH Mesembryanthemum crystallinum cD... 73 1e-18 emb[X13201|GHLEA7 Cotton set 5A Lea gene for seed protein D-7. emb|X15086|GHLEA29R Cotton set 5A Lea mRNA for seed protein D-29. 35 emb[X56882]TA3LEA Wheat mRNA for a group 3 late embryogenesis ab... 75 1e-18 emb|AW746385|AW746385 WS1_49_G03.g1_A002 Water-stressed 1 (WS1) ... 93 2e-18 emb|AW680063|AW680063 WS1_3_B02.g1_A002 Water-stressed 1 (WS1) S... 91 1e-17 emb|AF255052|AF255052 Triticum aestivum cold-responsive LEA/RAB-... 85 6e-17 emb|AF139915|AF139915 Triticum aestivum ABA-inducible protein WR... 85 6e-17 40 emb|AW164114|AW164114 Ljirnpest20-575-b9 Ljirnp Lambda HybriZap ... 88 7e-17 emb[Y10779]SSY10779 S.stapfianus pSD.42 mRNA. 86 3e-16 emb|AW569002|AW569002 si62c03.y1 Gm-r1030 Glycine max cDNA clone... emblAW508284|AW508284 si52b01.yl Gm-r1030 Glycine max cDNA clone... 62 4e-16 gb|BE034389|BE034389 MH04B07 MH Mesembryanthemum crystallinum cD... 72 7e-16 emb|AW681055|AW681055 WS1 8 F06.b1 A002 Water-stressed 1 (WS1) S... 75 7e-13 emb|AW746839|AW746839 WS1 55 D06.gl A002 Water-stressed 1 (WS1) ... 75 7e-13 emb|AW678335|AW678335 WS1 14 F02.gl A002 Water-stressed 1 (WS1) ... 75 7e-13 emb|AW678291|AW678291 WS1 14 D10.g1 A002 Water-stressed 1 (WS1) ... 74 1e-12 emb|AW679525|AW679525 WS1 29 F04.g1 A002 Water-stressed 1 (WS1) ... 74 1e-12 50 emb|Z18891|BPBP8GEN Betula pendula BP8 gene. emb|AW432699|AW432699 sh85b12.y1 Gm-c1016 Glycine max cDNA clone... 74 1e-12 emb|AW678194|AW678194 WS1_13_E06.g1_A002 Water-stressed 1 (WS1) ... 72 5e-12 emb|AW459847|AW459847 sh96a04.yl Gm-c1016 Glycine max cDNA clone... 70 2e-11 emb|X13203|GHLEA29 Cotton set 5A Lea gene for seed protein D-29. 55 emb|Z49713|PMDORORF6 P.menziesii mRNA (open reading frame) (DF77B). 59 3e-08 emb|Z49712|PMDORORF5 P.menziesii mRNA (open reading frame) (DF77A). 59 3e-08 emb|AJ225460|AJ225460 AJ225460 Abscisic acid-treated protonemata... 59 5e-08

emb|X89041|RFLASPPRO R.fluitans mRNA for landform specific protein. 58 6e-08 gb|M80664|SOYLEAB Soybean late embryogenesis abundant (LEA) prot... 58 9e-08 emb|AF166485|AF166485 Glycine max maturation protein pPM32 (PM32... 57 2e-07 gb|M19388|COTSPG G.hirsutum (cotton) storage protein (late embry... 57 2e-07

-WO 02/22675 ----PCT/US01/28506

```
gb|U47096|DCU47096 Daucus carota LEA protein mRNA, somatic embry... 57 2e-07
      gb|U02966|GMU02966 Glycine max Shi-shi 51 kDa seed maturation pr... 56 3e-07
      emb|Z49715|PMDORORF8 P.menziesii mRNA (open reading frame) (DF77D). 56 4e-07
      gb|L47932|L47932 BNAF1873 Mustard flower buds Brassica rapa cDNA... 56 4e-07
      emb|Z49714|PMDORORF7 P.menziesii mRNA (open reading frame) (DF77C). 55 8e-07
      emb|AW746616|AW746616 WS1_54_F07.b1_A002 Water-stressed 1 (WS1) ...
      emb|AW678229|AW678229 WS1_14_F02.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
      emb|AW924822|AW924822 WS1_72_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
      emb|AW924712|AW924712 WS1_71_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
10
      emb|AW679366|AW679366 WS1_24_E04.b1_A002 Water-stressed 1 (WS1) ...
      emb|AW746766|AW746766 WS1_55_D06.b1_A002 Water-stressed 1 (WS1) ...
                                                                            52 4e-06
      emb|AW678206|AW678206 WS1 14 D10.b1 A002 Water-stressed 1 (WS1) ...
      emb|AW747038|AW747038 WS1 65 C09.b1 A002 Water-stressed 1 (WS1) ...
      emb|AW678115|AW678115 WS1 13 E06.b1 A002 Water-stressed 1 (WS1) ...
15
      emb|AW679354|AW679354 WS1_24_G08.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
      emb|AI305014|AI305014 EST00119 mRNP Lambda ZapII Express Library... 51 8e-06
      emb|AF009953|AF009953 Glycine max 35 kDa seed maturation protein... 51 8e-06
      emb|Z22872|GMLEAPROA G.max Lea protein mRNA, complete CDS.
                                                                           51 1e-05
      emb|X92955|BOPC15 B.oleracea mRNA for pollen coat protein.
                                                                    51 le-05
20
      emb|AW680922|AW680922 WS1 8 F06.gl A002 Water-stressed 1 (WS1) S... 51 le-05
      emb|AW678045|AW678045 WS1_13_A03.b1_A002 Water-stressed 1 (WS1) ... 50 2e-05
      gb[L33614|L33614 BNAESTF503 Mustard flower buds Brassica rapa cD... 50 2e-05
      emb|X79466|HVES2A H.vulgare (Dbg 567) ES2A mRNA.
                                                                     39 4e-05
      emb[AJ000100]HVAJ100 Hordeum vulgare mRNA for cold-regulated pro... 39 4e-05
25
      emb|AJ130888|FSY130888 Fagus sylvatica mRNA for ABA-inducible pr... 49 4e-05
      emb|AW703962|AW703962 sk14e10.y1 Gm-c1023 Glycine max cDNA clone... 49 5e-05
      emb|AW509514|AW509514 ga73a10.yl Moss EST library PPU Physcomitr... 49 5e-05
      emb|AW679440|AW679440 WS1 24 C05.gl A002 Water-stressed 1 (WS1) ... 48 1e-04
      gb]L46517|L46517 BNAF1718 Mustard flower buds Brassica rapa cDNA... 47 1e-04
30
      emb|AW185164|AW185164 se87g01.yl Gm-c1023 Glycine max cDNA clone... 38 2e-04
      emb|AW679430|AW679430 WS1 24 G08.gl A002 Water-stressed l (WS1) ... 46 5e-04
      emb[X16131]DCDC8 D. carota DC8 gene for an embryonic-specific 66... 41 8e-04
      emb|AW754854|AW754854 PC06D01 Pine TriplEx pollen cone library P... 45 9e-04
      emb|AW679001|AW679001 WS1_21_C11.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
35
      emb|AW679463|AW679463 WS1_24_E04.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
      emb|AW981579|AW981579 PC14C08 Pine TriplEx pollen cone library P... 43 0.002
      emb|AF255053|AF255053 Triticum aestivum cold-responsive LEA/RAB-... 39 0.004
      emb|AW680686|AW680686 WS1 6 H05.g1 A002 Water-stressed 1 (WS1) S... 42 0.004
      emb|AW747334|AW747334 WS1_67_C01.g1_A002 Water-stressed 1 (WS1) ... 42 0.004
40
      emb|AW747282|AW747282 WS1_67_C01.b1_A002 Water-stressed 1 (WS1) ... 42 0.004
      emb|AW983308|AW983308 HVSMEg0010C18f Hordeum vulgare pre-anthesi... 35 0.005
      emb|AW679087|AW679087 WS1 22 A07.b1 A002 Water-stressed 1 (WS1) ... 42 0.006
      emb|AW981621|AW981621 PC14G04 Pine TriplEx pollen cone library P... 42 0.006
      emb|AJ225515|AJ225515 AJ225515 Abscisic acid-treated protonemata... 37 0.017
45
      emb|AW754577|AW754577 PC03H06 Pine TriplEx pollen cone library P... 40 0.021
      emb|AW458460|AW458460 sh09e04.y1 Gm-c1016 Glycine max cDNA clone... 39 0.040
      emb|AW981729|AW981729 PC18A04 Pine TriplEx pollen cone library P... 39 0.055
      gb|BE033848|BE033848 MG01A05 MG Mesembryanthemum crystallinum cD... 38 0.076
      emb|AI068981|AI068981 mgae0004dH11f Magnaporthe grisea Appressor... 38 0.076
      emb|AW679089|AW679089 WS1 22 A07.gl A002 Water-stressed 1 (WS1) ... 38 0.10
      Query= Z99708.249 at 12007 at /id_source genbank /description
      emb|cab16829.1| (299708) putative protein [arabidopsis thaliana]
      /blast score 1.00e-168 /ec number /family /chip nova /gb link
55
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708| /ncgi
      http://www.ncgr.org/cgi-bin/ff?z99708
           (885 letters)
```

60 Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching....

Score 5 (bits) Value Sequences producing significant alignments: emb|AI486681|AI486681 EST245003 tomato ovary, TAMU Lycopersicon ... 414 e-115 emb|AI488706|AI488706 EST247045 tomato ovary, TAMU Lycopersicon ... 373 e-102 emblAW185116|AW185116 se87a08.yl Gm-c1023 Glycine max cDNA clone... 364 e-100 emb|AW776370|AW776370 EST335435 DSIL Medicago truncatula cDNA cl... 316 1e-85 emb|AW441466|AW441466 EST310862 tomato fruit red ripe, TAMU Lyco... 311 4e-84 emb|AW775237|AW775237 EST331959 GVN Medicago truncatula cDNA clo... 278 4e-74 emb|AW564397|AW564397 LG1 292 F08.b1 A002 Light Grown 1 (LG1) So... 275 2e-73 emb|AW648604|AW648604 EST327154 tomato germinating seedlings, TA... 275 3e-73 emb|AW309188|AW309188 sg05d07.yl Gm-c1019 Glycine max cDNA clone... 274 8e-73 15 emb|AW329561|AW329561 N200812e rootphos(-) Medicago truncatula c... 204 3e-69 emblAI897460|AI897460 EST266903 tomato ovary, TAMU Lycopersicon ... 158 7e-67 emb|AI775112|AI775112 EST256212 tomato resistant, Cornell Lycope... 248 4e-65 emb|AI898201|AI898201 EST267644 tomato ovary, TAMU Lycopersicon ... 118 1e-51 20 emb|AW011189|AW011189 ST17G07 Pine TriplEx shoot tip library Pin... 172 4e-48 emb|AW622515|AW622515 EST313315 tomato root during/after fruit s... 189 3e-47 emb|AW933718|AW933718 EST359561 tomato fruit mature green, TAMU ... 188 7e-47 emb[AI897919]AI897919 EST267362 tomato ovary, TAMU Lycopersicon ... 102 6e-45 emb|AW623431|AW623431 EST321376 tomato flower buds 3-8 mm, Corne... 179 2e-44 25 emb|AI967352|AI967352 Ljimpest01-065-f5 Ljimp Lambda HybriZap ... 167 5e-44 emb|AW496876|AW496876 ga49e04.yl Moss EST library PPU Physcomitr... 175 5e-43 emb|AW616498|AW616498 EST322909 L. hirsutum trichome, Cornell Un... 174 1e-42 emb|AW687128|AW687128 NF006C08RT1F1065 Developing root Medicago ... 156 1e-41 emb|AW191300|AW191300 T113619e KV2 Medicago truncatula cDNA clon... 167 1e-40 30 emb|AW257178|AW257178 EST305315 KV2 Medicago truncatula cDNA clo... 144 7e-34 emb|AW699388|AW699388 gb07g07.y1 Moss EST library PPN Physcomitr... 139 2e-32 emblAV421449lAV421449 AV421449 Lotus japonicus young plants (two... 132 4e-30 emblAW626193lAW626193 EST320100 tomato radicle, 5 d post-imbibit... 132 5e-30 emb|AL109608|SPCC23B6 S.pombe chromosome III cosmid c23B6. 35 emb|AV426790|AV426790 AV426790 Lotus japonicus young plants (two... 123 2e-27 emb|AI778049|AI778049 EST258928 tomato susceptible, Cornell Lyco... 116 2e-25 emb|AW626687|AW626687 NXNV068E07 Nsf Xylem Normal wood Vertical ... 114 1e-24 emb|AW929355|AW929355 EST338143 tomato flower buds 8 mm to pre-a... 106 2e-22 emb|AW719259|AW719259 LjNEST1h10r Lotus japonicus nodule library... 105 4e-22 40 emb|Z69381|SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom... 60 1e-17 emb|Z71507|SCYNL231C S.cerevisiae chromosome XIV reading frame O... emb|AB001995|AB001995 Schizosaccharomyces pombe gene for Tellp, ... 82 6e-17 emb|AI442227|AI442227 sa49c11.yl Gm-c1004 Glycine max cDNA clone... 85 8e-16 emb|AI725484|AI725484 BNLGHi12268 Six-day Cotton fiber Gossypium... 54 2e-15 45. emb|X92494|SCBN11 S.cerevisiae BN11, N0647, APL1, N0665, N0670, ... 46 5e-13 emb|Z71540|SCYNL264C S.cerevisiae chromosome XIV reading frame O... emb|AI731920|AI731920 BNLGHi11386 Six-day Cotton fiber Gossypium... 44 2e-12 emb|AI729569|AI729569 BNLGHi13678 Six-day Cotton fiber Gossypium... 44 6e-11 emb|A1728685|A1728685 BNLGHill318 Six-day Cotton fiber Gossypium... 50 emb|AI725979|AI725979 BNLGHi13788 Six-day Cotton fiber Gossypium... emb|AJ273110|AJ273110 AJ273110 Metarhizium anisopliae ARSEF 2575... 52 6e-09 emb|AQ655616|AQ655616 Sheared DNA-2J3.TR Sheared DNA Trypanosoma... 61 1e-08 emb|AQ501933|AQ501933 V11E10 mTn-3xHA/lacZ Insertion Library Sac... 60 2e-08 55 7e-08 emb|X97320|CGSEC14GN C.glabrata SEC14 gene. 55 emb|Z49259|SC9582X S.cerevisiae chromosome XIII cosmid 9582. 55 9e-08 emb|X15483|SCSEC14G Yeast SEC14 gene for cytosolic factor. 55 9e-08 gb|BE053932|BE053932 GA Ea0031D10f Gossypium arboreum 7-10 dpa ... 46 6e-07 emb|AQ023632|AQ023632 CpGR0082A Cryptosporidium parvum genomic r... 55 7e-07 emb|AQ449556|AQ449556 500001H03.x1 CpIOWAM13mp18gDNA1 Cryptospor... 55 7e-07 60 emb|Z28091|SCYKL091C S.cerevisiae chromosome XI reading frame OR... 50 8e-07 emb|A86344|A86344 Sequence 1003 from Patent EP0866129. 54 le-06

	emb AF024652 AF024652 Glycine max polyphosphoinositide binding p 54 1e-06
	emb[AL114465]CNS01BNT Botrytis cinerea strain T4 cDNA library un 51 2e-06
	gb C96579 C96579 C96579 Marchantia polymorpha immature sex organ 42 4e-06
_	emb AQ855615 AQ855615 CpG1709A CpIOWAgDNA1 Cryptosporidium parvu 52 5e-06
5	gb L20972 YSJSEC14A Yarrowia lipolytica phosphatidylinositol-pho 51 9e-06
	emb X81937 CASEC14 C.albicans SEC14 gene. 49 3e-05
	gb U61975 CAU61975 Candida albicans phosphatidylinositol/phospha 49 3e-05
	gb BE123583 BE123583 NXNV_145_C08_F Nsf Xylem Normal wood Vertic 49 4e-05
10	emb AW739337 AW739337 gb40f01.yl Moss EST library PPN Physcomitr 49 4e-05 emb AW738979 AW738979 gb23b03.yl Moss EST library PPN Physcomitr 49 6e-05
10	emb AW702333 AW702333 TgESTzz74g03.y1 TgRH*-Tachyzoite cDNA Toxo 47 2e-04
	emb AI894440 AI894440 EST263895 tomato callus, TAMU Lycopersicon 46 3e-04
	emb AI727743 AI727743 BNLGHi8966 Six-day Cotton fiber Gossypium 45 8e-04
	emb AL114440 CNS01BN4 Botrytis cinerea strain T4 cDNA library un 45 0.001
15	emb AI729716 AI729716 BNLGHi14012 Six-day Cotton fiber Gossypium 45 0.001
	emb AW348860 AW348860 GM210010A10E4R Gm-r1021 Glycine max cDNA 3 44 0.001
	emb AI727901 AI727901 BNLGHi9413 Six-day Cotton fiber Gossypium 44 0.001
	emb Z69086 SPAC3H8 S.pombe chromosome I cosmid c3H8. 44 0.001
20	emb AI731713 AI731713 BNLGHi10565 Six-day Cotton fiber Gossypium 44 0.001
20	emb AI725627 AI725627 BNLGHi12489 Six-day Cotton fiber Gossypium 44 0.002 emb AW398657 AW398657 EST309157 L. pennellii trichome, Cornell U 43 0.003
	emb AW625133 AW625133 EST313950 tomato radicle, 5 d post-imbibit 43 0.003
	emb AI487421 AI487421 EST245743 tomato ovary, TAMU Lycopersicon 43 0.003
	emb AI486549 AI486549 EST244870 tomato ovary, TAMU Lycopersicon 43 0.003
25	emb AW508716 AW508716 si35e11.yl Gm-r1030 Glycine max cDNA clone 43 0.003
	gb BE020974 BE020974 sm54b08.yl Gm-c1028 Glycine max cDNA clone 43 0.003
	emb AI460982 AI460982 sa77d02.y1 Gm-c1004 Glycine max cDNA clone 43 0.004
	emb AA787291 AA787291 n1d01a1_r1 Aspergillus nidulans 24hr asexu 43 0.004
30	emb AW350019 AW350019 GM210006B20G9R Gm-r1021 Glycine max cDNA 3 43 0.004 emb AW689904 AW689904 NF025E09ST1F1000 Developing stem Medicago 42 0.005
50	emb AW254728 AW254728 ML1015 peppermint glandular trichome Menth 42 0.007
	emb AW267807 AW267807 EST305935 DSIR Medicago truncatula cDNA cl 41 0.010
	emb AW676817 AW676817 DG1 1 H07.b1 A002 Dark Grown 1 (DG1) Sorgh 41 0.010
	emb X87371 SCX731 S.cerevisiae DNA from chromosome X (cosmids 7, 41 0.010
35	emb Z49420 SCYJL145W S.cerevisiae chromosome X reading frame ORF 41 0.010
	emb AZ213346 AZ213346 Sheared DNA-77B10.TR Sheared DNA Trypanoso 41 0.014
	emb AW720085 AW720085 LjNEST13f5r Lotus japonicus nodule library 41 0.014
	emb AL078627 SPBC365 S.pombe chromosome II cosmid c365. 34 0.016 emb AV425459 AV425459 AV425459 Lotus japonicus young plants (two 40 0.019
40	emb AI495137 AI495137 sb03h08.y1 Gm-c1004 Glycine max cDNA clone 40 0.019
10	emb AW731571 AW731571 GA
	emb AI812357 AI812357 1D3 Pine Lambda Zap Xylem library Pinus ta 40 0.019
	emb AJ273448 AJ273448 AJ273448 Metarhizium anisopliae ARSEF 2575 40 0.019
	dbj D89132 D89132 Schizosaccharomyces pombe mRNA, partial cds, c 34 0.020
45	emb AW925728 AW925728 HVSMEg0005F19 Hordeum vulgare pre-anthesis 40 0.026
	One - A C004450 116 at 12001 at 1/4 assume and only /decembrism
	Query= AC004450.116_at 12091_at /id_source genbank /description gb aac64313.1 (ac004450) unknown protein [arabidopsis thaliana]
	/blast score 0 /ec_number /family /chip nova /gb_link
50	http://www3.ncbi.nlm.nih.gov/htbin-
- •	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac004450 /ncgi
	http://www.ncgr.org/cgi-bin/ff?ac004450
	(2633 letters)
55	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
	VVII VIIII 5
60	Score E
	Sequences producing significant alignments: (bits) Value

emb|AW310456|AW310456 sf36d02.x1 Gm-c1028 Glycine max cDNA clone... 243 5e-72 emb|AW623933|AW623933 EST321878 tomato flower buds 3-8 mm, Corne... 166 3e-69 emb[AW693705]AW693705 NF068B10ST1F1080 Developing stem Medicago ... 214 2e-65 emb|AW203623|AW203623 sf36d02.y1 Gm-c1028 Glycine max cDNA clone... 205 2e-60 emb|AW928464|AW928464 EST337252 tomato flower buds 8 mm to pre-a... 212 1e-53 emb|AW289771|AW289771 NXNV005G02F Nsf Xylem Normal wood Vertical... 189 4e-49 emb|AW720506|AW720506 LjNEST18d11r Lotus japonicus nodule librar... 142 3e-41 emb|AI166211|AI166211 a063p06u Hybrid aspen plasmid library Popu... 114 2e-37 10 emb|AI165948|AI165948 B004p66u Hybrid aspen plasmid library Popu... 62 2e-29 emb|AW508607|AW508607 si34b12.yl Gm-r1030 Glycine max cDNA clone... 78 3e-27 emblAW309153|AW309153 sf94h02.yl Gm-c1019 Glycine max cDNA clone... 91 9e-26 emb|AW830563|AW830563 sm28e08.yl Gm-c1028 Glycine max cDNA clone... 104 7e-23 emb|AI166124|AI166124 B008P77U Hybrid aspen plasmid library Popu... 105 2e-21 15 emb|AI487660|AI487660 EST245982 tomato ovary, TAMU Lycopersicon ... 103 6e-21 emb|AI489289|AI489289 EST247628 tomato ovary, TAMU Lycopersicon ... 103 6e-21 emb|AW185557|AW185557 se81d11.yl Gm-c1023 Glycine max cDNA clone... 85 3e-20 emb|AI898473|AI898473 EST267916 tomato ovary, TAMU Lycopersicon ... 100 4e-20 emb|AW695390|AW695390 NF094D01ST1F1012 Developing stem Medicago ... 77 9e-17 emb|AW277644|AW277644 sf84g03.yl Gm-c1019 Glycine max cDNA clone... 71 3e-12 20 emb|AW759290|AW759290 sl39d05.yl Gm-c1027 Glycine max cDNA clone... 67 6e-10 emb|AI759735|AI759735 sb63e04.y1 Gm-c1017 Glycine max cDNA clone... 66 2e-09 emb|AW100893|AW100893 sd62g04.y1 Gm-c1008 Glycine max cDNA clone... 62 1e-08 emb|AW694269|AW694269 NF074E05ST1F1038 Developing stem Medicago ... 58 2e-07 25 emb|AI988575|AI988575 sd04d10.yl Gm-c1020 Glycine max cDNA clone... 36 3e-07 emb|AQ638650|AQ638650 927P1-3G7.TP 927P1 Trypanosoma brucei geno... 52 2e-05 emb|AW561069|AW561069 EST316117 DSIR Medicago truncatula cDNA cl... 52 2e-05 emb|AW677337|AW677337 DG1_5_F09.g1_A002 Dark Grown 1 (DG1) Sorgh... 51 3e-05 emb|AW677330|AW677330 DG1 5 D09.g1 A002 Dark Grown 1 (DG1) Sorgh... 46 0.001 30 emb|Al736413|Al736413 sb28d01.yl Gm-c1009 Glycine max cDNA clone... 41 0.027 emb[X96932]NTASCOXRP N.tabacum gene encoding ascorbate oxidase-r... 40 0.086 emb|A46243|A46243 Sequence 6 from Patent WO9521929. 40 0.086 emb|AW931746|AW931746 EST357589 tomato fruit mature green, TAMU ... 39 0.16 emb|AW617831|AW617831 EST324230 L. hirsutum trichome, Cornell Un... 39 0.16 35 emb|AW672358|AW672358 LG1_359 D11.b1 A002 Light Grown 1 (LG1) So... 38 0.31 emb|AC004157|AC004157 Plasmodium falciparum chromosome 12 clone ... 38 0.42 emb|AW065005|AW065005 ST38E01 Pine TriplEx shoot tip library Pin... 37 0.58 emb|AQ254402|AQ254402 CpG0808B CpIOWAgDNA1 Cryptosporidium parvu... 36 1.1 emb|AF177330|AF177330 Saccharomyces cerevisiae iron transporter ... 36 1.1 emblAZ219717|AZ219717 Sheared DNA-88B11.TF Sheared DNA Trypanoso... 36 1.1 40 emb|AI729567|AI729567 BNLGHi13639 Six-day Cotton fiber Gossypium... 36 1.1 emb|Z21487|SCCHRIIFG S.cerevisiae RIM, MSI1, PGI, and ribosomal ... 36 1.1 emb|Z36076|SCYBR207W S.cerevisiae chromosome II reading frame OR... 36 1.1 emb|AW094274|AW094274 EST287454 tomato mixed elicitor, BTI Lycop... 35 2.1 45 emb|AF129037|AF129037 Magnolia hypoleuca chloroplast trnT-trnL i... 35 2.1 emb|AI211514|AI211514 p0g02a1.rl Aspergillus nidulans 24hr asexu... 35 2.8 emb|AW038170|AW038170 EST279827 tomato mixed elicitor, BTI Lycop... 35 2.8 emb|AE001274|AE001274 Leishmania major chromosome 1, complete se... 35 2.8 emb|Z69944|SPAC1F12 S.pombe chromosome I cosmid c1F12. 50 emb|AB028188|AB028188 Penicillium digitatum DNA fragment contain... 34 5.3 emb|AA898910|AA898910 NCP3E1T3 Perithecial Neurospora crassa cDN... emb|AI822825|AI822825 L30-661T3 Ice plant Lambda Uni-Zap XR expr... 34 7.3 emb|AL353821|NC68B2 Neurospora crassa DNA linkage group V Cosmid... 34 7.3 emb|AI724262|AI724262 RHIZ1 33 A04.y2 A001 Rhizome1 Sorghum hale... 34 7.3 55 emb|AW397716|AW397716 sg83e02.yl Gm-c1026 Glycine max cDNA clone... 34 7.3 Query= AL033545.26_at 12115_at /id_source genbank /description emb|caa22152.1| (al033545) extensin-like protein [arabidopsis thaliana] /blast score 1.00e-87 /ec number /family /chip nova 60 /gb_link http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|al033545| /ncgi

5

15

20

25

30

35

40

45

50

55

60

http://www.ncgr.org/cgi-bin/ff?al033545 (1140 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

Ε Score

10

Sequences producing significant alignments: (bits) Value emb|AI507807|AI507807 sb12h09.yl Gm-c1004 Glycine max cDNA clone... 52 7e-08 emb|AW443491|AW443491 EST308421 tomato mixed elicitor, BTI Lycop... 48 2e-07 emb|AW719418|AW719418 LjNEST4c12r Lotus japonicus nodule library... 50 2e-07 gb|BE020862|BE020862 sm53c05.y1 Gm-c1028 Glycine max cDNA clone ... 50 2e-07 emb|AI777049|AI777049 EST252016 tomato callus, TAMU Lycopersicon... 51 2e-07 emb|AW032807|AW032807 EST276366 tomato callus, TAMU Lycopersicon... 51 2e-07 emb|AI776903|AI776903 EST258003 tomato resistant, Cornell Lycope... 47 3e-07 emb|AW092951|AW092951 EST286131 tomato mixed elicitor, BTI Lycop... 47 3e-07 emb|AW203388|AW203388 sf29f06.yl Gm-c1028 Glycine max cDNA clone... 50 3e-07 emb|AW597294|AW597294-si71c07.y1 Gm-c1031 Glycine max cDNA clone... 50 3e-07 emb|AW622484|AW622484 EST313272 tomato root during/after fruit s... 47 3e-07 emb|AW707234|AW707234 sk22d10.yl Gm-c1028 Glycine max cDNA clone... 50 3e-07 emb[AW568382]AW568382 si70b03.yl Gm-c1031 Glycine max cDNA clone... 50 3e-07 emb|AW568746|AW568746 si72e11.yl Gm-c1031 Glycine max cDNA clone... 50 3e-07 emb|AV422321|AV422321 AV422321 Lotus japonicus young plants (two... 50 3e-07 emb|AW830420|AW830420 sm26e07.y1 Gm-c1028 Glycine max cDNA clone... 50 3e-07 emb|AW650542|AW650542 EST328996 tomato germinating seedlings, TA... 47 3e-07 emb|AI441446|AI441446 sa86a06.yl Gm-c1004 Glycine max cDNA clone... emb|AW234379|AW234379 sf24e05.y1 Gm-c1028 Glycine max cDNA clone... 50 3e-07 emb[AI437875]AI437875 sa40g10.y1 Gm-c1004 Glycine max cDNA clone... 50 3e-07 emb|AV416097|AV416097 AV416097 Lotus japonicus young plants (two... emb|AV413898|AV413898 AV413898 Lotus japonicus young plants (two... 50 3e-07 emb|AI441173|AI441173 sa52c02.y1 Gm-c1004 Glycine max cDNA clone... 50 3e-07 emb|AV415427|AV415427 AV415427 Lotus japonicus young plants (two... 50 3e-07 emb[AI772831]AI772831 EST253931 tomato resistant, Cornell Lycope... 47 3e-07 gb|BE020429|BE020429 sm40f03.y1 Gm-c1028 Glycine max cDNA clone ... 50 3e-07 emb|AI443594|AI443594 sa42b01.yl Gm-c1004 Glycine max cDNA clone... 50 3e-07 emb|AW569805|AW569805 si81g01.y1 Gm-c1031 Glycine max cDNA clone... 50 3e-07 emb|AW093202|AW093202 EST286382 tomato mixed elicitor, BTI Lycop... 46 4e-07 emb|AW906384|AW906384 EST342506 potato-stolon, Cornell Universit... 46 6e-07 emb|AW597346|AW597346 si91f06.y1 Gm-c1031 Glycine max cDNA clone... 50 6e-07 emb|AV423170|AV423170 AV423170 Lotus japonicus young plants (two... 50 6e-07 emb|AW351202|AW351202 GM210010B20H11R Gm-r1021 Glycine max cDNA ... emb|AW649092|AW649092 EST327546 tomato germinating seedlings, TA... 46 8e-07 emb[AV424931]AV424931 AV424931 Lotus japonicus young plants (two... 48 8e-07 emb|AW350777|AW350777 GM210009B10D3R Gm-r1021 Glycine max cDNA 3... 48 1e-06 emb|AW597304|AW597304 si71d07.yl Gm-c1031 Glycine max cDNA clone... 48 1e-06 emb|AW706307|AW706307 sj54f10.y1 Gm-c1033 Glycine max cDNA clone... 48 1e-06 emb|AW133241|AW133241 se16b08.y1 Gm-c1013 Glycine max cDNA clone... 48 1e-06 emb|AW568935|AW568935 si73c12.y1 Gm-c1031 Glycine max cDNA clone... 48 1e-06 gb|BE020648|BE020648 sm51g03.y1 Gm-c1028 Glycine max cDNA clone ... 48 1e-06 emb|AW567667|AW567667 si77d01.yl Gm-c1031 Glycine max cDNA clone... 48 1e-06 emb|AI495459|AI495459 sa98c07.yl Gm-c1004 Glycine max cDNA clone... 48 1e-06 emb|AW234280|AW234280 sf23c12.y1 Gm-c1028 Glycine max cDNA clone... 48 1e-06 emb|AW348755|AW348755 GM210003A22D8R Gm-r1021 Glycine max cDNA 3... 47 2e-06 emb|AW309755|AW309755 sf24d05.x1 Gm-c1028 Glycine max cDNA clone... 47 2e-06 emb|AW703937|AW703937 sk25h11.yl Gm-c1028 Glycine max cDNA clone... 47 2e-06

emb|AW596777|AW596777 sj16e12.v1 Gm-c1032 Glycine max cDNA clone... 47 2e-06

emb|AW620542|AW620542 sj06e05.y1 Gm-c1032 Glycine max cDNA clone... 47 2e-06 emb|AW706297|AW706297 sj54e12.y1 Gm-c1033 Glycine max cDNA clone... 47 2e-06

PCT/US01/28506 -----WO 02/22675

	emb AW666031 AW666031 sk31c05.y1 Gm-c1028 Glycine max cDNA clone 47 2e-06
	emb AW760039 AW760039 sl57c07.yl Gm-c1027 Glycine max cDNA clone 47 2e-06
	gb BE057556 BE057556 sn03h08.yl Gm-c1015 Glycine max cDNA clone 47 2e-06
	emb AW596055 AW596055 si97d01.yl Gm-c1032 Glycine max cDNA clone 47 2e-06
5	emb Al901127 Al901127 sc21a04.yl Gm-c1013 Glycine max cDNA clone 47 2e-06
	emb AW666132 AW666132 sk32f02.y1 Gm-c1028 Glycine max cDNA clone 48 2e-06
	emb AW756628 AW756628 sl25b06.yl Gm-c1027 Glycine max cDNA clone 47 2e-06
	emb AW234369 AW234369 sf24d05.yl Gm-c1028 Glycine max cDNA clone 47 2e-06
	emb AI441736 AI441736 sa82b04.yl Gm-c1004 Glycine max cDNA clone 47 2e-06
10	
10	
	emb AW317359 AW317359 sg48c11.yl Gm-c1025 Glycine max cDNA clone 45 2e-06
	emb AW306872 AW306872 sf49g05.yl Gm-c1009 Glycine max cDNA clone 50 2e-06
	emb AW597518 AW597518 sj48b01.yl Gm-c1033 Glycine max cDNA clone 50 2e-06
	emb AW307412 AW307412 sf56f11.y1 Gm-c1009 Glycine max cDNA clone 50 2e-06
15.	emb AW597680 AW597680 sj49e04.yl Gm-c1033 Glycine max cDNA clone 50 2e-06
	emb AW831618 AW831618 sm04g03.y1 Gm-c1027 Glycine max cDNA clone 47 2e-06
	emb AI736342 AI736342 sb27c03.yl Gm-c1009 Glycine max cDNA clone 50 2e-06
	emb AI441411 AI441411 sa59e12.yl Gm-c1004 Glycine max cDNA clone 50 2e-06
	emb AW666398 AW666398 sk36a11.yl Gm-c1028 Glycine max cDNA clone 47 3e-06
20	emb AW759615 AW759615 sl45f02.yl Gm-c1027 Glycine max cDNA clone 47 3e-06
	emb AW309747 AW309747 sf24c01_x1 Gm-c1028 Glycine max cDNA clone 47 4e-06
	emb AW309357 AW309357 sf16d03.x1 Gm-c1028 Glycine max cDNA clone 47 4e-06
	gb[BE022318]BE022318 sm73d03.yl Gm-c1028 Glycine max cDNA clone 47 4e-06
	emb AW234182 AW234182 sf22b12.yl Gm-c1028 Glycine max cDNA clone 47 4e-06
25	emb AW704401 AW704401 sk30f03.y1 Gm-c1028 Glycine max cDNA clone 47 4e-06
23	
	gb BE022257 BE022257 sm72g11.yl Gm-c1028 Glycine max cDNA clone 49 5e-06
	emb AW666281 AW666281 sk34f10.y1 Gm-c1028 Glycine max cDNA clone 49 5e-06
20	emb AW706178 AW706178 sj52g11.yl Gm-c1033 Glycine max cDNA clone 49 5e-06
30	emb AV422555 AV422555 AV422555 Lotus japonicus young plants (two 50 5e-06
	emb AI438033 AI438033 sa35a09.y1 Gm-c1004 Glycine max cDNA clone 49 5e-06
	emb AV406879 AV406879 AV406879 Lotus japonicus young plants (two 50 5e-06
	emb AI522822 AI522822 sa74b08.yl Gm-c1004 Glycine max cDNA clone 49 5e-06
	emb AV417663 AV417663 AV417663 Lotus japonicus young plants (two 50 5e-06
35	emb AV412992 AV412992 AV412992 Lotus japonicus young plants (two 50 5e-06
•	emb AV419296 AV419296 AV419296 Lotus japonicus young plants (two 50 5e-06
	emb AI442014 AI442014 sa66e07.yl Gm-c1004 Glycine max cDNA clone 47 5e-06
	gb L22305 ALFCORC Medicago sativa bimodular protein (corC) mRNA, 50 7e-06
	emb AW560195 AW560195 EST315243 DSIR Medicago truncatula cDNA cl 45 7e-06
40	emb AW559226 AW559226 EST306062 DSIR Medicago truncatula cDNA cl 45 7e-06
	emb AW570545 AW570545 sj63d10.yl Gm-c1033 Glycine max cDNA clone 48 7e-06
	emb AW309693 AW309693 sf23c12.x1 Gm-c1028 Glycine max cDNA clone 45 7e-06
	emb AW152920 AW152920 se32g01.yl Gm-c1015 Glycine max cDNA clone 48 7e-06
	emb AW830131 AW830131 sm23c07.y1 Gm-c1028 Glycine max cDNA clone 48 7e-06
45	emb AI736269 AI736269 sb26b02.yl Gm-c1008 Glycine max cDNA clone 48 7e-06
	emb AW595988 AW595988 si96d11.yl Gm-c1032 Glycine max cDNA clone 44 7e-06
	emb AW703893 AW703893 sk25d10.y1 Gm-c1028 Glycine max cDNA clone 48 7e-06
50	emb AI441694 AI441694 sa60a10.y1 Gm-c1004 Glycine max cDNA clone 48 7e-06
30	emb AI442516 AI442516 sa32e08.yl Gm-c1004 Glycine max cDNA clone 48 7e-06
	O 17 070770 100 110010 101
*	Query= AL078579.130_at 12240_at /id_source genbank /description
	emb cab43974.1 (al078579) putative protein [arabidopsis thaliana]
	/blast_score 0 /ec_number /family /chip nova /gb_link
55	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb al078579 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al078579
	(1899 letters)
<i>(</i> 0	- · · · · · · · · · · · · · · · · · · ·

Database: plantfungal 661,018 sequences; 426,114,510 total letters 60

	Searching	.done	
		Score E	
5	Sequences producing significant alignme		(bits) Value
			, ,
	emb A1896265 A1896265 EST265708 to	mato callus, TAN	MU Lycopersicon 69 5e-22
	emb AI896298 AI896298 EST265741 to emb AI352900 AI352900 MB73-10F PZ		
10	emb A1960998 A1960998 sc93g09.y1 Gi		
	emb AW618619 AW618619 EST320605	i L. pennellii trich	nome, Cornell U 67 4e-10
	emb AW618077 AW618077 EST314127		
	emb AW684309 AW684309 NF015D01		
1.5	emb AW477120 AW477120 ga42b04.yl		
15	emb AW459393 AW459393 sh23f12.y1		
	emb AW459655 AW459655 sh90b07.yl		
•	gb M82834 TRBAEMAJ Trypanosoma o emb AL031746 PFMAL1P3 Plasmodium		
	gb J03998 PFAGAR Plasmodium falcipa		
20	emb AQ361416 AQ361416 mgxb0004C		
	emb AQ160297 AQ160297_mgxb0005E	2r CUGI Rice B	last BAC Library P 39 0.15
	emb AQ399340 AQ399340 mgxb0016L0		
	emb AQ397636 AQ397636 mgxb0003C	21f CUGI Rice B	last BAC Library P 39 0.15
25	emb AQ254981 AQ254981 mgxb0007C		
23	emb AQ161580 AQ161580 mgxb0008O emb AQ400016 AQ400016 mgxb0006B		
	emb AQ399347 AQ399347 mgxb0003K		
	emb AQ161764 AQ161764 mgxb0009C		
	emb AV412173 AV412173 AV412173 I	otus japonicus yo	oung plants (two 35 1.4
30	gb L38454 PFAORFAE Plasmodium fale	ciparum (clone pS	31H) ORF mRNA, 27 1.8
	emb AQ162745 AQ162745 mgxb0016M		
	emb AQ398363 AQ398363 mgxb0014B6		
	emb AQ161887 AQ161887 mgxb0010E emb AQ161814 AQ161814 mgxb0009M		
35	emb AQ255508 AQ255508 mgxb0014J0	5r CUGI Rice B	ast BAC Library P 35 1.9
	emb AQ254973 AQ254973 mgxb0007C		
	emb AQ654450 AQ654450 Sheared DNA	A-25M9.TR Shea	red DNA Trypanosom 35 1.9
	emb AQ906953 AQ906953 GSSTc02993		
40	emb AL116053 CNS01CVX Botrytis cin		
40	gb BE052627 BE052627 GAEa0032JI emb AI668074 AI668074 TENG0996 T.	Greek animastica	boreum 7-10 dpa 34 2.6
	emb AF242312 AF242312 Euphorbia est	Ciuzi epiniasugo ila evelophilin m	RNA, partial 34 3.5
	emb AC004157 AC004157 Plasmodium	falciparum chron	nosome 12 clone 34 3.6
	emb AA550286 AA550286 1415m3 gmb	PfHB3.1, G. Ror	nan Reddy Plasmodi 34 3.6
45	emb Z49390 SCYJL115W S.cerevisiae c		
	emb AQ845473 AQ845473 LMAJFV1_I		
	emb AQ902283 AQ902283 LMAJFV1_1	m47104.x1 Leish	mania major FV1 ra 34 3.6
	emb AQ845786 AQ845786 LMAJFV1_1 gb L07593 YSCASF Saccharomyces cere	IBZ3N11.X1 LCISD Priciae ASE1 cen	mania major FV1 ra 34 3.6 e, complete cds. 34 3.6
50	emb[X53731]SCSPA2G S. cerevisiae SP.		34 4.8
	emb AQ324737 AQ324737 mgxb0019L2		
	emb AQ501529 AQ501529 V20F5 mTn-	3xHA/lacZ Inser	tion Library Sacc 34 4.8
	emb AQ161923 AQ161923 mgxb0010K2		
55	emb AW618616 AW618616 EST320602		
55	emb AI437671 AI437671 sa38b01.yl Gr emb AW703668 AW703668 sk11h05.yl		
	emb X97560 SC32KBF S.cerevisiae 32kl		
	emb Z73126 SCYLL021W S.cerevisiae of		
	emb AV414692 AV414692 AV414692 L	otus japonicus yo	oung plants (two 33 5.0
60	emb Z37997 SC9877 S.cerevisiae chrome	osome IX cosmid	9877. 33 5.0
	emblX52898lTCGAP T, cruzi gan gene f	or elyceraldehyde	-3-phosphat 33 5 0

	emb AF052832 AF052832 Trypanosoma cruzi CL Brener cosmid 1621 ch 33 5.0
	emb AV423850 AV423850 AV423850 Lotus japonicus young plants (two 33 5.0
	emb AC006281 AC006281 Plasmodium falciparum chromosome 12 clone 26 5.3
	emb AW459042 AW459042 sh18d12.yl Gm-c1016 Glycine max cDNA clone 33 6.5
5	gb L06323 THEGLUMEMP Theileria parva glutamine rich membrane pro 33 6.5
_	emb W66263 W66263 TgESTzy71f09.r1 TgME49 Tachyzoite cDNA Toxopla 33 6.5
	emb AQ948528 AQ948528 Sheared DNA-37G19.TR Sheared DNA Trypanoso 33 6.9
	emb AL035476 PFMAL4P3 Plasmodium falciparum chromosome 4 strain 33 6.9
	emb AI080842 AI080842 TENU3699 T. cruzi epimastigote normalized 33 6.9
10	gb U75347 ENU75347 Emericella nidulans fatty acid synthase, alph 33 6.9
	emb AQ659013 AQ659013 Sheared DNA-13G3.TR Sheared DNA Trypanosom 33 6.9
	emb AF100160 AF100160 Glycine max hydrophobic seed protein precu 33 6.9
	emb AF118381 AF118381 Brassica napus tonoplast intrinsic protein 33 8.9
	emb AW099672 AW099672 sd29e10.y2 Gm-c1012 Glycine max cDNA clone 33 8.9
15	emb AA519692 AA519692 TgESTzz27f06.rl TgME49 invivo Bradyzoite c 33 8.9
13	
	emb AQ255413 AQ255413 mgxb0012P02r CUGI Rice Blast BAC Library P 33 8.9
	emb Z73626 SCYPL270W S.cerevisiae chromosome XVI reading frame O 33 8.9
	emb X96876 SCCHRIVFY S.cerevisiae DNA of cosmid from chromosome 32 9.4
	gb U43564 SCU43564 Saccharomyces cerevisiae CDC53 gene, complete 32 9.4
20	emb Z29537 NTPROTINH N.tabacum (Samsun NN) gene for proteinase i 32 9.4
	_ emb AF155848 AF155848 Lysinema ciliatum chloroplast atpB-rbcL in 32 9.4
	gb U38804 PPU38804 Porphyra purpurea chloroplast, complete genome. 32 9.4
05	emb AI510981 AI510981 T7187 MVAT4 bloodstream form of serodeme W 32 9.4
25	emb AF102653 AF102653 Podranea ricasoliana ribulose 1,5-bisphosp 32 9.4
	emb Z74180 SCYDL132W S.cerevisiae chromosome IV reading frame OR 32 9.4
	Query= AJ011674.2 at 12278 at /id_source genbank /description
	"emb caa09731.1 (aj011674) receptor-like protein kinase, rlk3
30	[arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase
	/chip nova /gb link
	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb aj011674 /ncgi
25	http://www.ncgr.org/cgi-bin/ff?aj011674
35	(2196 letters)
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
40	Searchingdone
	Score E
:	Sequences producing significant alignments: (bits) Value
	(,
45.	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k 375 e-120
	emb[Y18260]BOY18260 Brassica oleracea mRNA for SRK15 protein, pa 332 e-105
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 339 e-105
	emb[Y14285]BOY14285 Brassica oleracea mRNA for SFR1 protein. 330 e-105
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds. 333 e-104
50	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par 332 e-104
	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 328 e-103
	gb[M76647]BNASKR6A Brassica oleracea receptor protein kinase (SK 329 e-100
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc 321 1e-99
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds. 316 2e-98
<i>E E</i>	
55	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine 323 2e-98
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase 324 4e-98
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial. 195 4e-97
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp 312 4e-95
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti 314 4e-95
60	emb AW620957 AW620957 sj98a07.yl Gm-c1023 Glycine max cDNA clone 285 3e-9
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR 306 6e-94

- WO 02/22675 ---PCT/US01/28506

gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 221 1e-93 dbi|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 270 3e-93 gb[U51741]ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 264 2e-90 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 289 2e-90 emblAB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 275 7e-90 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 274 9e-89 emb[Y12530]BOARLKGEN B.oleraceae gene encoding serine/threonine ... 127 6e-88 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 272 6e-88 gb[BE057261]BE057261 sm99f12.yl Gm-c1015 Glycine max cDNA clone ... 313 3e-84 10 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 122 2e-82 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 302 9e-81 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 128 3e-78 emb|AW760240|AW760240 s159g07.yl Gm-c1027 Glycine max cDNA clone... 283 4e-75 emb|AW831390|AW831390 sm22a06.y1 Gm-c1028 Glycine max cDNA clone... 213 3e-73 15 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 127 6e-73 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 266 3e-71 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 118 1e-70 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 114 4e-69 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 261 2e-68 20 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 182 4e-68 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 210 8e-68 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 110 9e-68 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 111 2e-67 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 109 2e-67 25 emb|AI896155|AI896155 EST265598 tomato callus, TAMU Lycopersicon... 186 3e-67 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 109 3e-66 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 120 2e-65 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 120 3e-65 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 116 le-64 30 emb|AW203661|AW203661 sf36g06.yl Gm-c1028 Glycine max cDNA clone... 208 2e-63 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 241 2e-62 emb|AI967314|AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two... 134 1e-60 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 171 3e-60 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 231 2e-59 35 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 231 2e-59 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 171 3e-59 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 136 1e-58 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 227 2e-58 emb|AW309544|AW309544 sf20h08.x1 Gm-c1028 Glycine max cDNA clone... 167 4e-57 40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 176 7e-56 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 219 8e-56 emb|AI901283|AI901283 sc31d08.yl Gm-c1014 Glycine max cDNA clone... 175 9e-56 emblY16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 131 1e-55 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 117 1e-53 45 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 116 4e-53 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 111 7e-53 emblAW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 140 9e-53 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 78 4e-52 emb|A1899009|A1899009 EST268452 tomato ovary, TAMU Lycopersicon ... 160 5e-52 50 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 205 1e-51 emblAI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 156 6e-51 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 156 6e-51 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 160 6e-51 emblAW039406iAW039406 EST281663 tomato mixed elicitor, BTI Lycop... 115 1e-50 55 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 183 1e-50 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 160 3e-50 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 125 2e-49 emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 196 5e-49 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 116 6e-49 60 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 100 8e-49 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 74 4e-48

emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 116 5e-47 emb[AW776492]AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 189 8e-47 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 160 9e-47 emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 188 le-46 5 gb[U51330]TAU51330 Triticum aestivum leaf rust resistance kinase... 78 1e-46 emb|AI967315|AI967315 Ljirnpest00-018 Ljirnp Lambda HybriZap two... 142 2e-46 emb|AW279355|AW279355 sf65g10.y1 Gm-c1013 Glycine max cDNA clone... 111 4e-46 emblAI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 130 5e-46 emb|AI775997|AI775997 EST257097 tomato resistant, Cornell Lycope... 186 5e-46 10 emb|AI930642|AI930642 sb37f05.yl Gm-c1013 Glycine max cDNA clone... 182 1e-44 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 78 1e-44 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 67 3e-44 emb|AW394449|AW394449 sh05d09.yl Gm-c1016 Glycine max cDNA clone... 119 4e-44 emb[AI938169]AI938169 sc40d07.y1 Gm-c1014 Glycine max cDNA clone... 179 6e-44 15 emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 114 7e-44 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 76 1e-43 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 125 1e-43 emb[Y14600]SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 74 1e-43 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 177 2e-43 20 emb|AI055189|AI055189 coau0003E19 Cotton Boll Abscission Zone cD... 107 4e-43 gb|BE058691|BE058691 sn19e05.yl Gm-c1016 Glycine max cDNA clone ... 92 4e-43 emb|Z18883|BOSRKRPB B.oleracea encoding S-receptor kinase relate... 176 4e-43

Query= AC002392.162 at 12307 at /id source genbank /description 25 gb|aad12037.1| (ac002392) putative receptor-like protein kinase [arabidopsis thaliana] /blast_score 0 /ec_mmber /family kinase /chip nova/gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002392| /ncgi 30 http://www.ncgr.org/cgi-bin/ff?ac002392

(2631 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

35

Searching.....

Score E

Sequences producing significant alignments:

(bits) Value

40 emb|AW774582|AW774582 EST333733 KV3 Medicago truncatula cDNA clo... 204 5e-74 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 245 1e-63 emb|Z73295|CRPK1 C.roseus mRNA for receptor-like protein kinase. 146 5e-56 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 112 7e-54 45 gb U59317 LPU59317 Lycopersicon pimpinellifolium serine/threonin... 108 7e-54 gb U13923 LEU13923 Lycopersicon pimpinellifolium serine/threonin... 108 7e-54 emb|AW222552|AW222552 EST299363 tomato fruit red ripe, TAMU Lyco... 210 3e-53 gb|BE053916|BE053916 GA Ea0031D03f Gossypium arboreum 7-10 dpa ... 209 8e-53 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 112 4e-52 50 emb|AW200786|AW200786 se93e06.yl Gm-c1027 Glycine max cDNA clone... 206 5e-52 emb|AW729859|AW729859 GA_Ea0026H04 Gossypium arboreum 7-10 dpa ... 206 7e-52 emb|AW774672|AW774672 EST333823 KV3 Medicago truncatula cDNA clo... 82 7e-51 gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 111 9e-50 gb/U59318/LEU59318 Lycopersicon esculentum serine/threonine prot... 102 3e-49

55 emb|AF121450|AF121450 Capsicum annuum protein kinase homolog C11... 104 1e-48 emb|AF108892|AF108892 AF108892 Capsicum annuum root 1st-branched... 194 3e-48 emb|AI967314|AI967314 Ljirnpest00-017 Ljirnp Lambda HybriZap two... 129 5e-48 gb|U59315|LPU59315 Lycopersicon pimpinellifolium serine/threonin... 103 1e-47

60 gb U02271 LEU02271 Lycopersicon pimpinellifolium Rio Grande-PtoR... 103 1e-47 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 185 3e-47

emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 113 5e-47 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 182 2e-46 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 112 2e-46 emb|AW773915|AW773915 EST332901 KV3 Medicago truncatula cDNA clo... 82 3e-46 emb|AF053127|AF053127 Malus domestica leucine-rich receptor-like... 130 4e-46 dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein... 110 4e-46 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 111 5e-46 dbilD38563|BOLRPKA Brassica campestris mRNA for receptor protein... 109 6e-46 emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 146 6e-46 10 emb|AI736063|AI736063 sb22d04.y1 Gm-c1007 Glycine max cDNA clone... 147 6e-46 emb|AW256717|AW256717 EST304854 KV2 Medicago truncatula cDNA clo... 82 7e-46 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 94 2e-45 dbj E05046 E05046 DNA encoding ZmPK1 homologue protein in tobacco. 94 2e-45 emb|AW979740|AW979740 EST341365 tomato root deficiency, Cornell ... 184 2e-45 15 emb|AI895365|AI895365 EST264808 tomato callus, TAMU Lycopersicon... 184 2e-45 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 82 3e-45 gb|U28007|LEU28007 Lycopersicon esculentum Pto kinase interactor... 127 1e-44 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 79 2e-44 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 79 2e-44 20 emb|AF121451|AF121451 Capsicum annuum protein kinase homolog C11... 105 5e-44 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 133 6e-44 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 81 2e-43 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 78 3e-43 gb[U20948]ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 99 1e-42 25 emb|AF121449|AF121449 Capsicum annuum protein kinase homolog C15... 99 1e-42 emb|AW219672|AW219672 EST302154 tomato root during/after fruit s... 125 1e-42 emb[AW030530[AW030530 EST273785 tomato callus, TAMU Lycopersicon... 162 1e-42 emb|AI898917|AI898917 EST268360 tomato ovary, TAMU Lycopersicon ... 122 1e-42 emb|AI489287|AI489287 EST247626 tomato ovary, TAMU Lycopersicon ... 122 2e-42 30 emb|A1730776|A1730776 BNLGHi7867 Six-day Cotton fiber Gossypium ... 151 2e-42 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 78 2e-42 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 115 6e-42 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 110 9e-42 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 132 9e-42 35 gb[M97667]BNASTKR Brassica napus ssp. oleifera serine/threonine ... 115 2e-41 emb|AW036763|AW036763 EST252152 tomato ovary, TAMU Lycopersicon ... 164 2e-41 emb|AW036762|AW036762 EST252151 tomato ovary, TAMU Lycopersicon ... 164 2e-41 emb|AW668493|AW668493 GA_Ea0014C20 Gossypium arboreum 7-10 dpa ... 127 4e-41 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 110 4e-41 40 emb|AW776704|AW776704 EST335769 DSIL Medicago truncatula cDNA cl... 113 2e-40 emb|AF131222|AF131222 Lophopyrum elongatum protein serine/threon... 97 2e-40 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 133 2e-40 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 111 3e-40 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 105 3e-40 emb|AW615998|AW615998 EST325448 tomato flower buds 0-3 mm, Corne... 117 3e-40 emb|AW218745|AW218745 EST301225 tomato root during/after fruit s... 120 5e-40 emb|AI731501|AI731501 BNLGHi9983 Six-day Cotton fiber Gossypium ... 98 6e-40 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 108 9e-40 emb|AF121448|AF121448 Capsicum annuum protein kinase homolog C11... 95 2e-39 50 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 165 2e-39 emb|AI486547|AI486547 EST244868 tomato ovary, TAMU Lycopersicon ... 123 2e-39 emb|AW094468|AW094468 EST287648 tomato mixed elicitor, BTI Lycop... 156 2e-39 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 108 3e-39 emb|AI771841|AI771841 EST252941 tomato ovary, TAMU Lycopersicon ... 164 4e-39 55 emb|AI485090|AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 164 4e-39 emb|Al731504|Al731504 BNLGHi9991 Six-day Cotton fiber Gossypium ... 78 4e-39 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 111 4e-39 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 107 6e-39 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 107 6e-39 60 emb|AW267961|AW267961 EST306183 DSIR Medicago truncatula cDNA cl... 94 7e-39 emb[Y18259]BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 107 1e-38

emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... emb|AJ485862|AJ485862 EST244183 tomato ovary, TAMU Lycopersicon ... 162 1e-38 emb|AI487456|AI487456 EST245778 tomato ovary, TAMU Lycopersicon ... 123 2e-38 gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 75 2e-38 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 107 3e-38 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 78 3e-38 emb|AW617255|AW617255 EST323666 L. hirsutum trichome, Cornell Un... 148 4e-38 gb[U51741]ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 71 4e-38 emb|AW774790|AW774790 EST333941 KV3 Medicago truncatula cDNA clo... 95 5e-38 10 emb[Y14286]BOY14286 Brassica oleracea SFR3 gene, partial. 105 5e-38 emb|AI898390|AI898390 EST267833 tomato ovary, TAMU Lycopersicon ... 121 1e-37 gb|BE020963|BE020963 sm54a06.y1 Gm-c1028 Glycine max cDNA clone ... 125 3e-37 emblAI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 73 5e-37 15 emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 81 7e-37 emb|AW687267|AW687267 NF007G07RT1F1055 Developing root Medicago ... 140 8e-37 emb|AW648736|AW648736 EST327106 tomato germinating seedlings, TA... 98 1e-36 emb|AW650851|AW650851 EST329305 tomato germinating seedlings, TA... 126 2e-36

20 Query= AB023448.2 s at 12332 s at /id source genbank /description dbj|baa82810.1| (ab023448) basic endochitinase [arabidopsis thaliana] /blast score 0 /ec number /family /chip nova /gb link /ncgi (1008 letters)

25 Database: plantfungal 661,018 sequences; 426,114,510 total letters

30 Score E

Sequences producing significant alignments:

(bits) Value

emblAF135130|AF135130 Arabis holboellii from Denmark class I chi... 438 0.0 emblX16939INTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 491 e-158 35 gb[M15173]TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 494 e-158 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 490 e-158 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 493 e-158 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 541 e-153 emb[X07130]STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 541 e-153 40 emb[Y10373]MTCHITIN1 M.truncatula mRNA for chitinase. 482 e-151 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 442 e-150 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 443 e-150 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 442 e-149 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 440 e-148 45 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 467 e-148 gb[U83592[MSU83592 Medicago sativa class I chitinase mRNA, compl... 310 e-146 gb[U83591]MSU83591 Medicago sativa class I chitinase mRNA, compl... 310 e-146 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 309 e-146 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 472 e-146 50 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 286 e-145 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 305 e-144 emb[X76041]TACHIG T.aestivum (Chinese spring) chi gene for endoc... 466 e-144 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 332 e-144

55 emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 333 e-144 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 469 e-144 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 435 e-143 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 284 e-143 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 296 e-143 60 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 459 e-141 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 455 e-140

	golivisatios acceptation Allium sativum chitinase mkna, 3 end. 448 e-140
	emb AB015655 AB015655 Cucurbita sp. mRNA for chitinase, complete 286 e-139
	emb AF000964 AF000964 Poa pratensis chitinase (Chi1) gene, compl 408 e-139
	gb[L34211]BLYCHI33A Hordeum vulgare chitinase (CHI33) gene, comp 448 e-138
5	gb[U02608 STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par 408 e-137
•	emb[X63899]PSCHITIN P.sativum mRNA for chitinase. 270 e-135
	emb AF061805 AF061805 Elaeagnus umbellata acidic chitinase mRNA, 430 e-134
	emb AF202731 AF202731 Glycine max endochitinase homolog (Chn1) m 273 e-134
	gb L34210 BLYCHI26A Hordeum vulgare chitinase (CHI26) gene, comp 475 e-133
10	emb A37990 A37990 Sequence 9 from Patent EP0616035. 475 e-133
	gb M62904 BLYCHI H. vulgare L. 26kD chitinase mRNA, complete cds. 475 e-133
	emb AF098302 AF098302 Brassica juncea chitinase mRNA, complete cds. 265 e-132
	gb U30324 TCU30324 Theobroma cacao class I chitinase gene, compl 238 e-131
	emb X95610 CSHITTB C.sativa mRNA for chitinase Ib. 259 e-130
15	gb[U48687]CSU48687 Castanea sativa endochitinase mRNA, complete 259 e-130
13	emb AF141372 AF141372 Petroselinum crispum chitinase precursor (463 e-130
	chiple 1415/2pt 1415/2 Fetosemini dispuni difficase precusor (405 e-150
	emb AF135137 AF135137 Arabis fecunda country USA class I chitina 459 e-128
	emb AF061806 AF061806 Elaeagnus umbellata basic chitinase mRNA, 297 e-128
	emb AB023464 AB023464 Arabis gemmifera ChiB gene for basic endoc 455 e-127
20	emb AF135152 AF135152 Arabis parishii country USA class I chitin 455 e-127
	emb AF135141 AF135141 Arabis gunnisoniana class I chitinase gene 455 e-127
'	emb AF135135 AF135135-Arabis drummondii class I chitinase gene, 455 e-127
	emb AF135143 AF135143 Arabis lemmonii country USA class I chitin 452 e-126
	emb X67693 STMREN S.tuberosum mRNA for endochitinase. 452 e-126
25	emb AF135132 AF135132 Arabis gunnisoniana from USA class I chiti 452 e-126
23	emb AF135144 AF135144 Arabis lemmonii country USA class I chitin 451 e-126
	children 135144 Analis ichimolii country OSA ciass i chim 451 e-120
	emb AF135140 AF135140 Arabis glabra country USA class I chitinas 449 e-125
	gb U30465 LEU30465 Lycopersicon esculentum class II chitinase (C 447 e-125
	emb AF135153 AF135153 Arabis parishii country USA class I chitin 445 e-124
30	gb L22032 ULMCHITIN Ulmus americana chitinase (pHS2) mRNA, compl 295 e-124
	emb AF135148 AF135148 Arabis lyallii class I chitinase gene, par 444 e-124
	emb AF135151 AF135151 Arabis microphylla country USA class I chi 444 e-124
	emb AF135150 AF135150 Arabis microphylla country USA class I chi 443 e-124
	emb AF135147 AF135147 Arabis lignifera country USA class I chiti 443 e-124
35	emb AF135136 AF135136 Arabis fecunda country USA class I chitina 443 e-124
	emb AF135145 AF135145 Arabis lignifera country USA class I chiti 443 e-123
	emb AF135146 AF135146 Arabis lignifera country USA class I chiti 441 e-123
	emb AF135149 AF135149 Arabis microphylla class I chitinase gene, 441 e-123
40	emb AF043247 AF043247 Solanum tuberosum class I chitinase (ChtC1 431 e-122
40	emb AF043248 AF043248 Solanum tuberosum class I chitinase (ChtC2 431 e-122
	emb Z15138 LECHI14 L.esculentum mRNA for chitinase (partial). 439 e-122
	emb AF135142 AF135142 Halimolobos perplexa var. perplexa class I 435 e-121
	emb AF135134 AF135134 Arabis blepharophylla class I chitinase ge 434 e-121
	gb[U01660]U01660 Populus trichocarpa x Populus deltoides acidic 207 e-121
45	emb AF135138 AF135138 Arabis glabra country USA class I chitinas 431 e-120
	emb AF135133 AF135133 Arabis blepharophylla country USA class I 423 e-118
	gb M95835 BNACH25A Brassica napus (clone BnCh25) endochitinase g 422 e-117
	emb AW034530 AW034530 EST278146 tomato callus, TAMU Lycopersicon 418 e-116
	emb AW560048 AW560048 EST315096 DSIR Medicago truncatula cDNA cl 350 e-112
50	emb AW687771 AW687771 NF013C08RT1F1065 Developing root Medicago 311 e-11
J U	
	emb AW033115 AW033115 EST276674 tomato callus, TAMU Lycopersicon 391 e-108
	emb AW034645 AW034645 EST278376 tomato callus, TAMU Lycopersicon 366 e-106
	emb AF082713 AF082713 AF082713 Capsicum annuum leaf mRNA Capsicu 364 e-106
	emb AW738053 AW738053 EST339480 tomato flower buds, anthesis, Co 379 e-104
55	emb AF141373 AF141373 Petroselinum crispum chitinase precursor (237 e-104
	emb Z70032 CSACHIT2 C.sinensis mRNA for class II acidic chitinase. 197 e-104
	emb AW030745 AW030745 EST274000 tomato callus, TAMU Lycopersicon 360 e-104
	emb AF141374 AF141374 Petroselinum crispum chitinase precursor (237 e-104
	emb AW033034 AW033034 EST276593 tomato callus, TAMU Lycopersicon 367 e-103
60	emb AW216454 AW216454 EST295084 tomato callus, TAMU Lycopersicon 373 e-102
J	embla W267781 IA W267781 FST305909 DSTR Medicago truncatula cDNA cl. 216 c. 102

emb|AW033757|AW033757 EST277328 tomato callus, TAMU Lycopersicon... 285 e-101 emb|AW037673|AW037673 EST279276 tomato mixed elicitor, BTI Lycop... 281 e-100 emb|AW216787|AW216787 EST295501 tomato callus, TAMU Lycopersicon... 364 e-100 emb|AI771248|AI771248 EST252264 tomato ovary, TAMU Lycopersicon... 363 1e-99 emb|AW031102|AW031102 EST274409 tomato callus, TAMU Lycopersicon... 275 1e-98 emb|X15349|HVENDCHT Barley (H.vulgare) mRNA for endochitinase. 359 2e-98 emb|AW622028|AW622028 EST312826 tomato root during/after fruit s... 269 9e-97 emb|Z15139|LECHI17 L.esculentum mRNA for chitinase. 242 2e-96 emb|AW032161|AW032161 EST275615 tomato callus, TAMU Lycopersicon... 334 2e-96 emb|AW560177|AW560177 EST315225 DSIR Medicago truncatula cDNA cl... 295 1e-95

Query= AL021637.176_s_at 12341_s_at /id_source genbank /description emb|caa16619.1| (al021637) vacuolar sorting receptor-like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1881 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

20

60

5

10

15

Searching......done

Score E.

Sequences producing significant alignments:

(bits) Value

25 gb[U79958]PSU79958 Pisum sativum BP-80 vacuolar sorting receptor... 810 0.0 emb|AB006809|AB006809 Cucurbita sp. mRNA for PV72, complete cds. 780 0.0 emb|AW267745|AW267745 EST305873 DSIR Medicago truncatula cDNA cl... 453 e-126 emb|AW931583|AW931583 EST357426 tomato fruit mature green, TAMU ... 308 e-112 30 emb|AW309187|AW309187 sg05d06.yl Gm-c1019 Glycine max cDNA clone... 405 e-112 gb|BE054150|BE054150 GA Ea0034H17f Gossypium arboreum 7-10 dpa ... 398 e-110 emb|AW622833|AW622833 EST306903 tomato flower buds 3-8 mm. Corne... 387 e-106 emb|AW689392|AW689392 NF018F12ST1F1000 Developing stem Medicago ... 371 e-102 emb|AW737948|AW737948 EST339375 tomato flower buds, anthesis, Co... 342 3e-94 35 emb|AW774434|AW774434 EST333585 KV3 Medicago truncatula cDNA clo... 263 2e-90 emb|AW932529|AW932529 EST358372 tomato fruit mature green, TAMU ... 326 3e-88 emb|AW615949|AW615949 EST325315 tomato flower buds 0-3 mm, Corne... 216 1e-87 emb|AI728635|AI728635 BNLGHi11276 Six-day Cotton fiber Gossypium... 281 8e-84 emb|AI782787|AI782787 EST263666 tomato susceptible, Cornell Lyco... 307 2e-82 40 emb|AI443067|AI443067 sa47a01.y1 Gm-c1004 Glycine max cDNA clone... 305 6e-82 emb|AW747297|AW747297 WS1 67 G06.b1 A002 Water-stressed 1 (WS1) ... 292 8e-78 emb|AI727826|AI727826 BNLGHi9195 Six-day Cotton fiber Gossypium ... 280 1e-77 emb|AI484571|AI484571 EST242801 tomato ovary, TAMU Lycopersicon ... 284 1e-75 emb|AW685785|AW685785 NF030C07NR1F1000 Nodulated root Medicago t... 166 1e-71 45 emb|AV406766|AV406766 AV406766 Lotus japonicus young plants (two... 260 2e-68 emb|AW509740|AW509740 ga63h11.yl Moss EST library PPU Physcomitr... 232 1e-65 emb|AV428420|AV428420 AV428420 Lotus japonicus young plants (two... 249 4e-65 emb|AW695542|AW695542 NF096C05ST1F1037 Developing stem Medicago ... 124 1e-58 emb|AW289687|AW289687 NXNV004E04F Nsf Xylem Normal wood Vertical... 226 4e-58 50 emb|AW064744|AW064744 ST35C06 Pine TriplEx shoot tip library Pin... 198 2e-56 emb|AW309191|AW309191 sg05d10.yl Gm-c1019 Glycine max cDNA clone... 171 3e-52 emb|AW096632|AW096632 EST289812 tomato mixed elicitor, BTI Lycop... 165 7e-52 emb|AW568619|AW568619 si60a11.yl Gm-r1030 Glycine max cDNA clone... 205 1e-51 emb|AF209910|AF209910 Prunus dulcis vacuolar sorting receptor pr... 160 5e-51 55 emb|AW623959|AW623959 EST321904 tomato flower buds 3-8 mm, Corne... 75 1e-50 emb[AW397829]AW397829 sg68h03.yl Gm-c1007 Glycine max.cDNA clone... 201 2e-50 emb|AW256542|AW256542 EST304679 KV2 Medicago truncatula cDNA clo... 151 2e-50 emb|AI967865|AI967865 Ljirnpest14-100-f3 Ljirnp Lambda HybriZap ... 197 3e-49

emb|AW680054|AW680054 WS1 3_A01.g1_A002 Water-stressed 1 (WS1) S... 150 6e-47

emb|AA660289|AA660289 00158 MtRHE Medicago truncatula cDNA 5', m... 107 9e-44 emb|AW056624|AW056624 ST53G07 Pine TriplEx shoot tip library Pin... 178 1e-43

emb|AW690002|AW690002 NF026G04ST1F1000 Developing stem Medicago ... 109 2e-43 emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 177 3e-43 emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 131 2e-39 emb|Al161766|Al161766 A006P54U Hybrid aspen plasmid library Popu... 93 3e-38 emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 149 5e-35 gb|BE125908|BE125908 DG1 59 E01.b1 A002 Dark Grown I (DG1) Sorgh... 149 5e-35 emb|AW201441|AW201441 sf03b09.yl Gm-c1027 Glycine max cDNA clone... 113 1e-34 emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 95 2e-34 gb|BE049814|BE049814 NXNV 144 F04 F Nsf Xylem Normal wood Vertic... 143 6e-33 10 emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 100 5e-30 emb|AW508719|AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone... 125 1e-27 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 117 4e-26 emb|AW317388|AW317388 sg48g10.yl Gm-c1025 Glycine max cDNA clone... 80 1e-25 emb|AW706755|AW706755 sk02f10.yl Gm-c1023 Glycine max cDNA clone... 118 2e-25 15 emb|AA660955|AA660955 00852 MtRHE Medicago truncatula cDNA 5' si... 74 7e-25 emb|AW616461|AW616461 EST322872 L. hirsutum trichome, Cornell Un... 69 2e-24 emb|AW348825|AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3... 68 8e-24 emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 80 1e-23 emb|AW774190|AW774190 EST333273 KV3 Medicago truncatula cDNA clo... 101 2e-20 20 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 66 6e-20 emb|AW093844|AW093844 EST287024 tomato mixed elicitor, BTI Lycop... 96 7e-19 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 67 2e-16 gb|BE060808|BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis... 87 4e-16 emb|AW620693|AW620693 sj08d10.y1 Gm-c1032 Glycine max cDNA clone... 76 1e-15 25 emblAW256398|AW256398 EST304465 KV2 Medicago truncatula cDNA clo... 74 6e-14 emb|AW037563|AW037563 EST278890 tomato mixed elicitor, BTI Lycop... 79 8e-14 emb|AW691052|AW691052 NF037B05ST1F1000 Developing stem Medicago ... 72 4e-13 emb|AW686287|AW686287 NF040A08NR1F1000 Nodulated root Medicago t... 77 4e-13 emb|AW685952|AW685952 NF036G09NR1F1000 Nodulated root Medicago t... 46 2e-11 30 emblAW760128|AW760128 s158d09.yl Gm-c1027 Glycine max cDNA clone... 58 1e-10 emb|AW119909|AW119909 sd54d08.yl Gm-c1016 Glycine max cDNA clone... 66 8e-10 emb|AI794754|AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone... 64 4e-09 emb|AW774852|AW774852 EST334003 KV3 Medicago truncatula cDNA clo... 64 4e-09 emb|AW127457|AW127457 M110648 DSIL Medicago truncatula cDNA clon... 58 3e-07 35 emb|AW443352|AW443352 EST308282 tomato mixed elicitor, BTI Lycop... 56 1e-06 emb|AW747372|AW747372 WS1 67 G06.g1 A002 Water-stressed 1 (WS1) ... 55 2e-06 emb|AI939286|AI939286 sc69h02.y1 Gm-c1016 Glycine max cDNA clone... 46 0.001 emb|AF198615|AF198615 Neospora caninum microneme protein Nc-P38 ... 43 0.009 emb|AI822258|AI822258 L0-701T3 Ice plant Lambda Uni-Zap XR expre... 36 0.019 40 gb|BE035779|BE035779 MO16H05 MO Mesembryanthemum crystallinum cD... 36 0.025 emb|AI822869|AI822869 L30-712T3 Ice plant Lambda Uni-Zap XR expr... 36 0.025 emb|AI822754|AI822754 LO-1287T3 Ice plant Lambda Uni-Zap XR expr... 36 0.025 emb|AI756736|AI756736 EtESTea24h07.yl Eimeria S5-2 Sporozoite st... 34 0.035 gb[M36941]BLYHORDCA Hordeum vulgare C-hordein gene, complete cds. 45 emb|AU036628|AU036628 Schizosaccharomyces pombe genomic clone ha... emb|AA948752|AA948752 LO-271M13R Ice plant Lambda Uni-Zap XR exp... 35 0.086 emb|AW760788|AW760788 sl35a03.yl Gm-c1027 Glycine max cDNA clone... 39 0.11 emb|AW830924|AW830924 sm19c06.yl Gm-c1027 Glycine max cDNA clone... 39 0.11 emblAO008266lAO008266 CpG0480B CpIOWAgDNA1 Cryptosporidium parvu... 39 0.16 50 emb|AW696326|AW696326 NF106G11ST1F1087 Developing stem Medicago ... 38 0.21 emb|AI974517|AI974517 T110467e KV0 Medicago truncatula cDNA clon... 38 0.21 emb|AV408651|AV408651 AV408651 Lotus japonicus young plants (two... 38 0.21 emb|AQ651638|AQ651638 Sheared DNA-7G23.TF Sheared DNA Trypanosom... 37 0.40 emb|AQ942781|AQ942781 Sheared DNA-42B17.TF Sheared DNA Trypanoso... 37 0.56 55 gb|BE036036|BE036036 MO18H02 MO Mesembryanthemum crystallinum cD... 36 0.76 gb|C95899|C95899 C95899 Marchantia polymorpha immature sex organ... 36 1.0 emblAA966307 V8c01a1.rl Aspergillus nidulans 24hr asexu... 36 1.0 emb|AI759219|AI759219 EtESTea26c02.yl Eimeria S5-2 Sporozoite st... 28 1.3 gb[U11583[YSCH9196 Saccharomyces cerevisiae chromosome VIII cosm... 35 1.4 60 emb|AQ639257|AQ639257 927P1-10E12.TV 927P1 Trypanosoma brucei ge... 35 1.4 emb|AQ943504|AQ943504 Sheared DNA-43F22.TF Sheared DNA Trypanoso... 35 1.4

~-WO-02/22675 PCT/US01/28506

emblAW623282|AW623282 EST321227 tomato flower buds 3-8 mm, Corne... dbj|D85226|D85226 Brassica campestris DNA for S glycoprotein, pa... 28 1.6 emb|AF001525|AF001525 Musa acuminata ripening-associated protein... 35 2.0

Query= X84728.6 s at 12349 s at /id source genbank/description gb|aaa17993.1| (m91192) phenylalanine ammonia-lyase [trifolium subterraneum] /blast score 0 /ec number /family /chip nova /gb link

(1962 letters)

10

Database: plantfungal 661,018 sequences; 426,114,510 total letters

15

Sequences producing significant alignments:

(bits) Value

gb|L11747|POPPALGA Populus tricocarpa X Populus deltoides (hybri... 354 0.0 20 emb|X99997|BFPAL B.finlaysoniana mRNA for phenylalanine ammonia-... 352 0.0 emb[X58180]MSPAL M.sativa PAL mRNA for phenylalanine ammonia-lyase. 351 0.0 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 350 0.0 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 350 0.0 emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 349 0.0 25 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 349 0.0 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 349 0.0 emb[X81158]PCPAL2 P.crispum mRNA for phenylalanine ammonia-lyase 2. 349 0.0 emb|X81159|PCPAL3 P.crispum mRNA for phenylalanine ammonia-lyase 3. 348 0.0 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 348 0.0 30 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 348 0.0 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 347 0.0 gb[M29232[IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 345 0.0 dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 344 0.0 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase.... 344 0.0 35 emb[X78269]NTPHEAL N.tabacum (Samsun NN) mRNA for phenylalanine ... 343 0.0 dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 343 0.0 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 342 0.0 emb[Y12461]HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 341 0.0 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 339 0.0 40 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 330 0.0 dbj[D10001]PEAPAL P.sativum mRNA for phenylalanine ammonia-lyase... 349 0.0 emb|X63103|STPAL1 S.tuberosum PAL-1 gene for phenylalanine ammon... 353 0.0 emblAJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 350 0.0 emb|AJ238753|CCL238753 Citrus clementina X Citrus reticulata mRN... 353 0.0 45 dbj|D10003|PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas... 349 0.0 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 349 0.0 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 355 0.0 gb[U16130]PAU16130 Persea americana phenylalanine ammonia lyase ... 331 0.0 dbj[D30656]POPPALA Populus kitakamiensis gene for phenylalanine ... 356 0.0 50 gb[M84466]TOBTPA1A Tobacco phenylalanine ammonialyase (tpa1) gen... 352 0.0 emblAB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 352 0.0 dbj[D85850]D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 347 0.0 emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 355 0.0

emb|X99705|TAPALGEN1 T.aestivum PAL gene. 342 0.0 55 gb[M91192]TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 345 0.0 gb[M90692]TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 347 0.0 emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 344 0.0 emb|Y07654|PCPAL1 P.crispum pal1 gene. 350 0.0 emb[X16772]PCPAL1EX2 P.crispum PAL-1 gene for phenylalanine ammo... 350 0.0

60 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 336 0.0 gb|M83314|TOMPHEAMLY Lycopersicon esculentum phenylalanine ammon... 353 0.0

	emb[X76130]CMPAL C.melo (cantaloupe) pal mRNA. 318 0.0
	dbj D30657 POPPALB Populus kitakamiensis gene for phenylalanine 333 0.0
	dbj D43802 POPPALG2BA Populus kitakamiensis gene for phenylalani 336 0.0
	emb AF081215 AF081215 Capsicum chinense phenylalanine ammonia-ly 346 0.0
5	dbj D10002 PEAPAL1 P.sativum gene for phenylalanine ammonia-lyas 349 0.0
J	emb Z49147 HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine 342 0.0
	emb X63104 STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon 353 0.0
	gb U39792 PTU39792 Pinus taeda phenylalanine ammonia-lyase (lpPA 311 0.0
	gb U39/92 P1U39/92 Pinus taeda pnenyiaiamile ammoliia-iyase (ipPA 311 U.U
10	gb[M11939]PHVPAL Phaseolus vulgaris L. phenylalanine ammonia-lya 354 0.0
10	dbj E04043 E04043 cDNA sequence coding for kidney bean phenylala 354 0.0
	emb AB015871 AB015871 Vitis vinifera gene for phenylalanine ammo 350 0.0
	emb Z49145 HVPAL2MR H.vulgare partial PAL mRNA for phenylalanine 341 0.0
	emb Z49146 HVPAL3MR H.vulgare partial PAL mRNA for phenylalanine 311 0.0
	emb X75967 VVPAL V.vinifera PAL mRNA for phenylalanine ammonia l 350 0.0
15	gb S46988 S46988 phenylalanine ammonia-lyase [soybeans, mRNA, 14 344 0.0
•	emb AF206634 AF206634 Prunus persica cultivar Loring phenylalani 336 0.0
	emb AF167487 AF167487 Eucalyptus globulus phenylalanine ammonia 334 e-178
	emb[X99725]TAPALGEN2 T.aestivum PAL gene, coding region. 300 e-137
	emblAW218834 AW218834 EST301314 tomato root during/after fruit s 347 e-134
20	emb AW031612 AW031612 EST275066 tomato callus, TAMU Lycopersicon 327 e-132
	emb AJ289609 BPE289609 Betula pendula partial pal gene for pheny 205 e-128
	emblAJ278116 BPE278116 Betula pendula partial pall gene for phen 205 e-128
	emblAW219303 AW219303 EST301785 tomato root during/after fruit s 339 e-126
	emb AW726548 AW726548 GA_ Ea0022A01 Gossypium arboreum 7-10 dpa 323 e-124
25	emb AI166817 AI166817 xylem.est.611 Poplar xylem Lambda ZAPII li 251 e-117
23	gb BE035366 BE035366 MM06H04 MM Mesembryanthemum crystallinum cD 235 e-11
	emb AW776946 AW776946 EST336011 DSIL Medicago truncatula cDNA cl 280 e-114
	gb BE020072 BE020072 sm38f08.yl Gm-c1028 Glycine max cDNA clone 233 e-112
	emb AF019965 AF019965 Pinus monticola phenylalanine ammonia lyas 205 e-110
30	emb[AF218453]AF218453 Coffea arabica clone 369.1.6r phenylalanin 247 e-105
30	emb[AW216505]AW216505 EST295219 tomato callus, TAMU Lycopersicon 209 e-104
	emb AI166477 AI166477 xylem.est.305 Poplar xylem Lambda ZAPII li 291 e-100
	emb AV428905 AV428905 AV428905 Lotus japonicus young plants (two 243 1e-98
35	emb AW220322 AW220322 EST302805 tomato root during/after fruit s 255 2e-98
33	emb AW734312 AW734312 sk81e07.yl Gm-c1016 Glycine max cDNA clone 324 6e-98
	emb AW034774 AW034774 EST278810 tomato callus, TAMU Lycopersicon 325 3e-93
	emb AW329762 AW329762 N201031e rootphos(-) Medicago truncatula c 337 1e-91
	emb AI777483 AI777483 EST258362 tomato susceptible, Cornell Lyco 294 3e-90
40	emb AW621418 AW621418 EST312216 tomato root during/after fruit s 330 2e-89
40	emb AW443181 AW443181 EST308111 tomato mixed elicitor, BTI Lycop 329 6e-89
	emb AW781748 AW781748 sl90e11.yl Gm-c1037 Glycine max cDNA clone 326 3e-88
	emb X68126 MSPALMR Malus sp. PAL mRNA for phenylalanine ammonia 324 1e-87
	emb AW760268 AW760268 sl48b08.yl Gm-c1027 Glycine max cDNA clone 323 3e-87
	emb AW278641 AW278641 sf63c08.yl Gm-c1013 Glycine max cDNA clone 316 4e-85
45	emb AF218454 AF218454 Coffea arabica clone 430.4 phenylalanine a 243 6e-85
	emb AI899698 AI899698 EST269141 tomato susceptible, Cornell Lyco 314 2e-84
	emb AW455294 AW455294 EST311832 tomato root during/after fruit s 313 3e-84
	emb AW685111 AW685111 NF026A05NR1F1000 Nodulated root Medicago t 236 6e-84
	emb AW667320 AW667320 GA_Ea0008P06 Gossypium arboreum 7-10 dpa 189 2e-83
50	gb BE021354 BE021354 sm57e05.y1 Gm-c1028 Glycine max cDNA clone 308 9e-83
	emb AI772657 AI772657 EST253757 tomato resistant, Cornell Lycope 299 2e-80
	emb A1894514 A1894514 EST263957 tomato callus, TAMU Lycopersicon 294 1e-78
	gb L11883 WHTWALI4A Triticum aestivum phenylalanine ammonia-lyas 87 4e-16
<i>E E</i>	O
55	Query= AL022347.131_at 12360_at /id_source genbank /description
	emb caa18468.1 (al022347) serine/threonine kinase-like protein
	[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova

emb|caa18468.1| (al022347) serine/threonine kinase-like protein
[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|al022347| /ncgi ~

http://www.ncgr.org/cgi-bin/ff?al022347

(1554 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

5 Searching.....done

Score E Sequences producing significant alignments: (bits) Value 10 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 251 1e-65 gb|BE034949|BE034949 ML07F03 ML Mesembryanthemum crystallinum cD... 231 8e-60 emb|AW031255|AW031255 EST274630 tomato callus, TAMU Lycopersicon... 231 1e-59 emb[X98520]BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 230 2e-59 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 227 1e-58 15 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 226 4e-58 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 225 7e-58 emb[Y18259]BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 225 7e-58 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 224 1e-57 gb[BE034855]BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 186 1e-57 20 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 222 6e-57 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 221 8e-57 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 221 2e-56 gb|BE057261|BE057261 sm99f12.yl Gm-c1015 Glycine max cDNA clone ... 220 3e-56 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 219 6e-56 25 gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 218 8e-56 gb[M97667]BNASTKR Brassica napus ssp. oleifera serine/threonine ... 216 3e-55 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 215 5e-55 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 213 3e-54 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 211 1e-53 30 emb[Y12531]BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 116 6e-53 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 207 2e-52 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 204 1e-51 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 198 4e-51 35 dbj[D38563]BOLRPKA Brassica campestris mRNA for receptor protein... 202 7e-51 gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 201 1e-50 emb|A1896155|A1896155 EST265598 tomato callus, TAMU Lycopersicon... 166 1e-50 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 196 2e-49 emb|AW760240|AW760240 s159g07.yl Gm-c1027 Glycine max cDNA clone... 196 4e-49 40 emb|AW033458|AW033458 EST277029 tomato callus, TAMU Lycopersicon... 196 4e-49 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 114 4e-48 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 113 7e-48 emb[Y12530]BOARLKGEN B.oleraceae gene encoding serine/threonine ... 115 1e-47 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 111 2e-47 45 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 112 3e-47 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 111 3e-47 emb[X79432]BOSRK3 B.oleracea SRK3 gene. 107 6e-47 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 108 6e-47 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 111 2e-46 50 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 120 3e-46 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 105 8e-46 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 184 2e-45 emb|AW039406|AW039406 EST281663 tomato mixed elicitor, BTI Lycop... 107 3e-45 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 106 4e-45 55 emblAW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 182 6e-45 dbi|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 109 9e-45 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 116 1e-43 emb|AI775997|AI775997 EST257097 tomato resistant, Cornell Lycope... 177 2e-43

emb|AI895623|AI895623 EST265066 tomato callus, TAMU Lycopersicon... 177 3e-43

emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 171 9e-42 emb|AW706972|AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone... 171 9e-42

60

-- WO-02/22675 --- -PGT/US01/28506

emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 111 4e-41 emb|AW216673|AW216673 EST295387 tomato callus, TAMU Lycopersicon... 169 6e-41 emb|AW154835|AW154835 EST290228 tomato root deficiency, Cornell ... 169 6e-41 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 97 3e-40 emb|AI898854|AI898854 EST268297 tomato ovary, TAMU Lycopersicon ... 163 4e-39 emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone... 162 7e-39 emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 160 4e-38 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 96 2e-37 emb|Z18883|BOSRKRPB B.oleracea encoding S-receptor kinase relate... 156 3e-37 10 emb[Y16999]TCA16999 Theobroma cacao microsatellite DNA, clone mT... 116 5e-37 emb|AW455306|AW455306 EST311844 tomato root during/after fruit s... 124 9e-37 emb|AI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 80 1e-36 emb|AI967314|AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two... 94 3e-36 emblAW223870lAW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 96 6e-36 15 emb|AW224241|AW224241 EST300968 tomato fruit red ripe, TAMU Lyco... 96 6e-36 emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... 110 8e-36 emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 87 1e-34 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 87 1e-34 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 100 2e-34 20 dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 100 2e-34 emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 88 3e-34 emb|Z18862|BOSRKRPD B.oleracea encoding S-receptor kinase protein. 80 5e-34 emb|AI896183|AI896183 EST265626 tomato callus, TAMU Lycopersicon... 96 5e-34 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 120 1e-33 emblAI055189lAI055189 coau0003E19 Cotton Boll Abscission Zone cD... 91 1e-33 ...25 emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 144 2e-33 emb|AV422094|AV422094 AV422094 Lotus japonicus young plants (two... 102 2e-33 emb|AI937984|AI937984 sc06e07.y1 Gm-c1012 Glycine max cDNA clone... 144 2e-33 emb|AW756743|AW756743 sl26f10.yl Gm-c1027 Glycine max cDNA clone... 143 3e-33 30 emblAW290044|AW290044 NXNV009D10F Nsf Xylem Normal wood Vertical... 91 4e-33 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 93 6e-33 emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycope... 142 6e-33 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 117 8e-33 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 76 2e-32 35 gb[U93048]DCU93048 Daucus carota somatic embryogenesis receptor-... 76 2e-32 emb|AW221202|AW221202 EST297671 tomato fruit mature green, TAMU ... 85 4e-32 emb|AI938653|AI938653 sb56g02.y1 Gm-c1018 Glycine max cDNA clone... 82 4e-32 emb|AW201125|AW201125 se98b06.yl Gm-c1027 Glycine max cDNA clone... 86 5e-32 emb|AW697111|AW697111 NF112D03ST1F1028 Developing stem Medicago ... 83 7e-32 40 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 138 8e-32 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 138 8e-32 emb|AI938169|AI938169 sc40d07.yl Gm-c1014 Glycine max cDNA clone... 138 1e-31 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 73 2e-31 emblAI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 88 2e-31 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 136 5e-31 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 88 7e-31 emb|Z18863|BOSRKPGA B.oleracea S-receptor kinase pseudogene. emb|AI895816|AI895816 EST265259 tomato callus, TAMU Lycopersicon... Query= AF081067.3 s at 12500 s at /id source genbank /description 50 gb|aac32192.1| (af081067) iaa-ala hydrolase; iaa-amino acid hydrolase [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1323 letters) 55. Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 60 Score E

(bits) Value

Sequences producing significant alignments:

emb|AW031251|AW031251 EST274626 tomato callus, TAMU Lycopersicon... 372 e-102 emb|AW032461|AW032461 EST276020 tomato callus, TAMU Lycopersicon... 363 2e-99 emb|AI938425|AI938425 sc45a04.yl Gm-c1015 Glycine max cDNA clone... 347 1e-94 5 emb|AW930806|AW930806 EST356649 tomato fruit mature green, TAMU ... 346 2e-94 emb|AW930422|AW930422 EST340795 tomato fruit mature green, TAMU ... 346 3e-94 gb|BE123972|BE123972 EST394097 DSIL Medicago truncatula cDNA clo... 278 8e-92 emb|AW776450|AW776450 EST335515 DSIL Medicago truncatula cDNA cl... 324 1e-87 emblAW034511lAW034511 EST278127 tomato callus, TAMU Lycopersicon... 323 2e-87 10 emb|AI965412|AI965412 sc71d05.y1 Gm-c1016 Glycine max cDNA clone... 322 3e-87 emb|AW185064|AW185064 se86c08.y1 Gm-c1023 Glycine max cDNA clone... 321 6e-87 emb|AI813025|AI813025 2H4 Pine Lambda Zap Xylem library Pinus ta... 321 6e-87 emb|AI895246|AI895246 EST264689 tomato callus, TAMU Lycopersicon... 317 1e-85 emb|AI896622|AI896622 EST266065 tomato callus, TAMU Lycopersicon... 312 3e-84 15 gb|BE021087|BE021087 sm55c04.yl Gm-c1028 Glycine max cDNA clone ... 277 2e-78 emb|AW746042|AW746042 WS1_39_B06.b1_A002 Water-stressed 1 (WS1) ... 277 1e-73 . gb|BE021086|BE021086 sm55c03.yl Gm-c1028 Glycine max cDNA clone ... 276 2e-73 emb|AW934118|AW934118 EST359961 tomato fruit mature green, TAMU ... 274 1e-72 emb|AW649568|AW649568 EST328022 tomato germinating seedlings, TA... 264 1e-69 emb|AW694276|AW694276 NF074C12ST1F1097 Developing stem Medicago ... 261 1e-68 20 emb|AW719214|AW719214 LjNEST1c1r Lotus japonicus nodule library,... 257 1e-67 emb|AW279413|AW279413 sf79c03.y1 Gm-c1019 Glycine max cDNA clone... 253 1e-66 emb[AW032091]AW032091 EST275545 tomato callus, TAMU Lycopersicon... 252 6e-66 emb|AW233984|AW233984 sf32g07.y1 Gm-c1028 Glycine max cDNA clone... 242 6e-63 25 emb|AI729732|AI729732 BNLGHi14072 Six-day Cotton fiber Gossypium... 241 8e-63 emb|AW233987|AW233987 sf32g10.y1 Gm-c1028 Glycine max cDNA clone... 239 4e-62 emb|AW648744|AW648744 EST327198 tomato germinating seedlings, TA... 237 1e-61 emb|AW931177|AW931177 EST357020 tomato fruit mature green, TAMU ... 237 1e-61 emb|AW616709|AW616709 EST323120 L. hirsutum trichome, Cornell Un... 237 1e-61 30 emb[AW686159]AW686159 NF034F08NR1F1000 Nodulated root Medicago t... 231 7e-60 emb|AW234471|AW234471 sf25e09.y1 Gm-c1028 Glycine max cDNA clone... 227 2e-58 emb|AW266116|AW266116 L30-2803T3 Ice plant Lambda Uni-Zap XR exp... 178 3e-58 emb|AI727696|AI727696 BNLGHi8625 Six-day Cotton fiber Gossypium ... 216 5e-58 emb]AW201351|AW201351 sf02a12.yl Gm-c1027 Glycine max cDNA clone... 183 3e-57 35 emb|AI728658|AI728658 BNLGHi11350 Six-day Cotton fiber Gossypium... 222 5e-57 emb[AW348121]AW348121 GM210001A11H6R Gm-r1021 Glycine max cDNA 3... 161 6eemb|AW596930|AW596930 sj84f04.yl Gm-c1034 Glycine max cDNA clone... 210 1e-53 emb|AW559656|AW559656 EST314768 DSIR Medicago truncatula cDNA cl... 208 1e-52 40 emb|AW220836|AW220836 EST297305 tomato fruit mature green, TAMU ... 204 1e-51 emb|AW782248|AW782248 sm03d05.yl Gm-c1027 Glycine max cDNA clone... 204 1e-51 emb|AW775988|AW775988 EST335053 DSIL Medicago truncatula cDNA cl... 201 1e-50 emb|AI444000|AI444000 sa29b03.yl Gm-c1004 Glycine max cDNA clone... 199 6e-50 emblAW202407|AW202407 sf14f07.yl Gm-c1027 Glycine max cDNA clone... 198 1e-49. emblAI779032|AI779032 EST259911 tomato susceptible, Cornell Lyco... 198 1e-49 45 emb|AW035625|AW035625 EST281363 tomato callus, TAMU Lycopersicon... 197 1e-49 emb|AI782331|AI782331 EST263210 tomato susceptible, Cornell Lyco... 191 1e-47 emb|AI440607|AI440607 sa68d03.yl Gm-c1004 Glycine max cDNA clone... 190 2e-47 emb|AW685271|AW685271 NF025F04NR1F1000 Nodulated root Medicago t... 189 4e-47 50 emblAW290830|AW290830 NXNV047E02F Nsf Xylem Normal wood Vertical... 188 6e-47 emb|AW039575|AW039575 EST282023 tomato mixed elicitor, BTI Lycop... 186 4e-46 emb|AW906099|AW906099 EST342220 potato stolon, Cornell Universit... 185 8e-46 emb|AW931325|AW931325 EST357168 tomato fruit mature green, TAMU ... 185 8e-46 emb[AW202273]AW202273 sf13b01.y1 Gm-c1027 Glycine max cDNA clone... 182 5e-45 55 emb|AW096584|AW096584 EST289764 tomato mixed elicitor, BTI Lycop... 181 1e-44 emb|AW559298|AW559298 EST306341 DSIR Medicago truncatula cDNA cl... 181 1e-44 emb|AW220837|AW220837 EST297306 tomato fruit mature green, TAMU ... 180 2e-44 emb|AW746169|AW746169 WS1 39 B06.gl A002 Water-stressed 1 (WS1) ... 127 4e-44 emb[AW677446]AW677446 DG1 7 D07.b1 A002 Dark Grown 1 (DG1) Sorgh... 178 7e-44 60 emb|AW559359|AW559359 EST314407 DSIR Medicago truncatula cDNA cl... 178 9e-44 emb|AW616711|AW616711 EST323122 L. hirsutum trichome, Cornell Un... 177 1e-43

---WO-02/22675 PCT/US01/28506

emb|AW310207|AW310207 sf32g10.x1 Gm-c1028 Glycine max cDNA clone... 176 4e-43 emb|AW617757|AW617757 EST324264 L. hirsutum trichome, Cornell Un... 173 2e-42 emb|AI054863|AI054863 coau0002F22 Cotton Boll Abscission Zone cD... 103 8e-42 emb|AW736524|AW736524 EST332538 KV3 Medicago truncatula cDNA clo... 169 5e-41 emb|AI775651|AI775651 EST256751 tomato resistant, Cornell Lycope... 168 1e-40 emb|AW310204|AW310204 sf32g07.x1 Gm-c1028 Glycine max cDNA clone... 166 5e-40 emb[AI489091]AI489091 EST247430 tomato ovary, TAMU Lycopersicon ... 162 4e-39 emb[AW567617]AW567617 si65e08.yl Gm-r1030 Glycine max cDNA clone... 157 le-37 emb|AJ005340|LUAJ5340 Linum usitatissimum mRNA for IAA amidohydr... 156 3e-37 emb|AW277663|AW277663 sf85a06.yl Gm-c1019 Glycine max cDNA clone... 155 1e-36 emb|AI736325|AI736325 sb27a06.yl Gm-c1009 Glycine max cDNA clone... 149 6e-35 emb[AW685732]AW685732 NF034F02NR1F1000 Nodulated root Medicago t... 122 1e-33 emb|AI781477|AI781477 EST262356 tomato susceptible, Cornell Lyco... 113 3e-32 emb|AW980900|AW980900 EST392053 GVN Medicago truncatula cDNA clo... 139 5e-32 15 emb|AI778980|AI778980 EST259859 tomato susceptible, Cornell Lyco... 138 1e-31 emb[AI773172]AI773172 EST254272 tomato resistant, Cornell Lycope... 133 2e-30 gb|BE054249|BE054249 GA_ Ea0033L21f Gossypium arboreum 7-10 dpa ... 120 3e-30 emb|AW220773|AW220773 EST297242 tomato fruit mature green, TAMU ... 128 1e-28 emb|AW398085|AW398085 EST297968 L. pennellii trichome, Cornell U... 100 1e-28 20 emb|AI725556|AI725556 BNLGHi12118 Six-day Cotton fiber Gossypium... 125 7e-28 emb|AV407386|AV407386 AV407386 Lotus japonicus young plants (two... 105 2e-25 emb|AV425676|AV425676 AV425676 Lotus japonicus young plants (two... 115 1e-24 emb|AW649713|AW649713 EST328167 tomato germinating seedlings, TA... 114 2e-24 emb|AW102170|AW102170 sd84c02.yl Gm-c1009 Glycine max cDNA clone... 114 2e-24 emb|AW091914|AW091914 EST285094 tomato mixed elicitor, BTI Lycop... 112 5e-24 25 emb|AW039945|AW039945 EST282436 tomato mixed elicitor, BTI Lycop... 112 5e-24 emb|AW928798|AW928798 EST337586 tomato flower buds 8 mm to pre-a... 111 1e-23 emb|AQ911427|AQ911427 LMAJFV1_ln04f02.x1 Leishmania major FV1 ra... 69 1e-21 emb|AW042912|AW042912 ST27A02 Pine TriplEx shoot tip library Pin... 92 7e-21 30 emb|AT000037|AT000037 AT000037 Apple young fruit cDNA library Ma... 101 1e-20 gb|BE049708|BE049708 NXNV_142_E09_F Nsf Xylem Normal wood Vertic... 100 3e-20 emb|AW684765|AW684765 NF021G11NR1F1000 Nodulated root Medicago t... 98 1e-19 emb|AW423725|AW423725 sh50h06.yl Gm-c1017 Glycine max cDNA clone... 98 1e-19 emb|AW278733|AW278733 sf96f12.yl Gm-c1019 Glycine max cDNA clone... 95 8e-19 35 emb|AW495793|AW495793 NXNV_065_E02_FF Nsf Xylem Normal wood Vert... 94 2e-18 emb|AW568805|AW568805 si61d03.yl Gm-r1030 Glycine max cDNA clone... 89 7e-17 emb|AQ948883|AQ948883 Sheared DNA-46E23.TF Sheared DNA Trypanoso... 69 1e-16 emb|AI974654|AI974654 T113109e KV2 Medicago truncatula cDNA clon... 79 4e-16 emb|AW255631|AW255631 ML690 peppermint glandular trichome Mentha... 86 7e-16 40 emb|AW102109|AW102109 sd83c02.yl Gm-c1009 Glycine max cDNA clone... emb|X68950|TRUROCAN T.repens gene for urocanase.

Query= AF049236.28_at 12521_at /id_source genbank /description gb|aac14413.1| (af049236) unknown [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1347 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

45

50

55

60

Score E

Sequences producing significant alignments:

(bits) Value

emb|AB012932|AB012932 Vigna radiata mRNA for Ca2+/H+ exchanger, ... 324 e-141 emb|AW119450|AW119450 sd47b12.yl Gm-c1016 Glycine max cDNA clone... 328 7e-89 emb|AW395054|AW395054 sh38h04.yl Gm-c1017 Glycine max cDNA clone... 323 2e-87 emb|AI748459|AI748459 sb53b12.yl Gm-c1016 Glycine max cDNA clone... 321 6e-87 emb|AB018526|AB018526 Ipomoea nil mRNA for H+/Ca2+ exchanger 2, ... 262 4e-86 emb|AW132719|AW132719 se09c07.yl Gm-c1013 Glycine max cDNA clone... 293 2e-78

--- WO 02/22675 --- PCT/US01/28506

```
gb|BE059799|BE059799 sn37c09.yl Gm-c1016 Glycine max cDNA clone ... 270 1e-71
      emb|AW424368|AW424368 sh64g04.yl Gm-c1015 Glycine max cDNA clone... 221 6e-70
      emb|AW283631|AW283631 LG1_242_D12.g1_A002 Light Grown 1 (LG1) So... 243 2e-63
      5
      emb|AW648038|AW648038 EST326492 tomato germinating seedlings, TA... 230 2e-59
      emb|AW132572|AW132572 se05h06.y1 Gm-c1013 Glycine max cDNA clone... 151 3e-52
      emb|AW399625|AW399625 EST310125 L. pennellii trichome, Cornell U... 154 4e-49
      gb|U18944|SCU18944 Saccharomyces cerevisiae putative transmembra... 195 5e-49
      gb|U36603|SCU36603 Saccharomyces cerevisiae vacuolar H+/Ca2+ exc... 195 5e-49
      emb|Z74176|SCYDL128W S.cerevisiae chromosome IV reading frame OR... 195 5e-49
      emb|AJ001273|SCMNR1W30 Saccharomyces cerevisiae MNR1 gene, strai... 194 1e-48
      emb|AW737408|AW737408 EST338751 tomato flower buds, anthesis, Co... 149 5e-48
      emb|AJ001272|SCMNR1MNR Saccharomyces cerevisiae mnr1 gene, strai... 191 1e-47
      emb|AI896399|AI896399 EST265830 tomato callus, TAMU Lycopersicon... 190 2e-47
15
      emb|AF053229|AF053229 Neurospora crassa calcium/proton exchanger... 167 3e-46
      emb|AW329785|AW329785 N201056e rootphos(-) Medicago truncatula c... 168 4e-46
      emb|AW471762|AW471762 si15e11.yl Gm-c1029 Glycine max cDNA clone... 99 8e-43
      emb|AW133119|AW133119 se14e12.yl Gm-c1013 Glycine max cDNA clone... 173 3e-42
      emb|AW459585|AW459585 sh89a07.y1 Gm-c1016 Glycine max cDNA clone... 164 1e-39
20
      emb|AL022598|SPCC1795 S.pombe chromosome III cosmid c1795.
                                                                     .150 1e-39
      emb|AL035247|SPCC895 S.pombe chromosome III cosmid c895.
                                                                    150 le-39
      emb|AW934664|AW934664 EST353556 tomato flower buds 0-3 mm, Corne... 120 1e-39
      emb|AW508855|AW508855 si41b10.y1 Gm-r1030 Glycine max cDNA clone... 136 3e-39
      emb|AW034341|AW034341 EST277912 tomato callus, TAMU Lycopersicon... 159 4e-38
25
      emb|AI484823|AI484823 EST243084 tomato ovary, TAMU Lycopersicon ... 106 2e-35
      emb|AW931722|AW931722 EST357565 tomato fruit mature green, TAMU ... 145 6e-34
      emb|AW289857|AW289857 NXNV007A07F Nsf Xylem Normal wood Vertical... 145 8e-34
      emb|AW423904|AW423904 sh57f03.y1 Gm-c1015 Glycine max cDNA clone... 144 1e-33
      emb|AW691013|AW691013 NF036F12ST1F1000 Developing stem Medicago ... 105 9e-33
30
      emb|AW737653|AW737653 EST339080 tomato flower buds, anthesis, Co... 140 3e-32
      emb|AI900767|AI900767 sb93a03.y1 Gm-c1017 Glycine max cDNA clone... 83 3e-31
      emb|AW329767|AW329767 N201036e rootphos(-) Medicago truncatula c... 136 3e-31
      emb|AW695100|AW695100 NF091E10ST1F1082 Developing stem Medicago ... 98 1e-30
      emb|AW596212|AW596212 si99e01.y1 Gm-c1032 Glycine max cDNA clone... 86 2e-30
35
      emb|AI899610|AI899610 EST269053 tomato susceptible, Cornell Lyco... 121 7e-30
      emb|AW688561|AW688561 NF009A06ST1F1000 Developing stem Medicago ... 80 2e-29
      emb|AW929865|AW929865 EST354135 tomato flower buds 8 mm to pre-a... 88 9e-29
      emb|AI780101|AI780101 EST260980 tomato susceptible, Cornell Lyco... 88 8e-28
      emb|AW689061|AW689061 NF014H11ST1F1000 Developing stem Medicago ... 87 3e-27
40
      emb|AW691346|AW691346 NF043G04ST1F1000 Developing stem Medicago ... 85 4e-27
      emb|AW697283|AW697283 NF115A12ST1F1088 Developing stem Medicago ... 85 5e-27
      emb|AW690182|AW690182 NF029D06ST1F1000 Developing stem Medicago ... 85 9e-27
      emb[AW694830]AW694830 NF080D09ST1F1077 Developing stem Medicago ... 85 1e-26
      emb|AI211369|AI211369 o6g04a1.rl Aspergillus nidulans 24hr asexu... 121 1e-26
45
      emb[AW394839]AW394839 sh36a06.yl Gm-c1017 Glycine max cDNA clone... 118 1e-25
      emb|AW119664|AW119664 sd50f07.y1 Gm-c1016 Glycine max cDNA clone... 117 1e-25
      emb|AW181027|AW181027 MgA0398r MgA Library Mycosphaerella gramin... 116 3e-25
      emb|AI771453|AI771453 EST252553 tomato ovary, TAMU Lycopersicon ... 84 3e-24
      emb|AW695020|AW695020 NF082E03ST1F1021 Developing stem Medicago ... 76 7e-24
50
      emb|AI211368|AI211368 o6g04a1.fl Aspergillus nidulans 24hr asexu... 111 9e-24
      emb|AW692971|AW692971 NF057G06ST1F1000 Developing stem Medicago ... 85 1e-23
      emb|AI966081|AI966081 sc27a12.yl Gm-c1013 Glycine max cDNA clone... 110 3e-23
      emb|AW696697|AW696697 NF109H04ST1F1043 Developing stem Medicago ... 58 8e-22
      emb|AW690067|AW690067 NF027E05ST1F1000 Developing stem Medicago ... 58 8e-22
55
      emb|AW218225|AW218225 EST303406 tomato radicle, 5 d post-imbibit... 105 1e-21
      emb|AW696232|AW696232 NF104B05ST1F1044 Developing stem Medicago ... 61 1e-19
      emb|AW041446|AW041446 EST284310 tomato mixed elicitor, BTI Lycop... 95 9e-19
      emb|AW041435|AW041435 EST284299 tomato mixed elicitor, BTI Lycop... 95 9e-19
      emb|AW693419|AW693419 NF064H07ST1F1000 Developing stem Medicago ... 58 5e-18
60
      emb|AW432234|AW432234 sh70h05.y1 Gm-c1015 Glycine max cDNA clone... 93 6e-18
      emb|AT002674|AT002674 AT002674 POSLM01 Pleurotus ostreatus cDNA ... 82 1e-14
```

emb|AW310634|AW310634 sg22e01.x1 Gm-c1024 Glycine max cDNA clone... 82 1e-14 emb|AA965697|AA965697 o3g02a1.fl Aspergillus nidulans 24hr asexu... 81 2e-14 emb|AI759554|AI759554 EtESTea22b04.x1 Eimeria S5-2 Sporozoite st... 52 2e-13 emb|AW923051|AW923051 DG1 48 G08.g1 A002 Dark Grown 1 (DG1) Sorg... 74 2e-12 emb|AW695860|AW695860 NF099D07ST1F1061 Developing stem Medicago ... 74 3e-12 emb|AW704472|AW704472 sk53e05.yl Gm-c1019 Glycine max cDNA clone... 74 3e-12 emb|AA901983|AA901983 NCM5F6T7 Mycelial Neurospora crassa cDNA c... 72 9e-12 gb|BE022406|BE022406 sm85d09.yl Gm-c1015 Glycine max cDNA clone ... 72 9e-12 emb|AW694605|AW694605 NF078B03ST1F1027 Developing stem Medicago ... 58 4e-11 10 emb|AI756356|AI756356 EtESTea42h07.y1 Eimeria S5-2 Sporozoite st... 67 3e-10 emb|AW875004|AW875004 00125 leafy spurge Lambda HybriZAP 2.1 two... 47 6e-10 emb|AL116004|CNS01CUK Botrytis cinerea strain T4 cDNA library un... 63 5e-09 emblAI488088|AI488088 EST246410 tomato ovary, TAMU Lycopersicon ... 59 7e-08 emb|AQ325110|AQ325110 mgxb0020F10r CUGI Rice Blast BAC Library P... 58 1e-07 emb|AW694277|AW694277 NF074D01ST1F1012 Developing stem Medicago ... 58 1e-07 15 emb|AI812387|AI812387 1G6 Pine Lambda Zap Xylem library Pinus ta... 54 3e-06 emb|AW985137|AW985137 NXNV_133_D09_F Nsf Xylem Normal wood Verti... 52 8e-06 emb|AW934474|AW934474 EST353378 tomato flower buds 0-3 mm, Corne... 51 1e-05 gb|BE059619|BE059619 sn34f03.yl Gm-c1016 Glycine max cDNA clone ... 50 4e-05' 20 emblAI043540lAI043540 L30-547T3 Ice plant Lambda Uni-Zap XR expr... 48 2e-04 emb|AW221661|AW221661 EST298472 tomato fruit red ripe, TAMU Lyco... 48 2e-04 emb|AW285659|AW285659 LG1_319_G05.g1_A002 Light Grown 1 (LG1) So... 46 5e-04 emb|AI489262|AI489262 EST247601 tomato ovary, TAMU Lycopersicon ... 46 5e-04 emb|AV422679|AV422679 AV422679 Lotus japonicus young plants (two... 46 7e-04 25 emb|AV424693|AV424693 AV424693 Lotus japonicus young plants (two... 46 7e-04 emb|AW287551|AW287551 LG1_242_D12.b1_A002 Light Grown 1 (LG1) So... 46 7e-04 emb|AV425896|AV425896 AV425896 Lotus japonicus young plants (two... 46 7e-04 gb|BE123551|BE123551 NXNV 149 F02 F Nsf Xylem Normal wood Vertic... 44 0.003 emblAV412612IAV412612 AV412612 Lotus japonicus young plants (two... 42 0.012 30 emb|AQ855371|AQ855371 CpG1905B CpIOWAgDNA1 Cryptosporidium parvu... 40 0.030 emb|AW038228|AW038228 EST279885 tomato mixed elicitor, BTI Lycop... 40 0.030 emb|AL114296|CNS01BJ4 Botrytis cinerea strain T4 cDNA library un... 40 0.057 emb|AW285641|AW285641 LG1_319_E05.g1_A002 Light Grown 1 (LG1) So... 39 0.079 35 Ouery= AF033205.2 at 12538 at /id source genbank /description gb|aac02973.1| (af033205) putative pectin methylesterase [arabidopsis thaliana] /blast score 6.00e-38 /ec number /family methylesterase /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbin-40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af033205| /ncgi http://www.ncgr.org/cgi-bin/ff?af033205 (236 letters) Database: plantfungal 45 661,018 sequences; 426,114,510 total letters Searching......done Score 50 Sequences producing significant alignments: (bits) Value emb|Z71753|NPPME3MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34 emb|Z71754|NPPME4MR N.plumbaginifolia mRNa for pectin methyleste... 142 3e-34 emb|Z71752|NPPME2MR N.plumbaginifolia mRNA for pectin methyleste... 142 3e-34 55 emb|AW429110|AW429110 EST306566 tomato flower buds 0-3 mm, Corne... 135 5e-32 emb|AW429158|AW429158 EST306614 tomato flower buds 0-3 mm, Corne... 135 5e-32 emb|AI781139|AI781139 EST262018 tomato susceptible, Cornell Lyco... 135 5e-32 emb|AI780635|AI780635 EST261610 tomato susceptible, Cornell Lyco... 135 5e-32 gb|U49330|SLU49330 Solanum lycopersicum pectin methylesterase (P... 135 5e-32 60 emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 134 1e-31 emb|AW154926|AW154926 EST290291 tomato root deficiency, Cornell ... 134 1e-31

emblX94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. emb|AW458218|AW458218 sh79h10.y1 Gm-c1016 Glycine max cDNA clone... 133 2e-31 emb|AF152172|AF152172 Solanum tuberosum cultivar Desiree pectin ... 132 3e-31 emb|AJ249786|NTA249786 Nicotiana tabacum partial mRNA for pectin... 132 3e-31 emb|AI494978|AI494978 sa93d09.yl Gm-c1004 Glycine max cDNA clone... 132 3e-31 gb|U82973|CSU82973 Citrus sinensis pectinesterase (PECS-1.1) gen... 131 6e-31 emb|AW774676|AW774676 EST333827 KV3 Medicago truncatula cDNA clo... 131 6e-31 emb|AW623150|AW623150 EST321095 tomato flower buds 3-8 mm, Corne... 131 6e-31 gb|U82976|CSU82976 Citrus sinensis pectinesterase mRNA, complete... 131 6e-31 emb[X97762]STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 131 7e-31 emb|X67425|PSPMEAG Pisum sativum pmeA gene for pectinesterase. emb|AF056493|AF056493 Pisum sativum pectin methylesterase mRNA, ... 131 1e-30 emb|AF081457|AF081457 Pisum sativum pectin methylesterase (rcpme... 131 1e-30 emb|AW329215|AW329215 N200427e rootphos(-) Medicago truncatula c... 130 2e-30 15 emb|AW257345|AW257345 EST305482 KV2 Medicago truncatula cDNA clo... 130 2e-30 emb|AI781140|AI781140 EST262019 tomato susceptible, Cornell Lyco... 129 3e-30 emb|AI441604|AI441604 sa68e03.y1 Gm-c1004 Glycine max cDNA clone... 129 3e-30 emblAI166540|AI166540 xylem.est.362 Poplar xylem Lambda ZAPII li... 129 4e-30 emb[X68029]PVVPE2 P.vulgaris PvVPE2 mRNA for pectin esterase. 20 emb|AW784073|AW784073 NXNV 117 D06 F Nsf Xylem Normal wood Verti... 126 2e-29 emb|AW429112|AW429112 EST306568 tomato flower buds 0-3 mm, Corne... 126 3e-29 emb|AW888107|AW888107 NXNV_129_C06_F Nsf Xylem Normal wood Verti... 125 5e-29 emb|AW774488|AW774488 EST333639 KV3 Medicago truncatula cDNA clo... 124 9e-29 emb|AF152171|AF152171 Solanum tuberosum cultivar Desiree pectin ... 121 8e-28 25 emb|A17010|A17010 tomato fruit pectin esterase seq ID no1. emblAW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 121 1e-27 emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 121 1e-27 emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 121 1e-27 gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 121 1e-27 30 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 121 1e-27 emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 121 1e-27 emb|X74638|LEPEC1 L.esculentum mRNA for pectin esterase. emb|AW696177|AW696177 NF103C11ST1F1085 Developing stem Medicago ... 121 1e-27 emb|AW760550|AW760550 sl51g07.yl Gm-c1027 Glycine max cDNA clone... 120 2e-27 35. emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 119 3e-27 gb|U50986|SLU50986 Solanum lycopersicum pectin methylesterase PM... 119 4e-27 gb|U70675|LEU70675 Lycopersicon esculentum fruit-specific pectin... 118 6e-27 gb|U70676|LEU70676 Lycopersicon esculentum pection methylesteras... 118 6e-27 emb|Z71751|NPPME1MR N.plumbaginifolia mRNA for pectin methyleste... 118 8e-27 40 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 118 8e-27 emb|AF229849|AF229849 Vigna radiata pectin methylesterase isofor... 118 8e-27 gb[U70677[LEU70677 Lycopersicon esculentum (LePME1) gene, partia... 118 8e-27 gb|U82974|CSU82974 Citrus sinensis pectinesterase (PECS-1.2) gen... 117 le-26 emb|AI897776|AI897776 EST267219 tomato ovary, TAMU Lycopersicon ... 117 2e-26 45 gb|U50985|SLU50985 Solanum lycopersicum pectin methylesterase PM... 116 3e-26 emb|AW758821|AW758821 NXNV 091 A04 F Nsf Xylem Normal wood Verti... 116 3e-26 emb|A17011|A17011 tomato fruit pectin esterase with pPel DNA seq... 116 3e-26 emb[X74639]LEPEC2 L.esculentum mRNA for pectin esterase clone. 116 3e-26 emb[X07910]LEPECES Tomato mRNA for pectin esterase. 116 3e-26 50 emb|A15983|A15983 L.esculentum mRNA for pectin esterase. 116 3e-26 emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 116 3e-26 emblAW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 115 5e-26 emb[X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 115 5e-26 emb|A24196|A24196 L.esculentum pectin esterase clone pPE1. 113 2e-25 55 emblAW687047|AW687047 NF005D06RT1F1057 Developing root Medicago ... 113 2e-25 emb|AW424141|AW424141 sh61d11.yl Gm-c1015 Glycine max cDNA clone... 112 6e-25 emb|AW398532|AW398532 EST309032 L. pennellii trichome, Cornell U... 111 8e-25 emb|AW163926|AW163926 Ljirnpest17-358-e10 Ljirnp Lambda HybriZap... 110 2e-24 60 emb[AW620942]AW620942 sj95g05.y1 Gm-c1023 Glycine max cDNA clone... 108 5e-24 emb|AI440753|AI440753 sa53f07.yl Gm-c1004 Glycine max cDNA clone... 108 7e-24

gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 84 2e-23 emb[AI731654|AI731654 BNLGHi10367 Six-day Cotton fiber Gossypium... 106 4e-23 emb|AI731653|AI731653 BNLGHi10366 Six-day Cotton fiber Gossypium... 106 4e-23 gb|U82975|CSU82975 Citrus sinensis pectinesterase (PECS-2.1) gen... 81 7e-23 gb|BE123534|BE123534 NXNV 149 D04 F Nsf Xylem Normal wood Vertic... 103 2e-22 emb|AI967495|AI967495 Ljirnpest03-197-b4 Ljirnp Lambda HybriZap ... 102 3e-22 emb|AB029461|AB029461 Salix gilgiana SgPME1 mRNA for pectin meth... 102 4e-22 emb|AW647968|AW647968 EST326422 tomato germinating seedlings, TA... 100 3e-21 emb|AW617630|AW617630 EST324041 L, hirsutum trichome, Cornell Un... 97 2e-20 emb[Y07899]CPSPE1 C.papaya mRNA for pectinesterase. 97 3e-20 emb|AW666437|AW666437 sk36e11.yl Gm-c1028 Glycine max cDNA clone... 95 7e-20 gb|L27101|PETPPE1A Petunia inflata pectinesterase (PPE1) gene, c... 92 6e-19 emb|X95991|PPPECESTR P.persica mRNA for pectin esterase. emb|AW598693|AW598693 sj94f11.yl Gm-c1023 Glycine max cDNA clone... 91 1e-18 15 emblAW256326|AW256326 EST304533 KV2 Medicago truncatula cDNA clo... 87 3e-17 emb|AW349192|AW349192 GM210004A21F6R Gm-r1021 Glycine max cDNA 3... 86 4e-17 emb|AW287387|AW287387 LG1 303 C07.b1 A002 Light Grown 1 (LG1) So... 82 6e-16 emb|AW278130|AW278130 sf40b03.yl Gm-c1009 Glycine max cDNA clone... 69 7e-16 emb|AW349615|AW349615 GM210006A11A5R Gm-r1021 Glycine max cDNA 3... 79 7e-15 20 emb|AA556385|AA556385 240 Loblolly pine C Pinus taeda cDNA clone... 71 1e-12 emb|AW218132|AW218132 EST303313 tomato radicle, 5 d post-imbibit... 55 2e-11 emb|AW648115|AW648115 EST326569 tomato germinating seedlings, TA... 64 2e-10 emb|AW220222|AW220222 EST302705 tomato root during/after fruit s... 62 4e-10 25 Query= AL079344.155 at 12556 at /id source genbank /description emblcab45330.1| (al079344) nucleotide pyrophosphatase-like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|a1079344| /ncgi 30 http://www.ncgr.org/cgi-bin/ff?al079344 (1386 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 35 Searching.....done Score E Sequences producing significant alignments: (bits) Value 40 emb|AW686852|AW686852 NF003B08RT1F1000 Developing root Medicago ... 226 3e-79 emb|AW563733|AW563733 LG1 248 C01.g1 A002 Light Grown 1 (LG1) So... 205 5e-52 gb|BE053112|BE053112 GA Ea0031A01f Gossypium arboreum 7-10 dpa ... 166 2e-50 emb|AV409759|AV409759 AV409759 Lotus japonicus young plants (two... 165 4e-44 45 emb|AW704801|AW704801 sk55f12.yl Gm-c1019 Glycine max cDNA clone... 148 3e-43 emb|AL034352|SPBC725 S.pombe chromosome II cosmid c725. gb|C96280|C96280 C96280 Marchantia polymorpha immature sex organ... 89 9e-37 emb|AW599232|AW599232 gb12b03.y1 Moss EST library PPN Physcomitr... 154 1e-36 emb|AW306350|AW306350 se49e12.yl Gm-c1017 Glycine max cDNA clone... 116 2e-33 50 emb|AV409781|AV409781 AV409781 Lotus japonicus young plants (two... 140 2e-32 emb|AI812708|AI812708 18B6 Pine Lambda Zap Xylem library Pinus t... 138 9e-32 emblAW626639|AW626639 NXNV067G03 Nsf Xylem Normal wood Vertical ... 119 4e-26 emb[X59720]SCCHRIII S.cerevisiae chromosome III complete DNA seq... 68 2e-13 gb[U18530]SCE9871 Saccharomyces cerevisiae chromosome V cosmids ... '61 3e-10 55 emb|AQ397058|AQ397058 mgxb0003P19f CUGI Rice Blast BAC Library P... 40 7e-06 emb|AV427570|AV427570 AV427570 Lotus japonicus young plants (two... 52 8e-06 gb[H74550]H74550 501 Random-primed Brassica napus cDNA clone RRM... 49 1e-04 emb|AW186036|AW186036 se62g09.y1 Gm-c1019 Glycine max cDNA clone... 46 5e-04 emb[AW832253]AW832253 sm21f10.yl Gm-c1027 Glycine max cDNA clone... 46 5e-04 60 emb[AW596708]AW596708 sj15g06.yl Gm-c1032 Glycine max cDNA clone... 46 5e-04 emb|AW156479|AW156479 se26f12.yl Gm-c1015 Glycine max cDNA clone... 44 0.002

```
emb|AQ845931|AQ845931 LMAJFV1_lm11d03.y1 Leishmania major FV1 ra... 44 0.002
      emb|AW330350|AW330350 TENU5096 T.cruzi epimastigote normalized c... 41 0.016
      emb|AI901162|AI901162 sc21e02.yl Gm-c1013 Glycine max cDNA clone... 41 0.016
      emb|AB004539|AB004539 Schizosaccharomyces pombe 38 kb genomic DN... 38 0.020
 5
      emb|AL021766|SPBC27B12 S.pombe chromosome II cosmid c27B12.
                                                                        38 0.020
      emb|AQ502678|AQ502678 V50A6 mTn-3xHA/lacZ Insertion Library Sacc... 40 0.059
      emb|AI919929|AI919929 1459 Pine Lambda Zap Xylem library Pinus t... 38 0.15
      emb|AQ872628|AQ872628 V26H10 mTn-3xHA/lacZ Insertion Library, st... 38 0.21
      emb|Z49337|SCYJL062W S.cerevisiae chromosome X reading frame ORF... 38 0.21
10
      emb|Z34288|SCXCDNA S.cerevisiae (S288C) X chromosome DNA (17137bp). 38 0.21
      emb|AW349789|AW349789 GM210006B10E8R Gm-r1021 Glycine max cDNA 3... 37 0.29
      emb|AW703931|AW703931 sk25h05.y1 Gm-c1028 Glycine max cDNA clone... 37 0.29
      emb|AW733463|AW733463 sk73h10.yl Gm-c1016 Glycine max cDNA clone... 28 0.38
      emb|AW100199|AW100199 sd26h06.yl Gm-c1012 Glycine max cDNA clone... 36 0.54
15
      emb|AW599349|AW599349 gb13g12.y1 Moss EST library PPN Physcomitr... 36 0.54
      emb|Z73136|SCYLL031C S.cerevisiae chromosome XII reading frame O... 29 0.61
      emb|AA898221|AA898221 NCC2C5T7 Conidial Neurospora crassa cDNA c... 35 1.0
      emb|AF130334|AF130334 Bruguiera cylindrica internal transcribed ... 35 1.9
      gb|B13384|B13384 jd152 Trypanosome Shotgun M13 genomic Trypanoso... 34 2.7
20
      emb|AQ500377|AQ500377 V40F1 mTn-3xHA/lacZ Insertion Library Sacc... 34 2.7
      emb|AW102097|AW102097 sd83a09.v1 Gm-c1009 Glycine max cDNA clone... 34 2.7
      emb|AW334235|AW334235 S32B4 AGS-1 Pneumocystis carinii f. sp. ca... 34 3.6
      emb|AW648115|AW648115 EST326569 tomato germinating seedlings, TA... 34 3.6
      emb|AQ500705|AQ500705 V33B7 mTn-3xHA/lacZ Insertion Library Sacc... 34 3.6
25
      emb|AW220222|AW220222 EST302705 tomato root during/after fruit s... 34 3.6
      emb|AC016528|AC016528 Leishmania major chromosome 35 clone L4123... 34 3.6
      gb|M55447|BLYRCAA2 Hordeum vulgare rubisco activase (RcaA2) mRNA... 34 3.6
      gb[BE054837]BE054837 GA_Ea0002C16f Gossypium arboreum 7-10 dpa ... 33 5.0
      gb|BE055267|BE055267 GA_Ea0004K24f Gossypium arboreum 7-10 dpa ... 33 5.0
30
      emb|AW109433|AW109433 gate0004K24f Gossypium arboreum 7-10 dpa f... 33 5.0
      emb|AW666951|AW666951 GA_Ea0006H12 Gossypium arboreum 7-10 dpa ... 33 5.0
      emblAW661478|AW661478 833006F08.yl C. reinhardtii CC-125 -S, Lam... 33 5.0
      emb|AW731558|AW731558 GA_Ea0030J12 Gossypium arboreum 7-10 dpa ... 33 5.0
      emb|AL031909|LMFL302 Leishmania major Friedlin chromosome 4 cosm... 33 5.0
35.
      emb|AW108953|AW108953 gate0002C16f Gossypium arboreum 7-10 dpa f... 33 5.0
      dbj|D83464|D83464 Candida intermedia 26S ribosomal RNA, partial ... 33 5.0
      emb|AW730349|AW730349 GA Ea0023E10 Gossypium arboreum 7-10 dpa ...
      emb|AW831354|AW831354 sm32e12.y1 Gm-c1028 Glycine max cDNA clone...
40
      emb|AI211253|AI211253 o0g06a1.rl Aspergillus nidulans 24hr asexu... 33 6.9
      emb|AF197953|AF197953 Toxoplasma gondii histone acetyltransferas... 33 6.9
      emb|AL353822|NC15E6 Neurospora crassa DNA linkage group V Cosmid... 33 6.9
      gb|U68555|SPU68555 Saccharomyces paradoxus 26S ribosomal RNA gen... 33 6.9
      emb|AB040996|AB040996 Saccharomyces sp. IFO 1815 gene for 26S rR... 33 6.9
45
      emb|AB040995|AB040995 Saccharomyces sp. IFO 1802 gene for 26S rR... 33 6.9
      emb|AW667927|AW667927 GA Ea0011M14 Gossypium arboreum 7-10 dpa ... 33 6.9
      emb|AE001274|AE001274 Leishmania major chromosome 1, complete se... 33 6.9
      emb|AF130335|AF130335 Bruguiera exaristata internal transcribed ... 33 6.9
      emb|AZ211966|AZ211966 Sheared DNA-106D6.TR Sheared DNA Trypanoso... 33 6.9
50
      emb|AV393427|AV393427 AV393427 Chlamydomonas reinhardtii C9 Chla... 33 6.9
      emb|AI664729|AI664729 TENG0690 T. Cruzi epimastigote normalised ... 33 6.9
      emb|AW720110|AW720110 LjNEST14a8r Lotus japonicus nodule library... 27 7.6
      gb[U30821|CPU30821 Cyanophora paradoxa cyanelle, complete genome.
      emb|AQ449508|AQ449508 500001C11.x1 CpIOWAM13mp18gDNA1 Cryptospor... 32 9.4
55
      emb|AU089911|AU089911 AU089911 Hordeum vulgare subsp. vulgare Up... 32 9.4
      emb|AW219224|AW219224 EST301706 tomato root during/after fruit s... 32 9.4
      emb|AA739819|AA739819 584 PtIFG2 Pinus taeda cDNA clone 8935M 3'... 32 9.4
      emb|AW335019|AW335019 S42B7 AGS-1 Pneumocystis carinii f. sp. ca... 32 9.4.
      emb|AU089924|AU089924 AU089924 Hordeum vulgare subsp. vulgare Up... 32 9.4
60
      emb|AQ641373|AQ641373 RPCI93-DpnII-28A9.TV RPCI93-DpnII Trypanos... 32 9.4
      emb|AW695807|AW695807 NF098G11ST1F1087 Developing stem Medicago ... 32 9.4
```

emb|AQ501198|AQ501198 V25G12 mTn-3xHA/lacZ Insertion Library Sac... 32 9.4

Query= X82624.2_at 12574_at /id_source genbank /description emb|caa57944.1| (x82624) srg2at [arabidopsis thaliana] /blast_score 1.00e-25 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|x82624| /ncgi http://www.ncgr.org/cgi-bin/ff?x82624 (147 letters)

10

5

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

15

Score E

Sequences producing significant alignments: (bits) Value emb|AW756217|AW756217 sl17e08.yl Gm-c1036 Glycine max cDNA clone... 96 1e-20 20 emb|AW561018|AW561018 EST316066 DSIR Medicago truncatula cDNA cl... 95 2e-20 gb[L47866]L47866 BNAF1507 Mustard flower buds Brassica rapa cDNA... 94 6e-20 emb[X94986]MEBGLA M.esculenta bglA gene. 94 6e-20 emb|AW257154|AW257154 EST305291 KV2 Medicago truncatula cDNA clo... 93 8e-20 gb[U39228]PAU39228 Prunus avium beta-glucosidase mRNA, partial cds. 93 8e-20 25 emb|AI729894|AI729894 BNLGHi5504 Six-day Cotton fiber Gossypium ... 93 8e-20 gb[U95298[MEU95298 Manihot esculenta linamarase (pLIN-GEN) gene,... 93 8e-20 gb|S35175|S35175 linamarase=beta-glucosidase [Manihot esculenta=... 92 2e-19 emb|AF072736|AF072736 Pinus contorta beta-glucosidase mRNA, comp... 92 2e-19 emb|AW568866|AW568866 si73c03.yl Gm-c1031 Glycine max cDNA clone... 91 4e-19 30 gb|U50201|PSU50201 Prunus serotina prunasin hydrolase precursor ... 90 5e-19 emb|AW560545|AW560545 EST315593 DSIR Medicago truncatula cDNA cl... 90 7e-19 emb|AI900802|AI900802 sb93e10.y1 Gm-c1017 Glycine max cDNA clone... 89 2e-18 gb|BE058816|BE058816 sn21c08.yl Gm-c1016 Glycine max cDNA clone ... 89 2e-18 emb|AW597982|AW597982 sj40c05.yl Gm-c1008 Glycine max cDNA clone... 89 2e-18 35 emb|AW395210|AW395210 sh45c06.yl Gm-c1017 Glycine max cDNA clone... 89 2e-18 emb|AW570004|AW570004 si85e02.y1 Gm-c1031 Glycine max cDNA clone... 89 2e-18 emb|AW733524|AW733524 sk74g01.yl Gm-c1016 Glycine max cDNA clone... 89 2e-18 emb|AW423986|AW423986 sh59a09.yl Gm-c1015 Glycine max cDNA clone... emb|AW423387|AW423387 sh65b01.yl Gm-c1015 Glycine max cDNA clone... 89 2e-18 40 emb|AW597368|AW597368 si91h08.yl Gm-c1031 Glycine max cDNA clone... 88 3e-18 emb|AW569966|AW569966 si83h05.yl Gm-c1031 Glycine max cDNA clone... 88 3e-18 emb|AW569751|AW569751 si79h11.yl Gm-c1031 Glycine max cDNA clone... emb|AW569883|AW569883 si82g07.yl Gm-c1031 Glycine max cDNA clone... 88 3e-18 emb|AW317654|AW317654 sg55e02.y1 Gm-c1025 Glycine max cDNA clone... 87 5e-18 45 emb|AW350857|AW350857 GM210009B10F4R Gm-r1021 Glycine max cDNA 3... 87 5e-18 emb|AW309715|AW309715 sf23f08.x1 Gm-c1028 Glycine max cDNA clone... 87 7e-18 emb|AF221526|AF221526 Prunus serotina prunasin hydrolase isoform... 86 9e-18 emb|AB003089|AB003089 Polygonum tinctorium mRNA for beta-glucosi... 86 9e-18 emb|AW279169|AW279169 sf67c06.yl Gm-c1013 Glycine max cDNA clone... 85 2e-17 50 gb[U72154|BNU72154 Brassica nigra beta-glucosidase (psr3.1) mRNA... 85 2e-17 emb|AW394514|AW394514 sh32a04.y1 Gm-c1017 Glycine max cDNA clone... 84 3e-17 emb[AW202129]AW202129 sf12c05.yl Gm-c1027 Glycine max cDNA clone... 84 3e-17 gb|U26025|PSU26025 Prunus serotina amygdalin hydrolase isoform A... 84 5e-17 dbi|D83177|CSAF26G Costus speciosus mRNA for furostanol glycosid... 83 9e-17 55 emb|AI774009|AI774009 EST255109 tomato resistant, Cornell Lycope... 63 2e-16 emb|AF143377|AF143377 AF143377 Pisum sativum library (Fristensky... 82 2e-16 emb|AI772446|AI772446 EST253546 tomato resistant, Cornell Lycope... 63 3e-16 emb|AW651266|AW651266 EST329720 tomato germinating seedlings, TA... 63 3e-16 emb|AW317658|AW317658 sg55f02.yl Gm-c1025 Glycine max cDNA clone... 81 3e-16 60 emb|AW042637|AW042637 ST24C01 Pine TriplEx shoot tip library Pin... 60 4e-16

emb|AW101162|AW101162 sd74h08.yl Gm-c1008 Glycine max cDNA clone... 81 4e-16

emb|AW132549|AW132549 se05f01.yl Gm-c1013 Glycine max cDNA clone... gb[L41869]BLYBGQ6 Hordeum vulgare L. beta-glucosidase (BGQ60) ge... 65 6e-16 emb|AB003110|AB003110 Trichoderma reesei bgl2 gene for bete-gluc... 80 8e-16 emb|AW760442|AW760442 sl50d01.yl Gm-c1027 Glycine max cDNA clone... 79 1e-15 emb|AJ005950|AJ005950 AJ005950 chickpea mRNA CAP-4 Cicer arietin... 79 1e-15 emb|X56734|TRBG361 Trifolium repens mRNA for non-cyanogenic beta... 78 2e-15 emb|AW201515|AW201515 sf04b02.yl Gm-c1027 Glycine max cDNA clone... 78 4e-15 emb|AA415086|AA415086 Mg0020 RCW Lambda Zap Express Library Pyri... '78 4e-15 emb|AI941073|AI941073 sb84a09.yl Gm-c1010 Glycine max cDNA clone... 63 5e-15 10 emb|AW311377|AW311377 sg38b12.yl Gm-c1025 Glycine max cDNA clone... 63 5e-15 emb|AW677220|AW677220 DG1 6 D11.g1 A002 Dark Grown 1 (DG1) Sorgh... 77 7e-15 gb|U33817|SBU33817 Sorghum bicolor dhurrinase mRNA, nuclear gene... 77 7e-15 emb|AW744827|AW744827 LG1 384 D09.g1 A002 Light Grown 1 (LG1) So... 77 7e-15 emb|AW923243|AW923243 DG1_50_B11.g1_A002 Dark Grown 1 (DG1) Sorg... 77 7e-15 15 emb|AW923628|AW923628 DG1 56 E12.g1 A002 Dark Grown 1 (DG1) Sorg... emb|AW922651|AW922651 DG1_20_B09.g1_A002 Dark Grown 1 (DG1) Sorg... 77 7e-15 emb|AW286529|AW286529 LG1 334 A07.g1 A002 Light Grown 1 (LG1) So... 77 7e-15 emb|AI974587|AI974587 T113037e KV2 Medicago truncatula cDNA clon... 65 9e-15 emb|AW676749|AW676749 DG1_14_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 76 1e-14 emb|AB003109|AB003109 Humicola grisea var. thermoidea bgl4 gene ... 76 1e-14 20 emb|AI723853|AI723853 RHIZ1_28_C08.yl_A001 Rhizome1 Sorghum hale... 76 1e-14 emb|AI724790|AI724790 RHIZ1_9_C08.y2_A001 Rhizomel Sorghum halep... 76 1e-14 emb|AW685200|AW685200 NF027E09NR1F1000 Nodulated root Medicago t... 65 1e-14 gb|BE124555|BE124555 EST393590 GVN Medicago truncatula cDNA clon... 65 le-14 25 emb|AW774242|AW774242 EST333393 KV3 Medicago truncatula cDNA clo... 65 1e-14 emb|AW286277|AW286277 LG1 329_G04.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 emb|AW286262|AW286262 LG1_329_E04.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 emb|AW284398|AW284398 LG1_289_B04.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 emb|AW283021|AW283021 LG1_301_G01.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 30 emb|AW284016|AW284016 LG1_264_G03.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 emb|AW282563|AW282563 LG1_312_A09.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 emb|AW282564|AW282564 LG1_312_A08.g1_A002 Light Grown 1 (LG1) So... 76 1e-14 emb|AW565734|AW565734 LG1 348 H08.g1 A002 Light Grown 1 (LG1) So... emb[X82577]BNBGL B.napus mRNA for beta-glucosidase. 35 emb|AF149311|AF149311 Rauvolfia serpentina raucaffricine-O-beta-... gb[BE021518[BE021518 sm59e05.yl Gm-c1028 Glycine max cDNA clone ... 74 4e-14 emb|AF082991|AF082991 Avena sativa beta-D-glucosidase beta subun... 73 9e-14 emb|AW423704|AW423704 sh50f06.yl Gm-c1017 Glycine max cDNA clone... 73 1e-13 emb[X78433]ASLBDG A.sativa L. mRNA for beta-D-glucosidase. 40 emb|AF163097|AF163097 Dalbergia cochinchinensis dalcochinin 8'-O... 62 2e-13 emb|AW733253|AW733253 sk70d08.yl Gm-c1016 Glycine max cDNA clone... 71 3e-13 emb|AW922447|AW922447 DG1_19_F09.g1_A002 Dark Grown 1 (DG1) Sorg... 60 5e-13 emb|AW671821|AW671821 LG1 351_F12.g1 A002 Light Grown 1 (LG1) So... 59 9e-13 gb|BE059820|BE059820 sn37e08.yl Gm-c1016 Glycine max cDNA clone ... 68 3e-12 45 emblAJ133406|DLA133406 Digitalis lanata mRNA for cardenolide 16-... 68 4e-12 emb|AW773684|AW773684 EST332670 KV3 Medicago truncatula cDNA clo... 61 6e-12 emb[AW099840]AW099840 sd17b01.y2 Gm-c1012 Glycine max cDNA clone... 60 6e-12 emb[X67838]BNDNAM B.napus DNA for myrosinase. emb|AW923660|AW923660 DG1_57_B08.g1_A002 Dark Grown 1 (DG1) Sorg... 66 1e-11 50 emb|AW284341|AW284341 LG1 275 C12.gl A002 Light Grown 1 (LG1) So... 66 1e-11 emb[X79080]BNMYRMC B.napus mRNA for myrosinase MC. emb|Z21977|BNMYR1A B.napus Myr1.Bn1 gene encoding myrosinase, th... 66 2e-11 emb|X56733|TRBG104 T.repens mRNA for cyanogenic beta-glucosidase... 52 2e-11 emb|AF016864|AF016864 Orpinomyces sp. PC-2 beta-glucosidase (bgl... 64 5e-11 55 emb[X59881]SAMYRMB1 S.alba thioglucoside glucohydrolase (myrosin... 63 7e-11 emb|AW927073|AW927073 HVSMEg0009H02 Hordeum vulgare pre-anthesis... 57 1e-10 gb[L11258]BNAMYROS Brassica campestris myrosinase gene, complete...

Query= AF024504.13_at 12630_at /id_source genbank /description 60 gb|aaf18681.1|af024504_11 (af024504) unknown protein [arabidopsis thaliana] /blast_score 1.00e-129 /ec_number /family /chip nova

/gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|af024504| /ncgi http://www.ncgr.org/cgi-bin/ff?af024504 (1374 letters)

5

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

10

Score E

Sequences producing significant alignments:

(bits) Value

emb|AW216758|AW216758 EST295472 tomato callus, TAMU Lycopersicon... 119 3e-34 15 emb|AW219044|AW219044 EST301526 tomato root during/after fruit s... 108 7e-33 emblAW031258|AW031258 EST274633 tomato callus, TAMU Lycopersicon... 108 7e-33 emb|AI772760|AI772760 EST253860 tomato resistant, Cornell Lycope... 108 7e-33 emb|AI486533|AI486533 EST244854 tomato ovary, TAMU Lycopersicon ... 71 5e-29 emb[AI898645]AI898645 EST268088 tomato ovary, TAMU Lycopersicon ... 71 6e-28 20 emblAW686482|AW686482 NF041H08NR1F1000 Nodulated root Medicago t... 112 8e-28 emb|AW704059|AW704059 sk27d01.yl Gm-c1028 Glycine max cDNA clone... 119 2e-27 emb|AW350257|AW350257 GM210007B20B11R Gm-r1021 Glycine max cDNA ... 122 5e-27 emb|AW759958|AW759958 s156c04.y1 Gm-c1027 Glycine max cDNA clone... 115 7e-25 emb|AW126130|AW126130 N100327e rootphos(-) Medicago truncatula c... 115 1e-24 25 emb|AI776363|AI776363 EST257463 tomato resistant, Cornell Lycope... 114 1e-24 emb|AI731720|AI731720 BNLGHi10579 Six-day Cotton fiber Gossypium... 112 5e-24 emb|AW034441|AW034441 EST278012 tomato callus, TAMU Lycopersicon... 103 5e-24 emb|AI896076|AI896076 EST265519 tomato callus, TAMU Lycopersicon... 102 1e-23 emb|AI898707|AI898707 EST268150 tomato ovary, TAMU Lycopersicon ... 71 2e-22 30 emb|AW310471|AW310471 sf36e11.x1 Gm-c1028 Glycine max cDNA clone... 105 6e-22 emb|AW219445|AW219445 EST302023 tomato root during/after fruit s... 105 8e-22 emb|AW648110|AW648110 EST326564 tomato germinating seedlings, TA... 105 1e-21 emb|AW831572|AW831572 sm34h08.y1 Gm-c1028 Glycine max cDNA clone... 100 2e-20 gb|BE124541|BE124541 EST393576 GVN Medicago truncatula cDNA clon... 89 8e-20 35 emb|AW671843|AW671843 LG1_352_B09.b1_A002 Light Grown 1 (LG1) So... 64 2e-18 emb|AW564955|AW564955 LG1_313_H09.b1_A002 Light Grown 1 (LG1) So... 64 2e-18 emb|AW329431|AW329431 N200666e rootphos(-) Medicago truncatula c... 93 4e-18 emb|AW929644|AW929644 EST338432 tomato flower buds 8 mm to pre-a... 73 7e-18 emb|AW907159|AW907159 EST343282 potato stolon, Cornell Universit... 60 2e-14 40 emb|AW565825|AW565825 LG1 352 B09.g1 A002 Light Grown 1 (LG1) So... 57 8e-14 emb|AW625736|AW625736 EST319643 tomato radicle, 5 d post-imbibit... 56 8e-14 emb|AI812987|AI812987 2D4 Pine Lambda Zap Xylem library Pinus ta... 52 4e-13 gblBE060164bE060164 HVSMEg0011B20f Hordeum vulgare pre-anthesis... 76 5e-13 emb|AW217067|AW217067 EST295781 tomato callus, TAMU Lycopersicon... 74 2e-12 45 emb|AW398760|AW398760 EST309260 L. pennellii trichome, Cornell U... 54 2e-12 emb|AW694156|AW694156 NF072H06ST1F1059 Developing stem Medicago ... 58 3e-12 emb|AW773860|AW773860 EST332846 KV3 Medicago truncatula cDNA clo... 58 3e-12 emb|AW394635|AW394635 sh33h09.y1 Gm-c1017 Glycine max cDNA clone... 55 3e-12 emb|AW203644|AW203644 sf36e11.yl Gm-c1028 Glycine max cDNA clone... 69 4e-12 50 emb|AI728748|AI728748 BNLGHi11497 Six-day Cotton fiber Gossypium... 57 4e-12 emb|AW697758|AW697758 Str1-D8 Sugar Beet germination cDNA librar... 46 5e-11 emb|AW030302|AW030302 EST273557 tomato callus, TAMU Lycopersicon... 53 7e-11 emb|AW982668|AW982668 HVSMEg0003O06f Hordeum vulgare pre-anthesi... 48 2e-10 emb|AW287116|AW287116 LG1 265 G01.b2 A002 Light Grown 1 (LG1) So... 64 2e-09 55 emb|AW734790|AW734790 sk88g11.y1 Gm-c1035 Glycine max cDNA clone... 42 5e-09 emb|AT000776|AT000776 AT000776 Brassica rapa guard cell Brassica... 62 7e-09 emb|A1775378|A1775378 EST256478 tomato resistant, Cornell Lycope... 42 1e-08 emblAW775488|AW775488 EST334553 DSIL Medicago truncatula cDNA cl... 58 2e-07 emb|AW928719|AW928719 EST337507 tomato flower buds 8 mm to pre-a... 39 2e-07 60 emb|AW282482|AW282482 LG1 313_B10.g1_A002 Light Grown 1 (LG1) So... 57 3e-07 emb|AW225609|AW225609 T210061e KV0 Medicago truncatula cDNA clon... 40 4e-07

---PCT/US01/28506 -WO 02/22675

	emb AT000645 AT000645 AT000645 Brassica rapa guard cell Brassica 56 6e-07
	emb AW731593 AW731593 GA_Ea0030P10 Gossypium arboreum 7-10 dpa 37 1e-06
	emb AW282432 AW282432 LG1_313_H09.g1_A002 Light Grown 1 (LG1) So 55 2e-06
_	emb A1736841 A1736841 sb34c09.yl Gm-c1012 Glycine max cDNA clone 50 5e-05
5	emb AW154916 AW154916 EST290281 tomato root deficiency, Cornell 40 6e-05
	emb AI054948 AI054948 coau0002J14 Cotton Boll Abscission Zone cD 49 7e-05 emb AI487433 AI487433 EST245755 tomato ovary, TAMU Lycopersicon 44 1e-04
	emb A1490477 A1490477 EST248846 tomato ovary, TAMU Lycopersicon 44 1e-04
•	emb A1895257 A1895257 EST264700 tomato callus, TAMU Lycopersicon 47 4e-04
10	emb AW564044 AW564044 LG1_281_A09.b1_A002 Light Grown 1 (LG1) So 47 4e-04
	emb AW565728 AW565728 LG1_348_E11.g1_A002 Light Grown 1 (LG1) So 47 4e-04
	emb AW922753 AW922753 DG1_45_C05.g1_A002 Dark Grown 1 (DG1) Sorg 47 4e-04
	emb AW746301 AW746301 WS1_40_G05.g1_A002 Water-stressed 1 (WS1) 47 4e-04
1.5	emb AW033344 AW033344 EST276915 tomato callus, TAMU Lycopersicon 40 5e-04
15	emb AI486814 AI486814 EST245136 tomato ovary, TAMU Lycopersicon 46 5e-04
	emb AI486642 AI486642 EST244963 tomato ovary, TAMU Lycopersicon 44 6e-04
	emb AW774292 AW774292 EST333443 KV3 Medicago truncatula cDNA clo 46 7e-04 emb AW472252 AW472252 si21g12.yl Gm-c1029 Glycine max cDNA clone 46 7e-04
	emb AW705448 AW705448 sk49c01.yl Gm-c1019 Glycine max cDNA clone 35 0.001
20 ·	emb A1728904 A1728904 BNLGHi11968 Six-day Cotton fiber Gossypium 41 0.002
	emb A1726718 A1726718 BNLGHi6425 Six-day Cotton fiber Gossypium 41_0.002
•	emb AW011001 AW011001 ST15E02 Pine TriplEx shoot tip library Pin 45 0.002
	emb AI563253 AI563253 EST00377 watermelon lambda zap library Cit 44 0.002
25	emb AW568784 AW568784 si61a06.yl Gm-r1030 Glycine max cDNA clone 44 0.002
25	emb AI485669 AI485669 EST243990 tomato ovary, TAMU Lycopersicon 44 0.003 emb AW154917 AW154917 EST290282 tomato root deficiency, Cornell 44 0.003
	emb AW154917 AW154917 EST290282 tomato root deficiency, Cornell 44 0.003 emb AI895825 AI895825 EST265268 tomato callus, TAMU Lycopersicon 44 0.003
	emb AF109661 AF109661 AF109661 Capsicum annuum root susceptible 42 0.004
	emb AI487481 AI487481 EST245803 tomato ovary, TAMU Lycopersicon 41 0.023
30	emb AV411141 AV411141 AV411141 Lotus japonicus young plants (two 41 0.023
	emb AW036093 AW036093 EST278179 tomato seed, TAMU Lycopersicon e 30 0.025
	emb AW036201 AW036201 EST278199 tomato seed, TAMU Lycopersicon e 40 0.031
	emb AW099579 AW099579 sd43g11.yl Gm-c1016 Glycine max cDNA clone 40 0.031
35	emb AW569827 AW569827 si82b01.y1 Gm-c1031 Glycine max cDNA clone 40 0.031 emb AW099588 AW099588 sd43h11.y1 Gm-c1016 Glycine max cDNA clone 40 0.031
55	emb AW306204 AW306204 se47d06.y1 Gm-c1017 Glycine max cDNA clone 40 0.031
	emb AW569325 AW569325 si76f02.yl Gm-c1031 Glycine max cDNA clone 40 0.031
	gb BE058656 BE058656 sn19a10.yl Gm-c1016 Glycine max cDNA clone 40 0.031
	emb AW559559 AW559559 EST314607 DSIR Medicago truncatula cDNA cl 40 0.043
40	emb AV427590 AV427590 AV427590 Lotus japonicus young plants (two 40 0.043
	emb A1777674 A1777674 EST258469 tomato susceptible, Cornell Lyco 40 0.043
	emb AI725930 AI725930 BNLGHi13647 Six-day Cotton fiber Gossypium 40 0.059 gb BE021933 BE021933 sm64c08.yl Gm-c1028 Glycine max cDNA clone 40 0.059
	gb BE021787 BE021787 sm62e01.y1 Gm-c1028 Glycine max cDNA clone 39 0.081
45	emb A1965348 A1965348 sc70c09.yl Gm-c1016 Glycine max cDNA clone 39 0.11
	emb AW729281 AW729281 GA_Ea0024J11 Gossypium arboreum 7-10 dpa 38 0.15
	emb AI485216 AI485216 EST243520 tomato ovary, TAMU Lycopersicon 36 0.20
	emb AI484866 AI484866 EST243127 tomato ovary, TAMU Lycopersicon 36 0.20
50	emb AI729570 AI729570 BNLGHi13679 Six-day Cotton fiber Gossypium 38 0.21
50	emb AW688707 AW688707 NF010F12ST1F1000 Developing stem Medicago 37 0.29
	emb AI483679 AI483679 EST249550 tomato ovary, TAMU Lycopersicon 37 0.39 emb AB029365 AB029365 Cephalotaxus harringtonia mitochondrial ge 29 0.83
	25 0.05
	Query= AC006920.138_at 12642_at /id_source genbank /description
55	gb aad22285.1 ac006920_9 (ac006920) unknown protein [arabidopsis
•	thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac006920 /ncgi http://www.ncgr.org/cgi-bin/ff?ac006920
60	(1512 letters)
	/ 10000D)

Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching.....done 5 Score E Sequences producing significant alignments: (bits) Value emb|AF223643|AF223643 Pisum sativum xyloglucan fucosyltransferas... 311 e-147 10 emb|AW719438|AW719438 LiNEST4f10r Lotus japonicus nodule library... 164 1e-64 emb|AA660464|AA660464 00349 MtRHE Medicago truncatula cDNA 5', m... 128 6e-38 emb|AW693268|AW693268 NF064A03ST1F1000 Developing stem Medicago ... 109 5e-32 emb|AW508697|AW508697 si35c12.yl Gm-r1030 Glycine max cDNA clone... 77 6e-31 emb|AW689377|AW689377 NF018E07ST1F1000 Developing stem Medicago ... 78 2e-30 15 gb|BE058474|BE058474 sn16f08.yl Gm-c1016 Glycine max cDNA clone ... 102 6e-21 emb|AW704030|AW704030 sk27a04.yl Gm-c1028 Glycine max cDNA clone... 64 5e-20 emb|AU089974|AU089974 AU089974 Hordeum vulgare subsp. vulgare Up... 45 1e-19 emb|AW720399|AW720399 LjNEST22c8r Lotus japonicus nodule library... 83 1e-18 emb|AU089968|AU089968 AU089968 Hordeum vulgare subsp. vulgare Up... 45 5e-17 20 emb|AV417193|AV417193 AV417193 Lotus japonicus young plants (two... 88 2e-16 emb[AQ855554]AQ855554 CpG1646A CpIOWAgDNA1 Cryptosporidium parvu... 35 1.1 emb|Z37536|LTND9 L.tarentolae ND9 mRNA encoding putative NADH de... 35 2.1 emb|AW934637|AW934637 EST353529 tomato flower buds 0-3 mm, Corne... emb|AF050740|AF050740 Plasmodium falciparum variant-specific sur... 35 2.1 25 emb|AI329848|AI329848 b8h09ne.r1 Neurospora crassa evening cDNA ... 35 2.1 emb|AW035275|AW035275 EST280638 tomato callus, TAMU Lycopersicon... 35 2.1 emb|AW933190|AW933190 EST359033 tomato fruit mature green, TAMU ... 35 2.1 emb|AL109832|SPAC630 S.pombe chromosome I cosmid c630. 34 2.9 emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 34 4.0 30 emb|A85491|A85491 Sequence 150 from Patent EP0866129. emb|AC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 34 4.0 emb|AA786891|AA786891 m7a05a1.rl Aspergillus nidulans 24hr asexu... 34 4.0 gb[BE124954]BE124954 EST393989 GVN Medicago truncatula cDNA clon... 27 4.7 emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 33 5.5 35 emb|AW617216|AW617216 EST323627 L. hirsutum trichome, Cornell Un... 33 5.5 emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 33 7.6 emb|AF056622|AF056622 Vitis vinifera putative Cu/Zn superoxide d... 33 7.6 40 Query= AC004077.149_s_at 12989_s_at /id_source genbank /description gb|aac26690.1| (ac004077) putative cytochrome p450 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi (1488 letters) 45 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching..... 50 Sequences producing significant alignments: (bits) Value emb|AW203670|AW203670 sf36h04.yl Gm-c1028 Glycine max cDNA clone... 334 1e-90 55 emb|AW268012|AW268012 EST306234 DSIR Medicago truncatula cDNA cl... 246 2e-83 emb|AW041000|AW041000 EST283864 tomato mixed elicitor, BTI Lycop... 307 1e-82 emb|AW472433|AW472433 si25b07.yl Gm-c1029 Glycine max cDNA clone... 306 3e-82 emb|AW560118|AW560118 EST315166 DSIR Medicago truncatula cDNA cl... 166 3e-64 emb|AW394771|AW394771 sh35b02.yl Gm-c1017 Glycine max cDNA clone... 213 3e-54 60 emb|AW622568|AW622568 EST313368 tomato root during/after fruit s... 181 5e-51

emb|AW737712|AW737712 EST339139 tomato flower buds, anthesis, Co... 162 1e-45

```
emb|AW694002|AW694002 NF071F03ST1F1029 Developing stem Medicago ... 135 2e-45
      gb[BE124930]BE124930 EST393965 GVN Medicago truncatula cDNA clon... 183 2e-45
      emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8.
                                                                     114 1e-38
      emb|AL111746|CNS019KA Botrytis cinerea strain T4 cDNA library un... 123 2e-38
 5
      emb|AL111744|CNS019K8 Botrytis cinerea strain T4 cDNA library un... 123 3e-37
      emb|AW922483|AW922483 DG1 19 A10.g1 A002 Dark Grown 1 (DG1) Sorg... 155 8e-37
      emb|Z49211|SC9711X S.cerevisiae chromosome XIII cosmid 9711.
                                                                    113 3e-36
      gb[U34636]SCU34636 Saccharomyces cerevisiae cytochrome P450 gene... 113 3e-36
      emb|AW928489|AW928489 EST337277 tomato flower buds 8 mm to pre-a... 149 5e-35
10
      emb|AL033396|CAC35A5 C.albicans cosmid Ca35A5.
      emb|AW310494|AW310494 sf36h04.x1 Gm-c1028 Glycine max cDNA clone... 124 2e-30
      emb|AA676046|AA676046 TENF0565 T.cruzi epimastigote normalized c... 125 1e-27
      gb[BE125362]BE125362 DG1 19 A10.b1 A002 Dark Grown 1 (DG1) Sorgh... 77 5e-21
      emb|AW496913|AW496913 ga50a07.yl Moss EST library PPU Physcomitr... 98 2e-19
15
      emb|AU012887|AU012887 AU012887 Schizosaccharomyces pombe late lo... 71 1e-12
      emb|AJ238612|CRO238612 Catharanthus roseus mRNA for cytochrome P... 45 2e-12
      emb|AW307234|AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone... 50 3e-12
      emb|AF124815|AF124815 Mentha spicata cytochrome p450 mRNA, compl... 38 4e-10
      emb|AV425399|AV425399 AV425399 Lotus japonicus young plants (two... 66 9e-10
20
      emb|AW234443|AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone... 51 4e-09
      emb|AI495626|AI495626-sb11c08.y1-Gm-c1004 Glycine max cDNA-clone... - 51- 4e-09
      emb|AF000403|AF000403 Lotus japonicus putative cytochorome P450 ... 38 1e-08
      emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 37 2e-08
      emb|AW699711|AW699711 gb30h12.y1 Moss EST library PPN Physcomitr... 61 2e-08
25
      emb|AA556134|AA556134 TENF0475 T.cruzi epimastigote normalized c... 61 2e-08
      emb|AA675972|AA675972 TENF0465 T.cruzi epimastigote normalized c... 61 2e-08
      emb|AF124817|AF124817 Mentha x piperita cytochrome p450 isoform ... 37 2e-08
      emb|AW255151|AW255151 ML1459 peppermint glandular trichome Menth... 37 1e-07
      emb|AW720567|AW720567 LjNEST9g11rc Lotus japonicus nodule librar... 34 1e-07
30
      emb|AW719774|AW719774 LjNEST9G11r Lotus japonicus nodule library... 34 1e-07
      gb[BE125544[BE125544 DG1 27 A10.b1 A002 Dark Grown 1 (DG1) Sorgh... 58 2e-07
      emb|AW255409|AW255409 ML430 peppermint glandular trichome Mentha... 37 3e-07
      emb|AW053855|AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... 32 3e-07
      emb|Y09291|TACYP51C6 T.aestivum mRNA for obtusifoliol 14-alpha-d... 35 6e-07
35
      emb[Y09292]TACYP51C1 T.aestivum mRNA for obtusifoliol 14-alpha-d... 35 7e-07
      emb|AW145717|AW145717 ga33h06.yl Moss EST library PPN Physcomitr... 55 1e-06
      gb|U74319|SBU74319 Sorghum bicolor obtusifoliol 14-alpha demethy... 32 1e-05
      emb|AW255953|AW255953 MW299 peppermint glandular trichome Mentha... 37 1e-05
      emb|AW163966|AW163966 Ljirnpest17-385-h1 Ljirnp Lambda HybriZap ... 34 1e-05
40
      emb|Z54096|SPAC13A11 S.pombe chromosome I cosmid c13A11.
                                                                      44 3e-05
      emb|AW666409|AW666409 sk36b12.y1 Gm-c1028 Glycine max cDNA clone... 51 3e-05
      emb|AW255274|AW255274 ML276 peppermint glandular trichome Mentha... 37 3e-05
      emb[Y10490]GMC450CP3 G.max mRNA for putative cytochrome P450, cl... 42 4e-05
45
      emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 50 4e-05
      emb|Al731081|Al731081 BNLGHi8648 Six-day Cotton fiber Gossypium ... 50 6e-05
      emb|AW733598|AW733598 sk75f08.yl Gm-c1016 Glycine max cDNA clone... 50 6e-05
      emb|AW254782|AW254782 ML1065 peppermint glandular trichome Menth... 37 6e-05
      emb|AW254794|AW254794 ML1076 peppermint glandular trichome Menth... 38 6e-05
50
      emb|AW256016|AW256016 MW370 perpermint glandular trichome Mentha... 37 6e-05
      emb|AW254868|AW254868 ML1290 peppermint glandular trichome Menth... 37 7e-05
      emb|AW310243|AW310243 sf33c07.x1 Gm-c1028 Glycine max cDNA clone... 49 1e-04
      emb|AW570532|AW570532 sj63c04.yl Gm-c1033 Glycine max cDNA clone... 49 1e-04
      emb|AI495064|AI495064 sa90d10.y1 Gm-c1004 Glycine max cDNA clone... 49 1e-04
55
      emb|AI855736|AI855736 sc23f01.yl Gm-c1013 Glycine max cDNA clone... 49 1e-04
      emb|AI900822|AI900822 sb93h05.y1 Gm-c1017 Glycine max cDNA clone... 49 1e-04
      emb|AW234028|AW234028 sf33c07.y1 Gm-c1028 Glycine max cDNA clone... 49 1e-04
      emb[AW706535]AW706535 sj57g05.yl Gm-c1033 Glycine max cDNA clone... 49 1e-04
      emb|AW254954|AW254954 ML1124 peppermint glandular trichome Menth... 37 1e-04
      emb|AW255346|AW255346 ML357 peppermint glandular trichome Mentha... 37 1e-04
      emb[AA824943]AA824943 CT226.complete Tomato Leaf cDNA from cv. V... 48 2e-04
```

	emb AW255059 AW255059 ML1354 peppermint glandular trichome Menth 37 3e-04
	emb AW255126 AW255126 ML1418 peppermint glandular trichome Menth 37 3e-04
	emb AW981162 AW981162 EST392356 DSIL Medicago truncatula cDNA cl 47 3e-04
_	emb AW299159 AW299159 EST305969 KV2 Medicago truncatula cDNA clo 47 3e-04
5	emb AW706489 AW706489 sj57b08.yl Gm-c1033 Glycine max cDNA clone 46 5e-04
	emb AW620257 AW620257 si93g06.yl Gm-c1031 Glycine max cDNA clone 46 7e-04
•.	emb AW704313 AW704313 sk17f11.y1 Gm-c1028 Glycine max cDNA clone 46 7e-04
	emb AW922821 AW922821 DG1_46_E11.g1_A002 Dark Grown 1 (DG1) Sorg 46 0.001
	emb A1895869 A1895869 EST265312 tomato callus, TAMU Lycopersicon 46 0.001
10	emb AJ238439 CAR238439 Cicer arietinum mRNA for a cytochrome P45 46 0.001
	emb AW348613 AW348613 GM210002B22F6R Gm-r1021 Glycine max cDNA 3 39 0.001
	emb AW255736 AW255736 ML798 peppermint glandular trichome Mentha 37 0.001
	emb AW101323 AW101323 sd77e08.yl Gm-c1009 Glycine max cDNA clone 39 0.001
	emb AW278093 AW278093 sf39f05.yl Gm-c1009 Glycine max cDNA clone 45 0.001
15	emb X70981 SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. 32 0.002
	emb AI725768 AI725768 BNLGHi12931 Six-day Cotton fiber Gossypium 45 0.002
	emb AB001379 AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto 45 0.002
	emb AB022732 AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy 45 0.002
	emb AW218488 AW218488 EST303671 tomato radicle, 5 d post-imbibit 32 0.002
20	emb AJ249800 CAR249800 Cicer arietinum partial mRNA for cytochro 44 0.003
	emb AW432266 AW432266 sh71d11.y1 Gm-c1015 Glycine max cDNA clone 44 0.003
	emb AF140614 AF140614 Manihot esculenta N-hydroxylating cytochro 32 0.003
	emb AF022457 AF022457 Glycine max cytochrome P450 monooxygenase 41 0.003
	emb AJ271708 ABI271708 Agaricus bisporus partial mRNA for cytoch 39 0.003
25	emb AW255619 AW255619 ML666 peppermint glandular trichome Mentha 33 0.003
	emb A1898152 A1898152 EST267595 tomato ovary, TAMU Lycopersicon 43 0.003
	emb AW152943 AW152943 se33a03.y1 Gm-c1015 Glycine max cDNA clone 44 0.004
	emb AJ012581 CAR012581 Cicer arietinum mRNA for cytochrome P450. 44 0.004
	emb AI485298 AI485298 EST243602 tomato ovary, TAMU Lycopersicon 43 0.004
30	emb AI728374 AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium 43 0.005
	emb AI485472 AI485472 EST243793 tomato ovary, TAMU Lycopersicon 43 0.005
	Query= AF003102.3 at 13435 at /id_source genbank /description
	gb aac49775.1 (af003102) ap2 domain containing protein rap2.9
35	[arabidopsis thaliana] /blast score 1.00e-33 /ec number /family
	/chip nova /gb link
	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb af003102 /ncgi
	http://www.ncgr.org/cgi-bin/ff?af003102
40	(417 letters)
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
45	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
50	emb AW760536 AW760536 sl51e12.yl Gm-c1027 Glycine max cDNA clone 82 2e-15
	emb AW981184 AW981184 EST392378 DSIL Medicago truncatula cDNA cl 57 5e-13
	emb AI728590 AI728590 BNLGHi11133 Six-day Cotton fiber Gossypium 60 7e-13
	emb AI731959 AI731959 BNLGHi11511 Six-day Cotton fiber Gossypium 60 7e-13
	emb AI775217 AI775217 EST256317 tomato resistant, Cornell Lycope 59 7e-13
55	emb AW458973 AW458973 sh17e01.y1 Gm-c1016 Glycine max cDNA clone 61 3e-12
	emb AW132527 AW132527 se05c02.y1 Gm-c1013 Glycine max cDNA clone 61 3e-12
	emb AW102493 AW102493 sd88h04.yl Gm-c1009 Glycine max cDNA clone 61 4e-12
	emb AV421249 AV421249 AV421249 Lotus japonicus young plants (two 62 2e-09
	emb AW691065 AW691065 NF040H08ST1F1000 Developing stem Medicago 61 3e-09
60	emb AW349295 AW349295 GM210004B12D12R Gm-r1021 Glycine max cDNA 46 8e-08
	emb AW101242 AW101242 sd97a09.y1 Gm-c1013 Glycine max cDNA clone 56 2e-07
	•

```
emb|AI898360|AI898360 EST267803 tomato ovary, TAMU Lycopersicon ...
                                                                         39 6e-07
      emb|AI496321|AI496321 sb05c05.yl Gm-c1004 Glycine max cDNA clone...
      emb|AW208239|AW208239 M110892e GVSN Medicago truncatula cDNA clo...
      emb|AI489067|AI489067 EST247406 tomato ovary, TAMU Lycopersicon ... 45 3e-04
 5
      emb|AI771636|AI771636 EST252736 tomato ovary, TAMU Lycopersicon ... '45 3e-04
      emb|AW219417|AW219417 EST301995 tomato root during/after fruit s... 45 3e-04
      emb|AI898830|AI898830 EST268273 tomato ovary, TAMU Lycopersicon ... 45 3e-04
      emb|AI489478|AI489478 EST247817 tomato ovary, TAMU Lycopersicon ... 45 3e-04
      emb|AI489770|AI489770 EST248109 tomato ovary, TAMU Lycopersicon ... 45 3e-04
10
      emb|AW672287|AW672287 LG1_358_A02.b1_A002 Light Grown 1 (LG1) So... 44 5e-04
      emb|AI771296|AI771296 EST252312 tomato ovary, TAMU Lycopersicon ... 44 7e-04
      emb|AI488844|AI488844 EST247183 tomato ovary, TAMU Lycopersicon ... 44 7e-04
      emb|AJ238740|CRO238740 Catharanthus roseus mRNA for AP2-domain D... 43 0.001
      emb[AV424732]AV424732 AV424732 Lotus japonicus young plants (two... 42 0.002
      emb|AW040122|AW040122 EST282621 tomato mixed elicitor, BTI Lycop... 33 0.002
15
      emb|AW040111|AW040111 EST282610 tomato mixed elicitor, BTI Lycop... 33 0.002
      emb|AI416505|AI416505 sa10g11.x1 Gm-c1003 Glycine max cDNA clone... 42 0.003
      emb|AW597629|AW597629 sj96g05.y1 Gm-c1023 Glycine max cDNA clone... 42 0.003
      emb|AI731684|AI731684 BNLGHi10485 Six-day Cotton fiber Gossypium... 42 0.003
      emb|AW727628|AW727628 GA_Ea0015E08 Gossypium arboreum 7-10 dpa ... 42 0.003
20
      emb|AW109338|AW109338 gate0004G15f Gossypium arboreum 7-10 dpa f... 42 0.003
      emb|AI416564|AI416564 sa10g11.yl Gm-c1003 Glycine max cDNA clone... 42 0.003
      gb|BE054117|BE054117 GA Ea0004G15f Gossypium arboreum 7-10 dpa ... 42 0.003
      emb|AW666769|AW666769 GA Ea0005O23 Gossypium arboreum 7-10 dpa ... 42 0.003
25
      emb|AI731460|AI731460 BNLGHi9812 Six-day Cotton fiber Gossypium ... 42 0.003
      emb|AW472387|AW472387 si24e07.y1 Gm-c1029 Glycine max cDNA clone... 42 0.003
     emb|AI731267|AI731267 BNLGHi9029 Six-day Cotton fiber Gossypium ... 42 0.003
      emb[AW832641]AW832641 sm15c04.yl Gm-c1027 Glycine max cDNA clone... 41 0.003
      emb|AW926228|AW926228 HVSMEg0006K15 Hordeum vulgare pre-anthesis... 41 0.004
30
      emb|AI795106|AI795106 sb76f04.y1 Gm-c1010 Glycine max cDNA clone... 41 0.004
      emb|AW694919|AW694919 NF081D08ST1F1073 Developing stem Medicago ... 41 0.004
      emb|AW706696|AW706696 sk01g02.y1 Gm-c1023 Glycine max cDNA clone... 41 0.004
      emb|AI900613|AI900613 sc13f09.y1 Gm-c1013 Glycine max cDNA clone... 41 0.004
      emb|AI937979|AI937979 sc06d12.y1 Gm-c1012 Glycine max cDNA clone... 41 0.004
35
      emb|AW220454|AW220454 EST302937 tomato root during/after fruit s... 41 0.005
      emb|AW127214|AW127214 M110154 GVN Medicago truncatula cDNA clone... 41 0.005
      emb|AW152963|AW152963 se33c03.y1 Gm-c1015 Glycine max cDNA clone... 41 0.005
      emb|AW693001|AW693001 NF058C04ST1F1000 Developing stem Medicago ... 40 0.007
      emb|AW278066|AW278066 sf39c09.y1 Gm-c1009 Glycine max cDNA clone... 40 0.007
40
      emb|AW318239|AW318239 sg62g03.yl Gm-c1007 Glycine max cDNA clone... 40 0.007
      emb|AW706818|AW706818 sk03g11.y1 Gm-c1023 Glycine max cDNA clone... 40 0.009
      emb|AI166481|AI166481 xylem.est.309 Poplar xylem Lambda ZAPII li... 40 0.013
      emb|AW759250|AW759250 sl38g10.yl Gm-c1027 Glycine max cDNA clone... 39 0.018
      emb|AW981151|AW981151 EST392345 DSIL Medicago truncatula cDNA cl... 39 0.018
45
      emb|AW981228|AW981228 EST392318 DSIL Medicago truncatula cDNA cl... 39 0.018
      emb|A1896723|A1896723 EST266166 tomato callus, TAMU Lycopersicon... 39 0.018
      emb|AW216598|AW216598 EST295312 tomato callus, TAMU Lycopersicon... 39 0.018
      emb|AW034686|AW034686 EST278417 tomato callus, TAMU Lycopersicon... 39 0.018
      emb|A1894724|A1894724 EST264167 tomato callus, TAMU Lycopersicon... 39 0.018
50
      emblAW031292lAW031292 EST274667 tomato callus, TAMU Lycopersicon... 39 0.018
      emb|AI487841|AI487841 EST246163 tomato ovary, TAMU Lycopersicon ... 39 0.018
      emb|AW032262|AW032262 EST275716 tomato callus, TAMU Lycopersicon... 39 0.018
      emb|AI486694|AI486694 EST245016 tomato ovary, TAMU Lycopersicon ... 39 0.018
      gb|U89256|LEU89256 Lycopersicon esculentum DNA-binding protein P... 39 0.024
55
      emb|AI988644|AI988644 sd05h06.yl Gm-c1020 Glycine max cDNA clone... 39 0.024
      emb|AW278190|AW278190 sf40g11.yl Gm-c1009 Glycine max cDNA clone... 39 0.024
      emb|AW030009|AW030009 EST273264 tomato callus, TAMU Lycopersicon... 39 0.024
      emb|A1894873|A1894873 EST264316 tomato callus, TAMU Lycopersicon... 39 0.024
      emb|AW257352|AW257352 EST305489 KV2 Medicago truncatula cDNA clo... 39 0.024
60
      emb|AW030386|AW030386 EST273641 tomato callus, TAMU Lycopersicon... 39 0.024
      emb[AV422393]AV422393 AV422393 Lotus japonicus young plants (two... 39 0.024
```

	emb AI973653 AI973653 sd07h05.y1 Gm-c1020 Glycine max cDNA clone 39 0.024
	emb AW349638 AW349638 GM210005B21A4R Gm-r1021 Glycine max cDNA 3 39 0.024 emb AW396250 AW396250 sh26c01.yl Gm-c1016 Glycine max cDNA clone 39 0.024
	emb A1896308 A1896308 EST265751 tomato callus, TAMU Lycopersicon 38 0.033
5	emb AW774176 AW774176 EST333259 KV3 Medicago truncatula cDNA clo 38 0.033
	emb AW776668 AW776668 EST335733 DSIL Medicago truncatula cDNA cl 38 0.033
	emb AW507898 AW507898 si46f03.yl Gm-r1030 Glycine max cDNA clone 38 0.033
	emb AW220395 AW220395 EST302878 tomato root during/after fruit s 38 0.033
10	emb AW184868 AW184868 se69f03.yl Gm-c1019 Glycine max cDNA clone 38 0.033
10	emb AW308784 AW308784 sf71h01.yl Gm-c1013 Glycine max cDNA clone 38 0.033
	emb AW574222 AW574222 EST316813 GVN Medicago truncatula cDNA clo 38 0.033 emb AW035882 AW035882 EST282389 tomato callus, TAMU Lycopersicon 38 0.033
	emb AW394770 AW394770 sh35b01.yl Gm-c1017 Glycine max cDNA clone 38 0.046
•	emb AW164648 AW164648 se75g05.y1 Gm-c1023 Glycine max cDNA clone 38 0.046
15	emb A1966402 A1966402 sc38e09.y1 Gm-c1014 Glycine max cDNA clone 38 0.046
	gb[L22964 SOYCPGAD3A Glycine soja chloroplast 3-omega faty acid 38 0.046
	emb AI442716 AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone 38 0.046
	emb AW776927 AW776927 EST335992 DSIL Medicago truncatula cDNA cl 38 0.046
	emb AI900861 AI900861 sb95d04.y1 Gm-c1012 Glycine max cDNA clone 38 0.046
20	emb AW930485 AW930485 EST340858 tomato fruit mature green, TAMU 38 0.046
	_emb AI899237 AI899237 EST268680 tomato ovary, TAMU Lycopersicon 38 0.046 emb AW034216 AW034216 EST277787 tomato callus, TAMU Lycopersicon 38 0.046
	emb A1856708 A1856708 sb42g10.y1 Gm-c1014 Glycine max cDNA clone 38 0.046
	emb AW185124 AW185124 se87b06.y1 Gm-c1023 Glycine max cDNA clone 38 0.046
25	emb AI895984 AI895984 EST265427 tomato callus, TAMU Lycopersicon 38 0.046
	emb AI778378 AI778378 EST259257 tomato susceptible, Cornell Lyco 38 0.046
	emb AI563167 AI563167 EST00291 watermelon lambda zap library Cit 38 0.046
	One— AI 022022 172 at 12066 at /id assess contact /dassistics
30	Query= AL022023.172_at 13966_at /id_source genbank /description emb caa17775.1 (al022023) putative protein [arabidopsis thaliana]
JU.	/blast score 1.00e-173 /ec number /family /chip nova /gb link
	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb al022023 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al022023
35	(1161 letters)
	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	,
40	Searchingdone
	Score E
	Sequences producing significant alignments: (bits) Value
45	emb AW185155 AW185155 se87e11.y1 Gm-c1023 Glycine max cDNA clone 134 2e-30
	emb AW278569 AW278569 sf46b12.y1 Gm-c1009 Glycine max cDNA clone 131 1e-29
	emb AW683973 AW683973 NF004E08NR1F1000 Nodulated root Medicago t 97 2e-19
	emb AI055338 AI055338 coau0003L11 Cotton Boll Abscission Zone cD 56 2e-07
50	emb AW693058 AW693058 NF059E03ST1F1021 Developing stem Medicago 49 9e-05
30	emb AW686062 AW686062 NF033A11NR1F1000 Nodulated root Medicago t 49 9e-05 gb BE060490 BE060490 HVSMEg0012H04f Hordeum vulgare pre-anthesis 37 0.22
	emb AW979446 AW979446 EST310344 tomato root deficiency, Cornell 35 1.0
	emb A1726520 A1726520 BNLGHi6046 Six-day Cotton fiber Gossypium 34 1.0
	gb[M86518]PFAHMGLP Plasmodium falciparum high mobility group-lik 35 1.1
55	emb AQ952389 AQ952389 Sheared DNA-32H3.TF Sheared DNA Trypanosom 35 1.1
•	emb AW775865 AW775865 EST334930 DSIL Medicago truncatula cDNA cl 35 1.1
	emb AQ988902 AQ988902 04D1B01NE.R1 C. parvum Lambda Zap Express 35 1.1
	emb AV425088 AV425088 AV425088 Lotus japonicus young plants (two 34 1.5
60	emb AA676132 AA676132 TENF0683 T.cruzi epimastigote normalized c 34 2.1
ou	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai 33 2.8
	emb AF108883 AF108883 Capsicum annuum small GTP-binding protein 28 3.6

```
emb[X75082]STCITS S.tuberosum mRNA for mitochondrial citrate-syn... 33 3.9
      emb|A46545|A46545 Sequence 1 from Patent WO9524487.
      emb|X07693|SPNUC2 Fission yeast nuc2 gene encoding nuclear scaff... 33 3.9
      emb|X83997|CPEAPC C.parasitica eapC gene.
      emb|AF143971|AF143971 Pinus taeda microsatellite PtTX3026 sequence. 33 3.9
      emb|AW667663|AW667663 GA Ea0010C16 Gossypium arboreum 7-10 dpa ... 33 5.0
      emb|AI053174|AI053174 TENU1594 T. cruzi epimastigote normalized ... 32 5.3
      emb|AW690972|AW690972 NF040A07ST1F1000 Developing stem Medicago ... 32 5.3
      emb|AB012123|AB012123 Candida albicans CHS5 gene, complete cds.
10
      emb|AW761626|AW761626 gb27h09.y1 Moss EST library PPN Physcomitr... 32 6.9
      emb[AI055163]AI055163 coau0003D12 Cotton Boll Abscission Zone cD... 32 6.9
      emb|AW761333|AW761333 sl66b07.y1 Gm-c1027 Glycine max cDNA clone... 32 6.9
      emb|AI822729|AI822729 L0-1261T3 Ice plant Lambda Uni-Zap XR expr... 32 6.9
      emb|AW931465|AW931465 EST357308 tomato fruit mature green, TAMU ... 32 7.3
15
      emb|AA555413|AA555413 CpEST.644 uniZAPCpIOWAsporoLib3 Cryptospor... 32 7.3
      gb[M80656]EIMPEM Eimeria maxima 230 kDa protein (pEM230) mRNA, 3... 32 7.3
      emb|AI026260|AI026260 L0-455T3 Ice plant Lambda Uni-Zap XR expre... 32 7.3
      emb|AQ640247|AQ640247 927P1-18B12.TV 927P1 Trypanosoma brucei ge... 32 7.3
      emb|AQ491970|AQ491970 GN616G2 mTn-3xHA/lacZ Insertion Library Sa... 32 7.3
20
      emb|AF143965|AF143965 Pinus taeda microsatellite PtTX3011 sequence. 32 7.3
      gb[U51031[YSCD9819 Saccharomyces cerevisiae chromosome IV cosmid... 32 7.3
      gb|L06487|YSCZIP1A Saccharomyces cerevisiae ZIP1 protein gene, c... 32 7.3
      emb|AQ850277|AQ850277 LMAJFV1_lm28b03.x1 Leishmania major FV1 ra... 32 9.4
      emb|AJ225402|AJ225402 AJ225402 Abscisic acid-treated protonemata... 32 9.4
25
      emb|AW735860|AW735860 EST336628 tomato flower buds 0-3 mm, Corne... 32 9.4
      emb|AW756470|AW756470 sl21g05.yl Gm-c1036 Glycine max cDNA clone... 32 9.4
      Query= AC002521.68 at 14381 at /id source genbank /description
      gb|aac05341.1| (ac002521) unknown protein [arabidopsis thaliana]
30
      /blast score 0 /ec number /family /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi
      http://www.ncgr.org/cgi-bin/ff?ac002521
           (999 letters)
35
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
      Searching......done
40
                                          Score E
      Sequences producing significant alignments:
                                                          (bits) Value
      emb[AI727718]AI727718 BNLGHi8830 Six-day Cotton fiber Gossypium ... 405 e-112
45
      emblAI894939IAI894939 EST264382 tomato callus, TAMU Lycopersicon... 405 e-112
      emblAI727173|AI727173 BNLGHi7479 Six-day Cotton fiber Gossypium ... 404 e-112
      emb|AW091566|AW091566 EST284842 tomato mixed elicitor, BTI Lycop... 364 e-100
      emb|AW201381|AW201381 sf02d09.y1 Gm-c1027 Glycine max cDNA clone... 301 le-98
      emb|AW397167|AW397167 sg67f10.y1 Gm-c1007 Glycine max cDNA clone... 287 1e-94
50
      emb|AW038822|AW038822 EST280778 tomato mixed elicitor, BTI Lycop... 282 3e-75
      emb|AI488594|AI488594 EST246933 tomato ovary, TAMU Lycopersicon ... 280 2e-74
      emb|AW926055|AW926055 HVSMEg0006C20 Hordeum vulgare pre-anthesis... 160 2e-71
      gb[T14872|T14872 crs323 lambdaZAPST Ricinus communis cDNA clone ... 187 4e-68
      emb|AW329252|AW329252 N200470e rootphos(-) Medicago truncatula c... 246 2e-64
55
      emb|AW932653|AW932653 EST358496 tomato fruit mature green, TAMU ... 246 2e-64
      emblAW508528|AW508528 si33a06.yl Gm-r1030 Glycine max cDNA clone... 177 8e-60
      emb[AW201152]AW201152 se98d11.y1 Gm-c1027 Glycine max cDNA clone... 137 1e-49
      emb[AW011518]AW011518 ST21G07 Pine TriplEx shoot tip library Pin... 178 5e-44
      emb|AW568929|AW568929 si74c04.y1 Gm-c1031 Glycine max cDNA clone... 169 3e-41
60
      emb[AW459302[AW459302 sh23c04.y1 Gm-c1016 Glycine max cDNA clone... 166 3e-40
      emb|AV392100|AV392100 AV392100 Chlamydomonas reinhardtii C9 Chla... 114 1e-36
```

	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb). 87 8e-28
	emb Z73600 SCYPL244C S.cerevisiae chromosome XVI reading frame O 87 9e-28
	emb AL096796 SPBC839 S.pombe chromosome II cosmid c839. 65 2e-25
	emb AL021816 SPBC24E9 S.pombe chromosome II cosmid c24E9. 65 2e-25
5	emb AW395997 AW395997 sh08a03.yl Gm-c1016 Glycine max cDNA clone 114 1e-24
_	emb AT000300 AT000300 AT000300 Apple young fruit cDNA library Ma 113 3e-24
	emb AI166335 AI166335 xylem.est.178 Poplar xylem Lambda ZAPII li 90 2e-17
	emb AQ649102 AQ649102 Sheared DNA-16A11.TR Sheared DNA Trypanoso 84 1e-15
10	emb AQ449927 AQ449927 500006A04.x1 CpIOWAM13mp18gDNA1 Cryptospor 65 1e-0
10	emb AL354298 L5768AY Leishmania major Friedlin cosmid L5768.1 t7 57 2e-07
	emb AW776002 AW776002 EST335067 DSIL Medicago truncatula cDNA cl 50 3e-05
	gb BE033570 BE033570 MF03F06 MF Mesembryanthemum crystallinum cD 47 2e-04
	emb AI727063 AI727063 BNLGHi7246 Six-day Cotton fiber Gossypium 44 0.002
	emb AW981371 AW981371 EST392524 DSIL Medicago truncatula cDNA cl 41 0.016
15	emb AL132839 SPAC1093 S.pombe chromosome I cosmid c1093. 40 0.040
	emb AW981366 AW981366 EST392519 DSIL Medicago truncatula cDNA cl 37, 0.20
	emb AZ044909 AZ044909 A975/R Soybean genomic clone Glycine max g 37 0.27
•	emb AW220332 AW220332 EST302815 tomato root during/after fruit s 36 0.37
	emb AI897952 AI897952 EST267395 tomato ovary, TAMU Lycopersicon 36 0.37
20	emb AW220428 AW220428 EST302911 tomato root during/after fruit s 36 0.37
20	emb AW932638 AW932638 EST358481 tomato fruit mature green, TAMU 36 0.37
	111.00.00.00.01.00.00.00.00.00.00.00.00.
	emb AC007862 AC007862 Trypanosoma brucei chromosome II clone RPC 35 0.97
25	emb AQ872760 AQ872760 V21H1 mTn-3xHA/lacZ Insertion Library, str 35 1.3
25	emb Z38062 SC9687 S.cerevisiae chromosome IX cosmid 9687. 35 1.3
	emb AW428965 AW428965 EST306505 tomato flower buds 0-3 mm, Corne 35 1.3
	emb X79743 SCBPPS S.cerevisiae BET1, PAN1 PRI1 and STS1 genes. 35 1.3
	emb AZ221045 AZ221045 Sheared DNA-64E9.TF Sheared DNA Trypanosom 35 1.3
	emb AF014809 AF014809 Lycopersicon esculentum proline transporte 35 1.3
30	emb AF106079 AF106079 Chlamydomonas reinhardtii dynein heavy cha 34 1.8
	gb[M80437]YSCSEQ Saccharomyces cerevisiae gene, complete cds. 34 2.5
	gb I05603 YSCCTR Saccharocyces cerevisiae choline transport prot 34 2.5
	emb Z72599 SCYGL077C S.cerevisiae chromosome VII reading frame O 34 2.5
	gb[T36987]T36987 EST102029 S. cerevisiae strain X2180-1A Sacchar 34 2.5
35	emb Z71519 SCYNL243W S.cerevisiae chromosome XIV reading frame O 33 3.4
	emb AW649403 AW649403 EST327857 tomato germinating seedlings, TA 33 3.4
	emb Z22811 SCSLA2PA S.cerevisiae of Sla2p gene. 33 3.4
	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom 33 3.4
	emb AI898010 AI898010 EST267453 tomato ovary, TAMU Lycopersicon 33 3.4
40	gb L12352 YSCMOP2G Saccharomyces cerevisiae transmembrane protei 33 3.4
	emb Z71518 SCYNL242W S.cerevisiae chromosome XIV reading frame O 33 3.4
	emb AQ649183 AQ649183 Sheared DNA-6F2.TR Sheared DNA Trypanosoma 33 4.7
	emb AW181050 AW181050 MgA0550r MgA Library Mycosphaerella gramin 33 4.7
	emb AQ841780 AQ841780 T134030 Soybean RFLP probe Glycine max gen 33 4.7
45	dbj D90206 CRECAH1G C. reinhardtii CAH1 gene for carbonic anhydr 33 4.7
•	emb X54487 CRCAH1 Chlamydomonas reinhardtii CAH1 gene for carbo 33 4.7
	emb AW596179 AW596179 si99a03.y1 Gm-c1032 Glycine max cDNA clone 33 4.7
	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD 33 4.7
	emb AW696344 AW696344 NF106H09ST1F1079 Developing stem Medicago 31 5.0
50	gb L36093 BLYPRX Barley peroxidase mRNA, complete cds. 32 6.5
	emb[X58396]HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 32 6.5
	emb AL121851 LMFL2581 Leishmania major Friedlin chromosome 23 co 32 6.5
	emb AW731480 AW731480 GAEa0030L23 Gossypium arboreum 7-10 dpa 32 6.5
	chipensessoride of a 10-12 of the state of t
55	gb BE058697 BE058697 sn19e12.yl Gm-c1016 Glycine max cDNA clone 32 6.5
,,	emb AL031324 SPCC1672 S.pombe chromosome III cosmid c1672. 32 6.5
	emb AC007865 AC007865 Trypanosoma brucei chromosome II clone RPC 28 6.8
	emb AW255798 AW255798 ML867 peppermint glandular trichome Mentha 26 7.0
	emb AW255452 AW255452 ML474 peppermint glandular trichome Mentha 26 7.0
۲۸	emb AI490316 AI490316 EST248642 tomato ovary, TAMU Lycopersicon 28 7.2
60	emb AF124817 AF124817 Mentha x piperita cytochrome p450 isoform 26 8.9
	emb AJ133001 CPL133001 Craterostigma plantagineum mRNA for phosp 32 8.9

```
emb|AW348239|AW348239 GM210001B12D9R Gm-r1021 Glycine max cDNA 3... 32 8.9
      emb|AQ903735|AQ903735 GSSTc04776 Trypanosome cruzi random genomi... 32 8.9
      emb|AB014483|AB014483 Nicotiana tabacum NtHSF1 mRNA for heat sho... 32 8.9
      emb|AF016328|AF016328 Hordeum vulgare Barperm2 (perm2) mRNA, par... 32 8.9
      emb|AW696053|AW696053 NF102A09ST1F1068 Developing stem Medicago ... 32 8.9
      emb|AW691566|AW691566 NF046E03ST1F1000 Developing stem Medicago ... 32 8.9
      emb|AW309484|AW309484 sf20a10.x1 Gm-c1028 Glycine max cDNA clone... 32 8.9
      emb|AI442542|AI442542 sa32h01.y1 Gm-c1004 Glycine max cDNA clone... 32 8.9
      emb[X55347]LPHSF24 Tomato mRNA for heat stress transcription fac... 32 8.9
      emb[X54488]CRCAH2 Chlamydomonas reinhardtii CAH2 gene for carbon... 32 8.9
      emb|A85864|A85864 Sequence 523 from Patent EP0866129.
      emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 32 8.9
      emb|AW184970|AW184970 se84g02.yl Gm-c1023 Glycine max cDNA clone... 32 8.9
      emb|Z46871|SOEXG1 S.occidentalis gene for exo-1,3-beta-glucanase... 32 8.9
15
      emb|AI163250|AI163250 A038p15u Hybrid aspen plasmid library Popu... 32 8.9
      emb|AL023592|SPCC550 S.pombe chromosome III cosmid c550.
      emb|AW668371|AW668371 GA_Ea0013L20 Gossypium arboreum 7-10 dpa ... 26 9.3
      emb|AW255363|AW255363 ML376 peppermint glandular trichome Mentha... 26 9.5
      gb|C96116|C96116 C96116 Marchantia polymorpha immature sex organ... 27 9.6
20
      emb|AW255126|AW255126 ML1418 peppermint glandular trichome Menth... 26 9.8
      Query= AC000348.23_at 14443_at /id_source genbank /description
      gb|aab61498.1| (ac000348) t7n9.22 [arabidopsis thaliana] /blast_score
      0/ec_number /family /chip nova/gb link
25
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000348| /ncgi
      http://www.ncgr.org/cgi-bin/ff?ac000348
           (1869 letters)
30
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
35
                                          Score
      Sequences producing significant alignments:
                                                         (bits) Value
      emb|AW622865|AW622865 EST306935 tomato flower buds 3-8 mm, Corne... 246 3e-64
      emb[AW907167]AW907167 EST343290 potato stolon, Cornell Universit... 152 7e-36
40
      emb|AW596038|AW596038 si97b04.yl Gm-c1032 Glycine max cDNA clone... 98 4e-28
      emb|AW774367|AW774367 EST333518 KV3 Medicago truncatula cDNA clo... 101 1e-25
      emb|AW459521|AW459521 sh42e12.yl Gm-c1017 Glycine max cDNA clone... 96 5e-24
      emb|AW777159|AW777159 Str2-E4 Sugar Beet germination cDNA librar... 82 1e-20
      emb|AW694460|AW694460 NF076E10ST1F1082 Developing stem Medicago ... 95 1e-18
45
      emb|AW651335|AW651335 EST329789 tomato germinating seedlings, TA... 82 8e-15
      emb|AW928691|AW928691 EST337479 tomato flower buds 8 mm to pre-a... 50 2e-09
      emb|AW226419|AW226419 ST82B05 Pine TriplEx shoot tip library Pin... 62 2e-08
      emb|AW398212|AW398212 EST298059 L. pennellii trichome, Cornell U... 60 4e-08
50
      emb|AT002124|AT002124 AT002124 Flower bud cDNA Brassica rapa sub... 44 0.004
      emb|AW666214|AW666214 sk33g11.yl Gm-c1028 Glycine max cDNA clone... 40 0.040
      gb[U51033]YSCP9513 Saccharomyces cerevisiae chromosome XVI cosmi... 38 0.19
      emb|AI725302|AI725302 1168 PtIFG2 Pinus taeda cDNA clone 9253r, ... 38 0.19
      emb|AB035928|AB035928 Malus transitoria mRNA for St-RNase, compl... 36 0.50
55
      emb|Z48618|SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), P... 36 0.68
      emb|Z72673|SCYGL151W S.cerevisiae chromosome VII reading frame O... 36 0.68
      emb|AF126872|AF126872 Magnaporthe grisea magnaporin mRNA, comple... 36 0.68
      emb|AF044679|AF044679 Leishmania major thiol specific antioxidan... 31 1.0
      emb|AC011617|AC011617 Leishmania major chromosome 35 clone L2993... 36 1.3
60
      emb|AB002141|AB002141 Pyrus pyrifolia mRNA for S5-RNase, complet... 35 1.3
      dbj|D88282|D88282 Pyrus serotina mRNA for S5-RNase, complete cds.
```

	emb AB025421 AB025421 Pyrus pyrifolia gene for S3-RNase, complet 35 1.3 emb AB002140 AB002140 Pyrus pyrifolia mRNA for S3-RNase, complet 35 1.3
	emb AL357592 LMFL5856 Leishmania major Friedlin chromosome 5 cos 35 1.3
5 .	emb AW180136 AW180136 MgA0212f MgA Library Mycosphaerella gramin 35 1.8
3	emb AW677734 AW677734 WS1_10_E07.g1_A002 Water-stressed 1 (WS1) 35 1.8 emb AI780435 AI780435 EST261314 tomato susceptible, Cornell Lyco 34 2.4
	emb AL355928 NCB1D4 Neurospora crassa DNA linkage group II BAC c 34 2.4
	emb AF188714 AF188714 Emericella nidulans chromosome VIII cosmid 34 2.4
	emb AF138284 AF138284 Emericella nidulans molybdopterin synthase 34 2.4
10	gb M23080 BLYHORA Hordeum vulgare alpha-hordothionin (Hth-1) gen 26 3.3
	emb AQ989014 AQ989014 35C1D04NE.R1 C. parvum Lambda Zap Express 34 3.3
	emb X55685 LEEXTEN5 Tomato extensin mRNA (clone uG-18). 34 3.3
	emb AB001337 AB001337 Saccharum officinarum mRNA for Sucrose-Pho 34 3.3
	emb AW565301 AW565301 LG1_342_G03.g1_A002 Light Grown 1 (LG1) So 34 3.3
15	emb AL035064 SPAC1687 S.pombe chromosome I cosmid c1687. 34 3.3
•	emb AJ223010 SCP223010 Schizosaccharomyces pombe pmt2 gene. 34 3.3
	emb AL356456 LMFLUNK01 Leishmania major Friedlin cosmid clones L 34 3.3
	emb AW683291 AW683291 NF010B07LF1F1060 Developing leaf Medicago 34 3.3
	emb X63357 HVNREHTH H.vulgare Hth-1 gene (promoter region). 26 3.3
20	emb AW710511 AW710511 e4c05ne.fl Neurospora crassa evening cDNA 34 4.4
	emb AQ411888 AQ411888 CpG0892A CpIOWAgDNA1 Cryptosporidium parvu 34 4.4
	emb AB036808 AB036808 Saccharomyces cerevisiae DNA, plasmid pTLU 33 4.6
	emb AA901701 AA901701 NCP2A2T7 Perithecial Neurospora crassa cDN 33 4.6
25	emb AF128526 AF128526 Theileria lestoquardi sporozoite antigen S 33 4.6
23	gb M76671 TOMEXTENB L.esculentum extensin (class II) gene, compl 33 4.6 emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai 33 4.6
	emb AB036809 AB036809 Saccharomyces cerevisiae DNA, plasmid pTLU 33 4.6
	emb AC004145 AC004145 Leishmania major chromosome 3 clone L5801 32 4.8
	gb L12467 YSCGCN1A Saccharomyces cerevisiae translational activa 33 6.1
30	emb AW725958 AW725958 GA_Ea0020E02 Gossypium arboreum 7-10 dpa 33 6.1
	emb X91837 SCCHVIIEU S.cerevisiae G1301, G1304, G1307, G1315, G1 33 6.1
	emb Z72717 SCYGL195W S.cerevisiae chromosome VII reading frame O 33 6.1
	emb X55694 LEEXTEN14 Tomato extensin mRNA (clone w10-1 L). 33 6.3
	emb X55693 LEEXTEN13 Tomato mRNA for a glycine-rich protein (clo 33 6.3,
35	emb AV427911 AV427911 AV427911 Lotus japonicus young plants (two 33 6.3
	emb AI897079 AI897079 EST266522 tomato ovary, TAMU Lycopersicon 33 6.3
	emb AW690872 AW690872 NF039H07ST1F1000 Developing stem Medicago 33 6.3
-	emb AW688252 AW688252 NF005C01ST1F1000 Developing stem Medicago 33 6.3
40	gb L38908 TOBEXTE Nicotiana tabacum extensin gene, complete cds. 33 6.3
40	dbj[D13951]TOBEXTS Tobacco gene for extensin, complete cds. 33 6.3
	dbj[E05393]E05393 DNA sequence encoding Nicotiana tabacum extensin. 33 6.3
	emb AA901958 AA901958 NCC2C12T7 Conidial Neurospora crassa cDNA 33 8.3 emb AW704352 AW704352 sk18c03.y1 Gm-c1028 Glycine max cDNA clone 33 8.3
	emb AF085735 AF085735 Trypanosoma triglae kinetoplast minicircle 33 8.3
45	emb AW457944 AW457944 sh97h02.yl Gm-c1016 Glycine max cDNA clone 33 8.3
	emb AW714167 AW714167 h6d08ne.fl Neurospora crassa evening cDNA 33 8.3
	emb AI320172 AI320172 c1f06nm.fl Neurospora crassa morning cDNA 33 8.3
	emb AQ941354 AQ941354 Sheared DNA-19O3.TR Sheared DNA Trypanosom 32 8.6
	emb AF046120 AF046120 Candida glabrata ATP-binding cassette tran 32 8.6
50	emb AW725268 AW725268 GA_Ea0015L23 Gossypium arboreum 7-10 dpa 32 8.6
	emb X77955 NCERG3 N.crassa (74-OR23-1VA) erg3 gene. 27 8.8
	Query= AL022605.63_at 14882_at /id_source genbank /description
	emb caa18753.1 (al022605) putative protein [arabidopsis thaliana]
55	/blast_score 1.00e-103 /ec_number /family /chip nova /gb_link
-	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb al022605 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al022605
	(645 letters)
60	•

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching..... 5 E Score Sequences producing significant alignments: (bits) Value emb|AW398164|AW398164 EST298047 L. pennellii trichome, Cornell U... 101 1e-44 emb|AW351246|AW351246 GM210011A20F7R Gm-r1021 Glycine max cDNA 3... 114 3e-43 10 emb|AW222063|AW222063 EST298874 tomato fruit red ripe, TAMU Lyco... 103 4e-40 emb|AW218145|AW218145 EST303326 tomato radicle, 5 d post-imbibit... 103 1e-39 emb|AW398260|AW398260 EST298107 L. pennellii trichome, Cornell U... 101 3e-39 emb|AW477271|AW477271 ga44c12.yl Moss EST library PPU Physcomitr... 94 1e-38 emb|AW568049|AW568049 si56g06.yl Gm-r1030 Glycine max cDNA clone... 102 1e-36 15 emblAW565775|AW565775 LG1 349 D04.g1 A002 Light Grown 1 (LG1) So... 108 5e-35 emb|AW218146|AW218146 EST303327 tomato radicle, 5 d post-imbibit... 108 5e-26 emb|AI488047|AI488047 EST246369 tomato ovary, TAMU Lycopersicon ... 78 3e-24 emb|AW671633|AW671633 LG1 349 D04.b1 A002 Light Grown 1 (LG1) So... 111 4e-24 emb|AI495965|AI495965 sb18d07.yl Gm-c1004 Glycine max cDNA clone... 102 3e-21 20 emb|AT002115|AT002115 AT002115 Flower bud cDNA Brassica rapa sub... 52 1e-09 emb[AT001714]AT001714 AT001714 Flower bud cDNA Brassica rapa sub... 52 3e-09 emb|AW621058|AW621058 sj95d05.yl Gm-c1023 Glycine max cDNA clone... 52 3e-08 emb|AW099304|AW099304 sd38a08.y1 Gm-c1016 Glycine max cDNA clone... 33 0.092 emb[AI774719]AI774719 EST255819 tomato resistant, Cornell Lycope... 35 0.12 25 emb|AW040524|AW040524 EST283484 tomato mixed elicitor, BTI Lycop... 35 0.12 emb|AB003068|AB003068 Trypanosoma cruzi clone TcCE5-9-1 mRNA, pa... 36 0.22 emb|AI781680|AI781680 EST262559 tomato susceptible, Cornell Lyco... 33 0.29 emb|AI778418|AI778418 EST259297 tomato susceptible, Cornell Lyco... 33 0.29 emb|AI775731|AI775731 EST256831 tomato resistant, Cornell Lycope... 35 0.78 30 emb|AF047694|AF047694 Vernicia fordii glutaredoxin mRNA, complet... 34 1.1 emb|AW599677|AW599677 ga91d04.yl Moss EST library PPN Physcomitr... 34 1.1 emb|AW039130|AW039130 EST281103 tomato mixed elicitor, BTI Lycop... 31 1.3 emb|AB003073|AB003073 Trypanosoma cruzi clone CE5-9-5 mRNA, part... 34 1.5 emb|AI899521|AI899521 EST268964 tomato susceptible, Cornell Lyco... 30 1.8 35 emb[AI055583]AI055583 coau0004G11 Cotton Boll Abscission Zone cD... 33 2.0 emb|AI776180|AI776180 EST257280 tomato resistant, Cornell Lycope... 30 2.4 emb|AL110509|SPAC1250 S.pombe chromosome I cosmid c1250. emb|Z74775|SCYOL033W S.cerevisiae chromosome XV reading frame OR... 33 2.8 gb|BE034215|BE034215 MH01C08 MH Mesembryanthemum crystallinum cD... 33 2.8 40 emb|AZ220957|AZ220957 Sheared DNA-94E5.TR Sheared DNA Trypanosom... 33 2.8 gb|L39015|YSCMSE1G Saccharomyces cerevisiae nuclear-encoded mito... 33 2.8 emb|AI398391|AI398391 NCSM1H10T7 Subtracted Mycelial Neurospora ... 33 2.8 emb|AI898738|AI898738 EST268181 tomato ovary, TAMU Lycopersicon ... 32 3.8 emb|AI487645|AI487645 EST245967 tomato ovary, TAMU Lycopersicon ... 32 3.8 emb|AW929266|AW929266 EST338054 tomato flower buds 8 mm to pre-a... 32 3.8 45 emb|AQ911385|AQ911385 LMAJFV1 ln03f07.x1 Leishmania major FV1 ra... 32 3.8 emb|AW677168|AW677168 DG1_5_E01.b1_A002 Dark Grown 1 (DG1) Sorgh... 32 3.8 emb|AI486591|AI486591 EST244912 tomato ovary, TAMU Lycopersicon ... 32 3.8 emb|AU011071|AU011071 AU011071 Schizosaccharomyces pombe late lo... 50 emb|AI776382|AI776382 EST257482 tomato resistant, Cornell Lycope... 29 4.3 emb|AW760067|AW760067 sl57f01.yl Gm-c1027 Glycine max cDNA clone... 28 4.7 emb|AW570039|AW570039 si85h08.yl Gm-c1031 Glycine max cDNA clone... 32 5.3 emb|Z36045|SCYBR176W S.cerevisiae chromosome II reading frame OR... 32 5.3 emb|AB012577|AB012577 Saccharomyces cerevisiae EHT1 gene for alc... 32 5.3 55 emb|AQ952955|AQ952955 Sheared DNA-52J12.TR Sheared DNA Trypanoso... 32 5.3 emb|AW704696|AW704696 sk39d04.yl Gm-c1028 Glycine max cDNA clone... 31 7.2 emb|AF091835|AF091835 Trypanosoma cruzi strain CL beta tubulin a... 31 7.2 gb|M96849|TRBBEALTUB Trypanosoma cruzi beta and alpha tubulin ge... 31 7.2 gb[M97956]TRBBEALTU Trypanosoma cruzi beta tubulin and alpha tub... 31 7.2 60 emb|AW686835|AW686835 NF043H11NR1F1000 Nodulated root Medicago t... 31 9.9 emb|AI304976|AI304976 EST00081 mRNP Lambda ZapII Express Library... 31 9.9

emb|AF026421|AF026421 Chlamydomonas reinhardtii clone CD191 star... 31 9.9 emb|AV391990|AV391990 Chlamydomonas reinhardtii C9 Chla... 31 9.9 emb|AW624834|AW624834 EST313651 tomato radicle, 5 d post-imbibit... 31 9.9 gb|L34658|FSOGAGPOL Fusarium oxysporum gag polyprotein (gag) gen... 31 9.9 emb|X64601|ANNIMTMR A.nidulans nimT mRNA for tyrosine phosphatase. 31 9.9

Query= U93215.38_at 15366_at /id_source genbank /description gb|aab63077.1| (u93215) unknown protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova/gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|u93215| /ncgi http://www.ncgr.org/cgi-bin/ff?u93215 (1761 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

5

10

25

30

35

40

45

50

55

60

Searching......done

Score E

Sequences producing significant alignments: (bits) Value

emb[AV411445]AV411445 AV411445 Lotus japonicus young plants (two... 198 le-49 emb|AV415235|AV415235 AV415235 Lotus japonicus young plants (two... 190 3e-47 emb|AV415282|AV415282 AV415282 Lotus japonicus young plants (two... 190 3e-47 emb|AW906097|AW906097 EST342218 potato stolon, Cornell Universit... 162 8e-39 emb|AV413830|AV413830 AV413830 Lotus japonicus young plants (two... 161 1e-38 emblAV419573|AV419573 AV419573 Lotus japonicus young plants (two... 82 5e-36 emb|AA660119|AA660119 EST00006 watermelon lambda zap express lib... 148 7e-36 emb|AI507855|AI507855 sa88a07.y1 Gm-c1004 Glycine max cDNA clone... 91 2e-35 emb|AW160273|AW160273 EST290131 L. pennellii trichome, Cornell U... 146 4e-34 emb|AV428532|AV428532 AV428532 Lotus japonicus young plants (two... 80 3e-30 emb|AV424557|AV424557 AV424557 Lotus japonicus young plants (two... 128 1e-28 emb|AW668007|AW668007 GA_Ea0012E04 Gossypium arboreum 7-10 dpa ... 117 2e-25 emb|AW922981|AW922981 DG1_48_B03.b1_A002 Dark Grown 1 (DG1) Sorg... 105_8e-22 emb|AW432282|AW432282 sh71f09.yl Gm-c1015 Glycine max cDNA clone... 100 3e-20 emb|AW621610|AW621610 EST312408 tomato root during/after fruit s... 100 5e-20 emb|AV419981|AV419981 AV419981 Lotus japonicus young plants (two... 95 2e-18 emb|AI937949|AI937949 sc06a10.y1 Gm-c1012 Glycine max cDNA clone... 88 3e-16 emb|AV406642|AV406642 AV406642 Lotus japonicus young plants (two... 67 6e-10 emb|AW497095|AW497095 ga53g06.yl Moss EST library PPU Physcomitr... 42 3e-06 emb|AW289850|AW289850 NXNV006F04F Nsf Xylem Normal wood Vertical... 40 4e-05 emb|AW279534|AW279534 sf90g12.yl Gm-c1019 Glycine max cDNA clone... 46 7e-04 emb|AQ911817|AQ911817 LMAJFV1 ln03b09.y1 Leishmania major FV1 ra... 46 7e-04 emb|AW689523|AW689523 NF021G01ST1F1000 Developing stem Medicago ... 39 0.007 emb|AW218923|AW218923 EST301405 tomato root during/after fruit s... 41 0.030 emb|AW695963|AW695963 NF101A10ST1F1072 Developing stem Medicago ... 40 0.041 emb|AW931531|AW931531 EST357374 tomato fruit mature green, TAMU ... 40 0.041 emb|AW691108|AW691108 NF041C09ST1F1000 Developing stem Medicago ... 39 0.14 emb|AA791402|AA791402 LO-136M13R Ice plant Lambda Uni-Zap XR exp... 38 0.20 emb|AI001408|AI001408 L0-330M13R Ice plant Lambda Uni-Zap XR exp... 38 0.20 emb|AI731457|AI731457 BNLGHi9807 Six-day Cotton fiber Gossypium ... 38 0.27 emb|AQ161167|AQ161167 mgxb0007I01r CUGI Rice Blast BAC Library P... 35 1.3 emb|AW690030|AW690030 NF027E08ST1F1000 Developing stem Medicago ... 35 1.8 gb|BE124825|BE124825 EST393860 GVN Medicago truncatula cDNA clon... 35 1.8 emb|AW684862|AW684862 NF022D06NR1F1000 Nodulated root Medicago t... 35 1.8 emb|AW686248|AW686248 NF039F10NR1F1000 Nodulated root Medicago t... 35 1.8 emb|AW696000|AW696000 NF100H02ST1F1026 Developing stem Medicago ... 35 1.8 emb|AW686364|AW686364 NF037B05NR1F1000 Nodulated root Medicago t... 35 1.8 emb|AW926002|AW926002 HVSMEg0006A15 Hordeum vulgare pre-anthesis... 35 2.5 emb|AA660722|AA660722 00613 MtRHE Medicago truncatula cDNA 5', m... 34 3.5

emb|AI054829|AI054829 coau0002E06 Cotton Boll Abscission Zone cD... 34 3.5 emb|AW719283|AW719283 LjNEST2b8r Lotus japonicus nodule library,... 34 3.5 emb|AW677540|AW677540 DG1 8 H03.b1_A002 Dark Grown 1 (DG1) Sorgh... emb|X78996|CSTETFP C.sativus mRNA for tetrafunctional protein. emb|AQ654502|AQ654502 Sheared DNA-25C14.TR Sheared DNA Trypanoso... 33 6.6 emb|AW981113|AW981113 EST392266 GVN Medicago truncatula cDNA clo... 33 6.6 gb|L40389|YSAERG11X Candida glabrata ERG11 gene, complete cds. emb|X79365|CSMFPB C.sativus MFP-b mRNA. gb|U05612|CSU05612 Colysis sintenensis chloroplast large subunit... 28 6.8 10 emb|X02433|MIPSCOX2 Pea mitochondrial gene for cytochrome oxidas... 24 6.9 emb|AQ654503|AQ654503 Sheared DNA-25C15.TR Sheared DNA Trypanoso... 33 9.0 emb|AI163319|AI163319 A039P66U Hybrid aspen plasmid library Popu... 33 9.0 emb|AQ641986|AQ641986 RPCI93-EcoRI-6N23.TJ RPCI93-EcoRI Trypanos... 33 9.0 emb|AL034558|PFMAL3P2 Plasmodium falciparum MAL3P2, complete seq... 33 9.0 15 emb|AQ649633|AQ649633 Sheared DNA-17K4.TF Sheared DNA Trypanosom... 33 9.0 emb|AI728749|AI728749 BNLGHi11499 Six-day Cotton fiber Gossypium... 33 9.0 emb|AQ940463|AQ940463 Sheared DNA-33A23.TR Sheared DNA Trypanoso... 33 9.0 emb|AQ647492|AQ647492 RPCI93-EcoRI-6G10.TJ RPCI93-EcoRI Trypanos... 33 9.0 emb|AW443117|AW443117 EST308047 tomato mixed elicitor, BTI Lycop... 33 9.0 20 emb|AA231646|AA231646 CDO328.F cDNA from oat Avena sativa cDNA c... 33 9.0 Query= AF000657.28 at 15415 at /id source genbank /description gb|aab72169.1| (af000657) hypothetical protein [arabidopsis thaliana] /blast_score 9.00e-96 /ec number /family /chip nova /gb link 25

http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|af000657| /ncgi

http://www.ncgr.org/cgi-bin/ff?af000657 (564 letters)

30 Database: plantfungal

40

45

50

55

60

661,018 sequences; 426,114,510 total letters

Searching......done

35

Score E

Sequences producing significant alignments:

(bits) Value

emb|AW622665|AW622665 EST313465 tomato root during/after fruit s... 166 8e-42 emb|AW625889|AW625889 EST319892 tomato radicle, 5 d post-imbibit... 166 1e-41 emblAI776839|AI776839 EST257939 tomato resistant, Cornell Lycope... 166 2e-40 emb|AI898331|AI898331 EST267774 tomato ovary, TAMU Lycopersicon ... 166 2e-40 emb|AI772887|AI772887 EST253987 tomato resistant, Cornell Lycope... 166 2e-40 emb|AI782639|AI782639 EST263518 tomato susceptible, Cornell Lyco... 161 2e-40 emb|AW035141|AW035141 EST280403 tomato callus, TAMU Lycopersicon... 162 3e-40 emb|AW559773|AW559773 EST314821 DSIR Medicago truncatula cDNA cl... 136 4e-40 emb|AI488935|AI488935 EST247274 tomato ovary, TAMU Lycopersicon ... 162 1e-39 emblAW626015|AW626015 EST319922 tomato radicle, 5 d post-imbibit... 161 4e-39 emb|AW035118|AW035118 EST280380 tomato callus, TAMU Lycopersicon... 159 1e-38 emb|AI442841|AI442841 sa27e02.x1 Gm-c1004 Glycine max cDNA clone... 131 2e-38 gb|BE057238|BE057238 sm99d06.yl Gm-c1015 Glycine max cDNA clone ... 133 4e-37 gb|BE021888|BE021888 sm63g06.yl Gm-c1028 Glycine max cDNA clone ... 151 4e-36 emb|AW782173|AW782173 sm02d12.yl Gm-c1027 Glycine max cDNA clone... 151 4e-36 emb|AW981240|AW981240 EST392330 DSIL Medicago truncatula cDNA cl... 127 5e-36 emb|AW624844|AW624844 EST313673 tomato radicle, 5 d post-imbibit... 150 6e-36 emb|AW348098|AW348098 GM210001A11F3R Gm-r1021 Glycine max cDNA 3... 121 1e-35 emb|AW348956|AW348956 GM210004A12C2R Gm-r1021 Glycine max cDNA 3... 127 2egb|BE058374|BE058374 sn15b11.yl Gm-c1016 Glycine max cDNA clone ... 127 2e-35 emb|AW570563|AW570563 sj63f09.yl Gm-c1033 Glycine max cDNA clone... 127 2e-35

emb|AW568265|AW568265 si69f02.yl Gm-r1030 Glycine max cDNA clone... 127 2e-35 emb|AW666011|AW666011 sk31a06.yl Gm-c1028 Glycine max cDNA clone... 127 2e-35

emb|AW306271|AW306271 se48e06.y1 Gm-c1017 Glycine max cDNA clone... 125 6e-35 emb|AI772066|AI772066 EST253166 tomato resistant, Cornell Lycope... 146 1e-34 emb|AW395160|AW395160 sh40f10.y1 Gm-c1017 Glycine max cDNA clone... 124 1e-34 emb|AW306309|AW306309 se49a06.yl Gm-c1017 Glycine max cDNA clone... 124 1e-34 5 gb|BE022272|BE022272 sm73a07.yl Gm-c1028 Glycine max cDNA clone ... 146 1e-34 gb|BE021996|BE021996 sm65c01.yl Gm-c1028 Glycine max cDNA clone ... 146 1e-34 emb|AW706543|AW706543 sj57h02.y1 Gm-c1033 Glycine max cDNA clone... 146 1e-34 emb|AW620987|AW620987 sj50d09.y1 Gm-c1033 Glycine max cDNA clone... 146 1e-34 emb|AW349990|AW349990 GM210006B20G11R Gm-r1021 Glycine max cDNA ... 146 1e-10 emb|AW706119|AW706119 sj52a11.yl Gm-c1033 Glycine max cDNA clone... 146 1e-34 emb|AW311107|AW311107 sg33a02.y1 Gm-c1025 Glycine max cDNA clone... 124 2e-34 emb|AW200806|AW200806 se93g05.y1 Gm-c1027 Glycine max cDNA clone... 123 3e-34 emb|AW830450|AW830450 sm27b08.y1 Gm-c1028 Glycine max cDNA clone... 145 3e-34 15 emb|AW458429|AW458429 sh09b05.y1 Gm-c1016 Glycine max cDNA clone... 127 4e-34 emb|AW559537|AW559537 EST314585 DSIR Medicago truncatula cDNA cl... 79 5e-34 emb|AW559584|AW559584 EST314632 DSIR Medicago truncatula cDNA cl... 79 5e-34 emb|AI939020|AI939020 sc64e06.yl Gm-c1016 Glycine max cDNA clone... 144 7e-34 emb|AW234019|AW234019 sf33b10.y1 Gm-c1028 Glycine max cDNA clone... 143 1e-33 20 emb|AW011055|AW011055 ST16B07 Pine TriplEx shoot tip library Pin... 142 2e-33 emb|AW687043|AW687043 NF005D02RT1F1016 Developing root Medicago ... 133 2e-33 gb[BE022312]BE022312 sm73c09.y1 Gm-c1028 Glycine max cDNA clone ... 142 3e-33 emb|AW620826|AW620826 sj47a07.y1 Gm-c1033 Glycine max cDNA clone... 119 3e-33 emb|AW666225|AW666225 sk34a04.y1 Gm-c1028 Glycine max cDNA clone... 140 9e-33 25 emb|AI494896|AI494896 sb06g10.yl Gm-c1004 Glycine max cDNA clone... 140 9e-33 emb|AI443387|AI443387 sa31d11.x1 Gm-c1004 Glycine max cDNA clone... 139 1e-32 emb|AW203753|AW203753 sf37h02.y1 Gm-c1028 Glycine max cDNA clone... 139 2e-32 emb|AW559725|AW559725 EST314717 DSIR Medicago truncatula cDNA cl... 78 4e-32 emb|AW289859|AW289859 NXNV007A04F Nsf Xylem Normal wood Vertical... 137 4e-32 30 emb|AW234737|AW234737 sf18f10.y1 Gm-c1028 Glycine max cDNA clone... 136 2e-31 emb|AW351059|AW351059 GM210010B10G3R Gm-r1021 Glycine max cDNA 3... 136 2eemb|AW684772|AW684772 NF021H06NR1F1000 Nodulated root Medicago t... 120 5e-31 emb|AW775144|AW775144 EST334295 KV3 Medicago truncatula cDNA clo... 76 9e-31 35 emb|AI495113|AI495113 sb03f02.yl Gm-c1004 Glycine max cDNA clone... 133 1e-30 emb|AW472306|AW472306 si23e07.yl Gm-c1029 Glycine max cDNA clone... 117 2e-30 emblAW035139|AW035139 EST280401 tomato callus, TAMU Lycopersicon... 131 5e-30 emb|AI496590|AI496590 sb13g02.y1 Gm-c1004 Glycine max cDNA clone... 129 2e-29 emb|AW351151|AW351151 GM210011A10E12R Gm-r1021 Glycine max cDNA ... 81 2e-29 40 emb|AW460064|AW460064 si08g11.y1 Gm-c1029 Glycine max cDNA clone... 105 4e-29 emb|AW432674|AW432674 sh83h05.y1 Gm-c1016 Glycine max cDNA clone... 126 1e-28 emb|AW507521|AW507521 si53a07.y1 Gm-r1030 Glycine max cDNA clone... 106 1e-28 emb|AI461088|AI461088 sa73g10.yl Gm-c1004 Glycine max cDNA clone... 123 8e-28 emb|AI461045|AI461045 sa73c04.y1 Gm-c1004 Glycine max cDNA clone... 123 8e-28 45 emb|AW010003|AW010003 ST01B12 Pine TriplEx shoot tip library Pin... 123 8e-28 gb|BE021390|BE021390 sm48e04.yl Gm-c1028 Glycine max cDNA clone ... 122 2e-27 gb|BE022539|BE022539 sm86c09.yl Gm-c1015 Glycine max cDNA clone ... 121 4e-27 emb|AW559258|AW559258 EST306094 DSIR Medicago truncatula cDNA cl... 118 3e-26 emb|AW760707|AW760707 sl36a09.yl Gm-c1027 Glycine max cDNA clone... 95 8e-26 50 emb|AI941013|AI941013 sb83c06.yl Gm-c1010 Glycine max cDNA clone... 95 8e-26 emb|AW745074|AW745074 LG1_386_D11.b1_A002 Light Grown 1 (LG1) So... 91 3e-25 emb|AI900284|AI900284 sc03d11.yl Gm-c1012 Glycine max cDNA clone... 111 4e-25 emb|AW666457|AW666457 sk36g12.y1 Gm-c1028 Glycine max cDNA clone... 114 7e-25 emb|AI522845|AI522845 sa74e03.yl Gm-c1004 Glycine max cDNA clone... 114 7e-25 55 emb[AW350289]AW350289 GM210008A10D4R Gm-r1021 Glycine max cDNA 3... 113 9eemb|AW233771|AW233771 sf26e08.y1 Gm-c1028 Glycine max cDNA clone... 105 1e-24 gb|BE021431|BE021431 sm49a02.y1 Gm-c1028 Glycine max cDNA clone ... 111 4e-24 emb|AW495792|AW495792 NXNV 065 D12 FF Nsf Xylem Normal wood Vert... 110 8e-24 60 emb|AI441701|AI441701 sa60b06.yl Gm-c1004 Glycine max cDNA clone... 110 8e-24 emb|AW686910|AW686910 NF003H08RT1F1000 Developing root Medicago ... 79 9e-24

emb|AW310235|AW310235 sf33b10.x1 Gm-c1028 Glycine max cDNA clone... 110 1e-23 emb|AI495196|AI495196 sa89d04.y1 Gm-c1004 Glycine max cDNA clone... 100 4e-23 emb|AI442650|AI442650 sa43f05.y1 Gm-c1004 Glycine max cDNA clone... 106 1e-22 emb|AW926095|AW926095 HVSMEg0006F02 Hordeum vulgare pre-anthesis... 106 1e-22 emb|AW309915|AW309915 sf26e08.x1 Gm-c1028 Glycine max cDNA clone... 105 2e-22 emb|AI812367|AI812367 1E2 Pine Lambda Zap Xylem library Pinus ta... 104 5e-22 gb|BE022988|BE022988 sm69b05.yl Gm-c1028 Glycine max cDNA clone ... 103 1e-21 emb|AI748713|AI748713 sb61a02.y1 Gm-c1010 Glycine max cDNA clone... 82 1e-21 gb|BE020169|BE020169 sm39e04.y1 Gm-c1028 Glycine max cDNA clone ... 103 1e-21 10 gb|BE021658|BE021658 sm60g09.yl Gm-c1028 Glycine max cDNA clone ... 101 3e-21 emb|AI855670|AI855670 sc32f08.yl Gm-c1014 Glycine max cDNA clone... 100 2e-20 emb|AI920195|AI920195 1725 Pine Lambda Zap Xylem library Pinus t... 73 2e-20 emb|AW686987|AW686987 NF004G02RT1F1018 Developing root Medicago ... 99 2e-20 emb|AW684941|AW684941 NF023D03NR1F1000 Nodulated root Medicago t... 88 1e-19 15 emb|AI494665|AI494665 sb18f10.y1 Gm-c1004 Glycine max cDNA clone... 89 1e-19 emb|AW277935|AW277935 sf87g05.yl Gm-c1019 Glycine max cDNA clone... 97 1e-19 gb|BE023344|BE023344 sm70f11.yl Gm-c1028 Glycine max cDNA clone ... 78 2e-19 emb|AV422621|AV422621 AV422621 Lotus japonicus young plants (two... 60 2e-19 emb|AW127416|AW127416 M110599 DSIL Medicago truncatula cDNA clon... 95 4e-19 20 Ouery= AL030978.64_at 15431_at /id_source genbank /description emb|caa19722.1| (al030978) putative protein [arabidopsis thaliana] /blast score 2.00e-51/ec number /family /chip nova/gb link http://www3.ncbi.nlm.nih.gov/htbin-25 post/entrez/query?db=n&form=6&dopt=g&uid=gb|a1030978| /ncgi http://www.ncgr.org/cgi-bin/ff?al030978 (393 letters) Database: plantfungal 30 661,018 sequences; 426,114,510 total letters Searching.....done E Score 35 Sequences producing significant alignments: (bits) Value emb|AW218792|AW218792 EST301272 tomato root during/after fruit s... 104 2e-30 emb|AW218791|AW218791 EST301271 tomato root during/after fruit s... 104 2e-30 emblAI781536|AI781536 EST262415 tomato susceptible, Cornell Lyco... 104 2e-30 emb|AI894486|AI894486 EST263929 tomato callus, TAMU Lycopersicon... 100 3e-29 40 emb|AW255546|AW255546 ML580 peppermint glandular trichome Mentha... 96 4e-25 emb|AW781055|AW781055 sl88d08.yl Gm-c1037 Glycine max cDNA clone... 95 5e-25 emb|AW980335|AW980335 EST391488 GVN Medicago truncatula cDNA clo... 94 1e-24 emb|AW982334|AW982334 HVSMEg0002O20f Hordeum vulgare pre-anthesi... 86 1e-24 45 gb|H74448|H74448 150 Standard Brassica napus cDNA clone R29F, mR... 92 4e-24 emb|AI960943|AI960943 sc93a04.y1 Gm-c1019 Glycine max cDNA clone... 92 5e-24 emb|AU036790|AU036790 AU036790 Cryptomeria japonica seedling lea... 88 5e-24 emb|AW598247|AW598247 sj42f01.yl Gm-c1008 Glycine max cDNA clone... 80 3e-23 emb|AW100651|AW100651 sd58b12.y1 Gm-c1008 Glycine max cDNA clone... 89 4e-23 50 emblAW208200|AW208200 M110845e GVSN Medicago truncatula cDNA clo... 88 5e-23 emb|AW559726|AW559726 EST314718 DSIR Medicago truncatula cDNA cl... 83 2e-22 emb|AW101120|AW101120 sd74c08.y1 Gm-c1008 Glycine max cDNA clone... 94 2e-22 emb|AW926990|AW926990 HVSMEg0009D05 Hordeum vulgare pre-anthesis... 103 8e-22 gb|BE124173|BE124173 EST394298 DSIL Medicago truncatula cDNA clo... 94 1e-21 55 emb|AT000903|AT000903 AT000903 Brassica rapa guard cell Brassica... 54 2e-20 emb[AW690635]AW690635 NF031H11ST1F1000 Developing stem Medicago ... 75 6e-20 emb|AW126039|AW126039 N100235e rootphos(-) Medicago truncatula c... 75 6e-20 emb|AW126127|AW126127 N100324e rootphos(-) Medicago truncatula c... 75 7e-20 emb|AI812959|AI812959 2A11 Pine Lambda Zap Xylem library Pinus t... 75 2e-19 60 emb|AI043565|AI043565 L30-578T3 Ice plant Lambda Uni-Zap XR expr... 75 3e-19

emb|AW396602|AW396602 sg80b06.yl Gm-c1026 Glycine max cDNA clone... 95 3e-19

```
gb|BE059263|BE059263 sn28d04.y1 Gm-c1016 Glycine max cDNA clone ... 95 3e-19
      emb|AW736823|AW736823 NXNV 083 D01 F Nsf Xylem Normal wood Verti... 73 3e-19
      emb|AW461253|AW461253 NXNV060C05F Nsf Xylem Normal wood Vertical... 70 7e-18
      emb|AW126244|AW126244 N100089e rootphos(-) Medicago truncatula c... 53 2e-17
      emb|AW683890|AW683890 NF003A10NR1F1000 Nodulated root Medicago t... 49 4e-17
      emb|AW922806|AW922806 DG1 46 G06.g1 A002 Dark Grown 1 (DG1) Sorg... 84 4e-17
      emb|AW290613|AW290613 NXNV044B04F Nsf Xylem Normal wood Vertical... 65 9e-17
      emblAW567768|AW567768 si54f04.yl Gm-r1030 Glycine max cDNA clone... 64 7e-16
      emblAW568036lAW568036 si56f04.yl Gm-r1030 Glycine max cDNA clone... 64 7e-16
10
      emb|AW461226|AW461226 NXNV048H05F Nsf Xylem Normal wood Vertical... 74 9e-15
      emb|AW720025|AW720025 LjNEST15c3r Lotus japonicus nodule library... 78 2e-14
      emb|AI812590|AI812590 13F9 Pine Lambda Zap Xylem library Pinus t... 54 1e-13
      emb|AW350351|AW350351 GM210008A10G1R Gm-r1021 Glycine max cDNA 3... 73 1e-12
      emb|AI779006|AI779006 EST259885 tomato susceptible, Cornell Lyco... 73 1e-12
15
      emb|AA557075|AA557075 917 Loblolly pine N Pinus taeda cDNA clone... 70 2e-12
      emb|AI899615|AI899615 EST269058 tomato susceptible, Cornell Lyco... 72 2e-12
      emb|AW394975|AW394975 sh37h12.y1 Gm-c1017 Glycine max cDNA clone... 69 1c-11
      emb|AU036851|AU036851 AU036851 Cryptomeria japonica seedling lea... 69 1e-11
      emb|AW394753|AW394753 sh34h05.yl Gm-c1017 Glycine max cDNA clone... 68 2e-11
20
      emb|AI965467|AI965467 sc72c05.yl Gm-c1018 Glycine max cDNA clone... 68 3e-11
      emb|AI495151|AI495151 sa88f06.y1 Gm-c1004 Glycine max cDNA clone... 67 6e-11
      gb|BE034744|BE034744 ML03G11 ML Mesembryanthemum crystallinum cD... 44 2e-10
      emb|AI771301|AI771301 EST252317 tomato ovary, TAMU Lycopersicon ... 64 6e-10
      emb|AW424128|AW424128 sh61c09.y1 Gm-c1015 Glycine max cDNA clone... 63 8e-10
25
      emb|AI736289|AI736289 sb26d05.yl Gm-c1008 Glycine max cDNA clone... 59 1e-08
      emb|AW888120|AW888120 NXNV 129 D10 F Nsf Xylem Normal wood Verti... 56 2e-08
      emb|AW784020|AW784020 NXNV_103 A11 F Nsf Xylem Normal wood Verti... 54 8e-08
      emb|AI938510|AI938510 sb46e12.yl Gm-c1015 Glycine max cDNA clone... 55 2e-07
      emb|AT000179|AT000179 AT000179 Apple young fruit cDNA library Ma... 41 0.004
30
      emb|AW234162|AW234162 sf22a01.y1 Gm-c1028 Glycine max cDNA clone... 40 0.006
      gb|BE033785|BE033785 MF06D08 MF Mesembryanthemum crystallinum cD...
      gb|BE034795|BE034795 ML04D08 ML Mesembryanthemum crystallinum cD...
      emb|AW309614|AW309614 sf22a01.x1 Gm-c1028 Glycine max cDNA clone...
      gb|L01433|SOYSCAM4X Soybean calmodulin (SCaM-4) mRNA, complete cds. 40 0.008
35
      gb|U20292|STU20292 Solanum tuberosum clone PCM3 calmodulin gene,... 40 0.008
      emb|AW458431|AW458431 sh09b07.yl Gm-c1016 Glycine max cDNA clone...
      emb|AW704882|AW704882 sk40g04.yl Gm-c1019 Glycine max cDNA clone...
      emb|AW706736|AW706736 sk02d02.y1 Gm-c1023 Glycine max cDNA clone...
      gb[M88307]BNACALM Brassica juncea calmodulin mRNA, complete cds.
                                                                         38 0.030
40
      gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 38 0.030
      emb|AW266313|AW266313 L30-3052T3 Ice plant Lambda Uni-Zap XR exp... 38 0.041
      emb|AW317381|AW317381 sg48f11.yl Gm-c1025 Glycine max cDNA clone... 38 0.041
      emb|AI973796|AI973796 sd10d10.y1 Gm-c1020 Glycine max cDNA clone... 37 0.078
      emb|AW704342|AW704342 sk18b05.yl Gm-c1028 Glycine max cDNA clone... 36 0.15
45
      gb|U13736|PSU13736 Pisum sativum Alaska calmodulin-like protein ... 35 0.20
      emb|AI080805|AI080805 TENU3514 T. cruzi epimastigote normalized ... 35 0.28
      emb|AW696965|AW696965 NF110H11ST1F1095 Developing stem Medicago ... 34 0.52
      emb|AW695301|AW695301 NF093G03ST1F1023 Developing stem Medicago ... 34 0.52
      emb|AW776108|AW776108 EST335173 DSIL Medicago truncatula cDNA cl... 34 0.52
50
      emb|AW691424|AW691424 NF044G02ST1F1000 Developing stem Medicago ... 34 0.52
      emblAW559907lAW559907 EST314955 DSIR Medicago truncatula cDNA cl... 34 0.52
      emb|AW689882|AW689882 NF026C01ST1F1000 Developing stem Medicago ... 34 0.52
      emblAW267797|AW267797 EST305925 DSIR Medicago truncatula cDNA cl... 34 0.52
      emb|AA660947|AA660947 00844 MtRHE Medicago truncatula cDNA 5' si... 34 0.52
55
      emb|AW696479|AW696479 NF106F05ST1F1046 Developing stem Medicago ... 34 0.52
      emb|AW693088|AW693088 NF060A07ST1F1052 Developing stem Medicago ... 34 0.52
      emb|AW687985|AW687985 NF001G08ST1F1000 Developing stem Medicago ... 34 0.52
      emb|AW692657|AW692657 NF057H03ST1F1000 Developing stem Medicago ... 34 0.52
      emb|AW559906|AW559906 EST314954 DSIR Medicago truncatula cDNA cl... 34 0.52
60
      emb|AI075569|AI075569 TENU3146 T. cruzi epimastigote normalized ... 33 0.99
      emb|AQ656273|AQ656273 Sheared DNA-25J5.TF Sheared DNA Trypanosom... 33 1.4
```

emb|AQ643265|AQ643265 RPCI93-DpnII-30O24.TJ RPCI93-DpnII Trypano... 33 1.4 emb|AW145395|AW145395 ga19g01.yl Moss EST library PPU Physcomitr... 33 1.4 emb|AF216527|AF216527 Dunaliella tertiolecta calcium-dependent p... 33 1.4 emb|AF137317|AF137317 Pariana radiciflora phytochrome B (PHYB) g... 32 1.9 gblU25841[YSCP9677 Saccharomyces cerevisiae chromosome XVI cosmi... 32 2.6 emb|AL354107|L2187X Leishmania major Friedlin cosmid L2187 t3Hyg... 31 3.5 emb|Y10156|BNMYAP12 B.napus for myrosinase-associated protein, c... 31 3.5 emb|AA901634|AA901634 NCM7H7T7 Mycelial Neurospora crassa cDNA c... 31 3.5 emb|AA519327|AA519327 TgESTzz40d01.s1 TgME49 invivo Bradyzoite c... 31 3.5 10. emb|AL109820|SPAC1952 S.pombe chromosome I cosmid c1952. emb|AV388698|AV388698 AV388698 Chlamydomonas reinhardtii C9 Chla... 31 4.8 emb|AQ852174|AQ852174 LMAJFV1 lm62c09.x1 Leishmania major FV1 ra... 31 4.8 emb|AW772887|AW772887 925001C07.yl C. reinhardtii CC-2290, norma... 31 4.8 gb|BE024237|BE024237 894001F07.yl C. reinhardtii CC-1690, normal... 31 4.8 15 Query= AC006067.63 at 15846 at /id source genbank /description gb|aad15461.1] (ac006067) unknown protein [arabidopsis thaliana] /blast score 1.00e-117/ec number /family /chip nova/gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006067| /ncgi 20 http://www.ncgr.org/cgi-bin/ff?ac006067 (777 letters) Database: plantfungal 25 661,018 sequences; 426,114,510 total letters Searching done Score E 30 Sequences producing significant alignments: (bits) Value emb|AI938176|AI938176 sc40e07.yl Gm-c1014 Glycine max cDNA clone... 226 1e-58 emb|AI938151|AI938151 sc40a07.yl Gm-c1014 Glycine max cDNA clone... 226 2e-58 emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 222 3e-35 gb[BE057559]BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ... 210 1e-53 emb|AW133238|AW133238 se16b04.y1 Gm-c1013 Glycine max cDNA clone... 200 8e-51 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48 emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48 40 emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47 emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47 emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47 emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47 emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycope... 133 2e-44 emb|AW832123|AW832123 sm30h02.yl Gm-c1028 Glycine max cDNA clone... 178 3e-44 emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 177 9e-44 emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 177 9e-44 emb|AI487153|AI487153 EST245475 tomato ovary, TAMU Lycopersicon ... 166 3e-40 emb|AW568464|AW568464 si59b03.yl Gm-r1030 Glycine max cDNA clone... 163 2e-39 50 emb|AW153022|AW153022 se33h12.yl Gm-c1015 Glycine max cDNA clone... 158 6e-38 emb|AI896759|AI896759 EST266202 tomato callus, TAMU Lycopersicon... 157 8e-38 emb|AW094322|AW094322 EST287502 tomato mixed elicitor, BTI Lycop... 128 5e-29 gb|BE125244|BE125244 DG1 18_B07.b1 A002 Dark Grown 1 (DG1) Sorgh... 127 1e-28 emblAW922420|AW922420 DG1 18 B07.g1 A002 Dark Grown 1 (DG1) Sorg... 123 2e-27 gbBE024006BE024006 sm95c09.yl Gm-c1015 Glycine max cDNA clone ... 122 2e-27 gb/T14912/T14912 crs394 lambdaZAPST Ricinus communis cDNA clone ... 72 3e-27 emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 119 2e-26 emb|AW030966|AW030966 EST274273 tomato callus, TAMU Lycopersicon... 96 1e-25 emb|AI938035|AI938035 sc40e07.x1 Gm-c1014 Glycine max cDNA clone... 116 3e-25 60 emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 111 7e-24 emb|AI938013|AI938013 sc40a07.x1 Gm-c1014 Glycine max cDNA clone... 110 1e-23

	emb AI776842 AI776842 EST257942 tomato resistant, Cornell Lycope 110 2e-23
	emb AA556663 AA556663 518 Loblolly pine CA Pinus taeda cDNA clon 61 2e-20
	emb AI736542 AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone 68 2e-17
	emb AI899328 AI899328 EST268771 tomato ovary, TAMU Lycopersicon 82 6e-15
5	gb[BE021003]BE021003 sm54e07.y1 Gm-c1028 Glycine max cDNA clone 55 1e-12
	emb AW217201 AW217201 EST295915 tomato callus, TAMU Lycopersicon 73 2e-12
	emb AI443600 AI443600 sa42b08.yl Gm-c1004 Glycine max cDNA clone 72 5e-12
	gb[BE123900[BE123900 EST394025 DSIL Medicago truncatula cDNA clo 58 7e-08
	- F. i i
10	
IU	
	emb AW184959 AW184959 se84d10.yl Gm-c1023 Glycine max cDNA clone 52 6e-06
	emb AW185963 AW185963 se61h02.yl Gm-c1019 Glycine max cDNA clone 52 6e-06
	emb AW153055 AW153055 se34d02.yl Gm-c1015 Glycine max cDNA clone 45 7e-04
	emb AI727849 AI727849 BNLGHi9260 Six-day Cotton fiber Gossypium 39 0.056
15	emb AI965877 AI965877 sc79a11.yl Gm-c1018 Glycine max cDNA clone 30 0.082
	emb AF157837 AF157837 Trypanosoma cruzi putative 90 kDa surface 35 0.52
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai 35 0.98
	emb AL112108 CNS019UC Botrytis cinerea strain T4 cDNA library un 34 1.4
	emb AF101023 AF101023 Picea abies clone PAA12E3 family 2 repetit 34 1.4
20	emb AA520766 AA520766 TgESTzz67g11.rl TgME49 invivo Bradyzoite c 34 1.4
	emb AA519752 AA519752 TgESTzz28f05.rl TgME49 invivo Bradyzoite c34 1.4
*	emb AA785314 AA785314 g6d11a1.fl Aspergillus nidulans 24hr asexu 34 1.9
	emb AQ367507 AQ367507 toxb0002H01r CUGI Tomato BAC Library Lycop 34 1.9
	emb AW348996 AW348996 GM210003B22A1R Gm-r1021 Glycine max cDNA 3 33 2.6
25	emb AW348959 AW348959 GM210004A12C6R Gm-r1021 Glycine max cDNA 3 33 2.6
	emb AL034559 PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq 33 2.6
	emb AW348503 AW348503 GM210002B12C1R Gm-r1021 Glycine max cDNA 3 33 2.6
	emb AW398499 AW398499 EST308999 L. pennellii trichome, Cornell U 33 2.6
	emb AW349705 AW349705 GM210005B21C6R Gm-r1021 Glycine max cDNA 3 33 2.6
30	emb AW596289 AW596289 sj01e09.y1 Gm-c1032 Glycine max cDNA clone 33 3.5
30	emb AF199419 AF199419 Trypanosoma cruzi 90 kDa surface protein (33 3.5
	emb AW102268 AW102268 sd85e07.yl Gm-c1009 Glycine max cDNA clone 33 3.5
	emb AI441442 AI441442 sa86a02.y1 Gm-c1004 Glycine max cDNA clone 33 3.5
35	emb X78037 MIOB250 O.berteriana mitochondrial DNA for orf250. 33 3.5
35	emb AC004688 AC004688 Plasmodium falciparum chromosome 12 clone 32 4.8
	emb AW719534 AW719534 LjNEST5c5rW Lotus japonicus nodule library 32 4.8
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S 32 4.8
	emb AF119172 AF119172 Cyanophora paradoxa alpha-tubulin (atub) g 32 4.8
40	emb AW101722 AW101722 sd69d02.yl Gm-c1008 Glycine max cDNA clone 32 4.8
40	gb U56098 AOU56098 Aspergillus oryzae putative DNA binding prote 32 4.8
	emb AI507866 AI507866 sa88b06.yl Gm-c1004 Glycine max cDNA clone 32 4.8
	gb[BE125213[BE125213 DG1_16_E11.b1_A002 Dark Grown 1 (DG1) Sorgh 32 4.8
	emb AA785315 AA785315 g6d11a1.rl Aspergillus nidulans 24hr asexu 32 4.8
	gb BE059192 BE059192 sn27d12.yl Gm-c1016 Glycine max cDNA clone 32 4.8
45	emb Z71334 SCYNL058C S.cerevisiae chromosome XIV reading frame O 32 6.6
	emb AW219947 AW219947 EST302430 tomato root during/after fruit s 32 6.6
	emb X56235 SCHYP1 Yeast (S.cerevisiae) HYP1 gene for hypusine co 32 6.6
	emb AL121851 LMFL2581 Leishmania major Friedlin chromosome 23 co 32 6.6
	emb AW686452 AW686452 NF041F08NR1F1000 Nodulated root Medicago t 32 6.6
50	emb Z67961 SPAC30D11 S.pombe chromosome I cosmid c30D11. 32 6.6
	emb AW395281 AW395281 sh46b07.yl Gm-c1017 Glycine max cDNA clone 32 6.6
	emb AL034563 SPBC660 S.pombe chromosome II cosmid c660. 32 6.6
	emb AW667846 AW667846 GA_ Ea0010O22 Gossypium arboreum 7-10 dpa 32 6.6
	emb AI043302 AI043302 TENU0942 T. cruzi epimastigote normalized 32 6.6
55	emb AI043452 AI043452 TENUI011 T. cruzi epimastigote normalized 32 6.6
	emb AW773882 AW773882 EST332868 KV3 Medicago truncatula cDNA clo 32 6.6
	emb AW219946 AW219946 EST302429 tomato root during/after fruit s 32 6.6
	a mainta a san ann ann ann ann ann ann ann ann
	gb U12141 SCU12141 Saccharomyces cerevisiae chromosome XIV left 32 6.6 emb AQ653810 AQ653810 Sheared DNA-8B13.TF Sheared DNA Trypanosom 32 6.6
60	
w	emb AW219759 AW219759 EST302241 tomato root during/after fruit s 32 6.6 emb AI069155 AI069155 mgae0005dA02f Magnaporthe grisea Appressor 27 7.0
	CHURA DOY LODA DOY LOD MOREUDINGADO MARONANOTOR ORGER ANDRESSOR 77.70

```
emb|AC023488|AC023488 Trypanosoma brucei chromosome IV clone RPC... 31 9.1
      emb|AW509230|AW509230 sh92h07.y1 Gm-c1016 Glycine max cDNA clone... 31 9.1
      emb|AW932541|AW932541 EST358384 tomato fruit mature green, TAMU ... 31 9.1
      emb|AF206700|AF206700 Neurospora crassa heterokaryon incompatibi... 31 9.1
      emb|AW621293|AW621293 EST312091 tomato root during/after fruit s... 31 9.1
      dbj|D15051|BLYIDS2NK Hordeum vulgare gene for ids2, complete cds.
      gb|BE021558|BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ... 31 9.1
      emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop... 31 9.1
      emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 31 9.1
10
      emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1
      Query= AC006067.63 g at 15847 g at /id source genbank /description
      gblaad15461.1 (ac006067) unknown protein [arabidopsis thaliana]
      /blast_score 1.00e-117 /ec_number /family /chip nova /gb_link /ncgi
15
           (777 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
20
      Searching.....done
                                          Score
      Sequences producing significant alignments:
                                                          (bits) Value
25
      emb|AI938176|AI938176 sc40e07.yl Gm-c1014 Glycine max cDNA clone... 226 1e-58
      emb|AI938151|AI938151 sc40a07.yl Gm-c1014 Glycine max cDNA clone... 226 2e-58
      emb|AW348772|AW348772 GM210003A22G1R Gm-r1021 Glycine max cDNA 3... 222 3e-
30
      gb[BE057559]BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ... 210 1e-53
      emb|AW133238|AW133238 se16b04.yl Gm-c1013 Glycine max cDNA clone... 200 8e-51
      emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48
      emb|AW930095|AW930095 EST340552 tomato fruit mature green, TAMU ... 190 9e-48
      emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47
35
      emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47
      emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47
      emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47
      emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycope... 133 2e-44
      emblAW832123|AW832123 sm30h02.yl Gm-c1028 Glycine max cDNA clone... 178 3e-44
40
      emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 177 9e-44
      emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 177 9e-44
      emb|AI487153|AI487153 EST245475 tomato ovary, TAMU Lycopersicon ... 166 3e-40
      emb[AW568464]AW568464 si59b03.yl Gm-r1030 Glycine max cDNA clone... 163 2e-39
      emb|AW153022|AW153022 se33h12.yl Gm-c1015 Glycine max cDNA clone... 158 6e-38
45.
      emb|AI896759|AI896759 EST266202 tomato callus, TAMU Lycopersicon... 157 8e-38
      emb|AW094322|AW094322 EST287502 tomato mixed elicitor, BTI Lycop... 128 5e-29
      gb|BE125244|BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 1e-28
      emb|AW922420|AW922420 DG1 18 B07.g1 A002 Dark Grown 1 (DG1) Sorg... 123 2e-27
      gb|BE024006|BE024006 sm95c09.yl Gm-c1015 Glycine max cDNA clone ... 122 2e-27
50
      gb|T14912|T14912 crs394 lambdaZAPST Ricinus communis cDNA clone ... 72 3e-27
      emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 119 2e-26
      emb|AW030966|AW030966 EST274273 tomato callus, TAMU Lycopersicon... 96 1e-25
      emb|AI938035|AI938035 sc40e07.x1 Gm-c1014 Glycine max cDNA clone... 116 3e-25
      emb|AI771551|AI771551 EST252651 tomato ovary, TAMU Lycopersicon ... 111 7e-24
55
      emb|AI938013|AI938013 sc40a07.x1 Gm-c1014 Glycine max cDNA clone... 110 1e-23
      emb|AI776842|AI776842 EST257942 tomato resistant, Cornell Lycope... 110 2e-23
      emb|AA556663|AA556663 518 Loblolly pine CA Pinus taeda cDNA clon... 61 2e-20
      emb|AI736542|AI736542 sb30b04.yl Gm-c1009 Glycine max cDNA clone... 68 2e-17
      emb|AI899328|AI899328 EST268771 tomato ovary, TAMU Lycopersicon ... 82 6e-15
60
      gb[BE021003[BE021003 sm54e07.yl Gm-c1028 Glycine max cDNA clone ... 55 le-12
      emb|AW217201|AW217201 EST295915 tomato callus, TAMU Lycopersicon... 73 2e-12
```

	emb Al443600 Al443600 sa42b08.yl Gm-c1004 Glycine max cDNA clone 72 5e-12
	gb BE123900 BE123900 EST394025 DSIL Medicago truncatula cDNA clo 58 7e-08
	gb BE022589 BE022589 sm86h09.y1 Gm-c1015 Glycine max cDNA clone 57 2e-07
	gb BE022911 BE022911 sm89a12.y1 Gm-c1015 Glycine max cDNA clone 55 6e-07
5	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone 52 6e-06
	emb AW185963 AW185963 se61h02.y1 Gm-c1019 Glycine max cDNA clone 52 6e-06
	emb AW153055 AW153055 se34d02.y1 Gm-c1015 Glycine max cDNA clone 45 7e-04
	emb AI727849 AI727849 BNLGHi9260 Six-day Cotton fiber Gossypium 39 0.056
10	emb AI965877 AI965877 sc79al1.yl Gm-c1018 Glycine max cDNA clone 30 0.082
10	emb AF157837 AF157837 Trypanosoma cruzi putative 90 kDa surface 35 0.52
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai 35 0.98
	emb AL112108 CNS019UC Botrytis cinerea strain T4 cDNA library un 34 1.4
	emb AF101023 AF101023 Picea abies clone PAA12E3 family 2 repetit 34 1.4
	emb AA520766 AA520766 TgESTzz67g11.rl TgME49 invivo Bradyzoite c 34 1.4
15	emb AA519752 AA519752 TgESTzz28f05.rl TgME49 invivo Bradyzoite c 34 1.4
	emb AA785314 AA785314 g6d11a1.fl Aspergillus nidulans 24hr asexu 34 1.9
	emb AQ367507 AQ367507 toxb0002H01r CUGI Tomato BAC Library Lycop 34 1.9
	emb AW348996 AW348996 GM210003B22A1R Gm-r1021 Glycine max cDNA 3 33 2
	emb AW348959 AW348959 GM210004A12C6R Gm-r1021 Glycine max cDNA 3 33 2
20	emb AL034559 PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq 33 2.6
	-emb AW348503 AW348503 GM210002B12C1R Gm-r1021 Glycine max cDNA 3 33 2.
	emb AW398499 AW398499 EST308999 L. pennellii trichome, Cornell U 33 2.6
	· · · · · · · · · · · · · · · · · · ·
25	emb AW596289 AW596289 sj01e09.y1 Gm-c1032 Glycine max cDNA clone 33 3.5
23	emb AF199419 AF199419 Trypanosoma cruzi 90 kDa surface protein (33 3.5
	emb AW102268 AW102268 sd85e07.yl Gm-c1009 Glycine max cDNA clone 33 3.5
	emb AI441442 AI441442 sa86a02.y1 Gm-c1004 Glycine max cDNA clone 33 3.5
	emb X78037 MIOB250 O.berteriana mitochondrial DNA for orf250. 33 3.5
•	emb AC004688 AC004688 Plasmodium falciparum chromosome 12 clone 32 4.8
30	emb AW719534 AW719534 LjNEST5c5rW Lotus japonicus nodule library 32 4.8
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S 32 4.8
	emb AF119172 AF119172 Cyanophora paradoxa alpha-tubulin (atub) g 32 4.8
	emb AW101722 AW101722 sd69d02.yl Gm-c1008 Glycine max cDNA clone 32 4.8
	gb U56098 AOU56098 Aspergillus oryzae putative DNA binding prote 32 4.8
35	emb AI507866 AI507866 sa88b06.yl Gm-c1004 Glycine max cDNA clone 32 4.8
	gb[BE125213]BE125213 DG1_16_E11.b1_A002 Dark Grown 1 (DG1) Sorgh 32 4.8
	emb AA785315 AA785315 g6d11a1.rl Aspergillus nidulans 24hr asexu 32 4.8
	gb BE059192 BE059192 sn27d12.yl Gm-c1016 Glycine max cDNA clone 32 4.8
	emb Z71334 SCYNL058C S.cerevisiae chromosome XIV reading frame O 32 6.6
40	emb AW219947 AW219947 EST302430 tomato root during/after fruit s 32 6.6
	emb X56235 SCHYP1 Yeast (S.cerevisiae) HYP1 gene for hypusine co 32 6.6
	emb AL121851 LMFL2581 Leishmania major Friedlin chromosome 23 co 32 6.6
	emb AW686452 AW686452 NF041F08NR1F1000 Nodulated root Medicago t 32 6.6
	emb Z67961 SPAC30D11 S.pombe chromosome I cosmid c30D11. 32.6.6
45	emb AW395281 AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone 32 6.6
	emb AL034563 SPBC660 S.pombe chromosome II cosmid c660. 32 6.6
	emb AW667846 AW667846 GA_Ea0010O22 Gossypium arboreum 7-10 dpa 32 6.6
	emb AI043302 AI043302 TENU0942 T. cruzi epimastigote normalized 32 6.6
50	emb AI043452 AI043452 TENU1011 T. cruzi epimastigote normalized 32 6.6
50	emb AW773882 AW773882 EST332868 KV3 Medicago truncatula cDNA clo 32 6.6
	emb AW219946 AW219946 EST302429 tomato root during/after fruit s 32 6.6
	gb[U12141 SCU12141 Saccharomyces cerevisiae chromosome XIV left 32 6.6
	emb AQ653810 AQ653810 Sheared DNA-8B13.TF Sheared DNA Trypanosom 32 6.6
	emb AW219759 AW219759 EST302241 tomato root during/after fruit s 32 6.6
55	emb AI069155 AI069155 mgae0005dA02f Magnaporthe grisea Appressor 27 7.0
	emb AC023488 AC023488 Trypanosoma brucei chromosome IV clone RPC 31 9.1
	emb AW509230 AW509230 sh92h07.yl Gm-c1016 Glycine max cDNA clone 31 9.1
	emb AW932541 AW932541 EST358384 tomato fruit mature green, TAMU 31 9.1
	emb AF206700 AF206700 Neurospora crassa heterokaryon incompatibi 31 9.1
60	emb AW621293 AW621293 EST312091 tomato root during/after fruit s 31 9.1
	dbjD15051BLYIDS2NK Hordeum vulgare gene for ids2, complete cds. 31 9.1

gb|BE021558|BE021558 sm49e02.yl Gm-c1028 Glycine max cDNA clone ... 31 9.1

```
emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop...
      emb|AL049181|PFMAL13P4 Plasmodium falciparum chromosome 13 strai... 31 9.1
      emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1
 5
      Query= AC006587.164 at 15859 at /id source genbank /description
      gb|aad21491.1| (ac006587) unknown protein [arabidopsis thaliana]
      /blast score 4.00e-17 /ec number /family /chip nova /gb_link
      http://www3.ncbi.nlm.nih.gov/htbin-
10
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006587|/ncgi
      http://www.ncgr.org/cgi-bin/ff?ac006587
           (504 letters)
      Database: plantfungal
15
            661,018 sequences; 426,114,510 total letters
      Searching.....
                                          Score
                                                 E
20
      Sequences producing significant alignments:
                                                          (bits) Value
      emb|AC006279|AC006279 Plasmodium falciparum chromosome 12 clone ... 36 0.16
      emb|AW932996|AW932996 EST358839 tomato fruit mature green, TAMU ... 36 0.16
      emblAC005140|AC005140 Plasmodium falciparum chromosome 12 clone ... 36 0.22
25
      emb|AC005139|AC005139 Plasmodium falciparum chromosome 12, *** S... 36 0.22
      gb|M73214|TETH3H4A Tetrahymena vorax histone H3 (histone H3II) g... 36 0.22
      emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 35 0.30
      gb[M17221]YSCRNR2 S.cerevisiae ribonucleotide reductase (RNR2) s... 35 0.30
      emb|AE001384|AE001384 Plasmodium falciparum chromosome 2, sectio... 35 0.30
30
      gb|BE034256|BE034256 MH02B11 MH Mesembryanthemum crystallinum cD... 35 0.41
      emblAC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 35 0.41
      emblAL031748[PFMAL1P5 Plasmodium falciparum chromosome 1 strain ... 35 0.41
      emblAE001383|AE001383 Plasmodium falciparum chromosome 2, sectio... 35 0.41
      gb|BE023268|BE023268 sm80b05.yl Gm-c1015 Glycine max cDNA clone ... 35 0.41
35
      emb|Z97348|PFMAL3P1 Plasmodium falciparum MAL3P1, complete seque... 35 0.41
      emb[X56950]PFCALM P. falciparum gene for calmodulin.
      gblM59349|PFACALMOD Plasmodium falciparum calmodulin gene, compl... 35 0.41
      emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 35 0.41
      emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 35 0.56
40
      gb|M37892|TETRPROL21 Tetrahymena thermophila ribosomal protein L... 35 0.56
      gb[T09806]T09806 0387m7 gmbPfHB3.1, G. Roman Reddy Plasmodium fa... 35 0.56
      gb[T09805]T09805 0387m3 gmbPfHB3.1, G. Roman Reddy Plasmodium fa... 35 0.56
      emb|AE001399|AE001399 Plasmodium falciparum chromosome 2, sectio... 34 0.77
      emb|AQ501167|AQ501167 V26E6 mTn-3xHA/lacZ Insertion Library Sacc... 34 0.77
      emb|AQ934965|AQ934965 CpG2344B CpIOWAgDNA1 Cryptosporidium parvu... 34 0.77
      emb|AQ934964|AQ934964 CpG2344A CpIOWAgDNA1 Cryptosporidium parvu...
      emb|AL111484|CNS019D0 Botrytis cinerea strain T4 cDNA library un... 28 0.94
      emb|AQ942015|AQ942015 Sheared DNA-41C1.TR Sheared DNA Trypanosom... 34 1.1
      emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 34 1.1
50
      emb|AC005507|AC005507 Plasmodium falciparum chromosome 12 clone ... 34 1.1
      emb|AL031745|PFMAL1P2 Plasmodium falciparum chromosome 1 strain ... 34 1.1
      gb]N98036]N98036 2094C3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 34 1.1
      gb L27838 PFARHPR Plasmodium yoelii rhoptry protein, complete cds. 29 1.1
      emb|AW686975|AW686975 NF004F02RT1F1025 Developing root Medicago ...
55
      gb|U84395|PFU84395 Plasmodium falciparum sarcalumenin/eps15 homo... 33 1.5
      emb|AQ657627|AQ657627 Sheared DNA-24C13.TR Sheared DNA Trypanoso... 33 1.5
      emb|AW286528|AW286528 LG1 334 A05.g1 A002 Light Grown 1 (LG1) So... 33 1.5
      emb|AV427431|AV427431 AV427431 Lotus japonicus young plants (two... 33 1.5
      emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 33 1.5
60
      emb|AA550506|AA550506 1663m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 33 1.5
      emb|AW286549|AW286549 LG1_334_C05.g1_A002 Light Grown 1 (LG1) So... 33 1.5
```

	emb AQ023572 AQ023572 CpGR0492A Cryptosporidium parvum genomic r 33 1.5
	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain 33 1.5
	gb U36927 PYU36927 Plasmodium yoelii rhoptry protein gene, compl 33 1.5
	emb AC006281 AC006281 Plasmodium falciparum chromosome 12 clone 33 1.5
5	emb AL034556 PFMAL3P5 Plasmodium falciparum MAL3P5, complete seq 33 1.5
	emb AJ002233 PFJ002233 Plasmodium falciparum genomic gene for su 29 1.6
	emb AC005505 AC005505 Plasmodium falciparum chromosome 12 clone 33 2.0
10	emb AL049180 PFMAL13P1 Plasmodium falciparum chromosome 13 strai 33 2.0
10	emb AV419396 AV419396 AV419396 Lotus japonicus young plants (two 33 2.0
	gb U49822 SDU49822 Saccharomyces douglasii mitochondrial tRNA-Se 33 2.0
	emb AV412618 AV412618 AV412618 Lotus japonicus young plants (two 33 2.0
	emb AW458882 AW458882 sh16a07.yl Gm-c1016 Glycine max cDNA clone 33 2.0
	emb AV428274 AV428274 AV428274 Lotus japonicus young plants (two 33 2.0
15	emb AL096783 PFMAL13P9 Plasmodium falciparum chromosome 13 strai 33 2.0
	gb M35612 YSCMTARSA Yeast (S.cerevisiae) mitochondrial autonomou 33 2.0
	emb AL031744 PFMAL1P1 Plasmodium falciparum chromosome 1 strain 32 2.8
	emb AF093584 AF093584 Plasmodium vivax merozoite surface protein 32 2.8
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone 32 2.8
20	emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S 32 2.8
	emb AE001410 AE001410 Plasmodium falciparum chromosome 2, sectio 32 2.8
,	emb X74069 SCALP1 S.cerevisiae APL1 gene for basic-amino-acid pe 32 2.8
•	
	emb AC005504 AC005504 Plasmodium falciparum chromosome 12, *** S 32 2.8 emb AW727908 AW727908 GA_Ea0028M15 Gossypium arboreum 7-10 dpa 32 2.8
25	11, 200, 100, 11, 200, 100, 100, 100, 10
23	emb AE001395 AE001395 Plasmodium falciparum chromosome 2, sectio 32 2.8
	emb AF030694 AF030694 Plasmodium falciparum strain Dd2 heat shoc 32 2.8
	emb AQ647469 AQ647469 RPCI93-EcoRI-6E20.TJ RPCI93-EcoRI Trypanos 32 2.8
	emb Z38061 SC9168 S. cerevisiae chromosome IX cosmid 9168. 32 2.8
20	emb AL110675 CNS018QK Botrytis cinerea strain T4 cDNA library un 32 2.8
30	emb AL008970 PFMAL3P4 Plasmodium falciparum MAL3P4, complete seq 31 2.9
	emb AW035978 AW035978 EST282837 tomato callus, TAMU Lycopersicon 32 3.8
	emb AF126285 AF126285 Pleurotus ostreatus linear mitochondrial p 32 3.8
	emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai 32 3.8
	emb AW691746 AW691746 NF043G06ST1F1000 Developing stem Medicago 32 3.8
35	emb Z98551 PFMAL3P6 Plasmodium falciparum MAL3P6, complete seque 32 3.8
	emb AW030017 AW030017 EST273272 tomato callus, TAMU Lycopersicon 32 3.8
	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai 32 3.8
	emb AC018661 AC018661 Leishmania major chromosome 35 clone L3836 32 3.8
	emb AQ909783 AQ909783 GSSTc08262 Trypanosome cruzi random genomi 32 3.8
40	emb AQ906056 AQ906056 GSSTc07178 Trypanosome cruzi random genomi 32 3.8
	emb AQ905917 AQ905917 GSSTc010600 Trypanosome cruzi random genom 32 3.8
	emb X16104 SBKAFGK1 Sorghum DNA for kafirin, pGK1. 32 3.8
	emb AW684444 AW684444 NF017A07NR1F1000 Nodulated root Medicago t 32 3.8
	emb AC011016 AC011016 Leishmania major chromosome 35 clone L218 32 3.8
45	emb AL033503 CAC49C4 C.albicans cosmid Ca49C4. 32 3.8
	emb AW761381 AW761381 sl66g01.yl Gm-c1027 Glycine max cDNA clone 32 3.8
	emb AW220823 AW220823 EST297292 tomato fruit mature green, TAMU 32 3.8
	114 00000 (014 00000 (0 m)
50	1)4.4.6660.4.6)4.4.6660.4.6.000
J 0	emb AA557046 AA557046 888 Loblolly pine N Pinus taeda cDNA clone 32 3.8
	emb AW692198 AW692198 NF048F08ST1F1000 Developing stem Medicago 32 3.8
	emb AQ935320 AQ935320 CpG2407A CpIOWAgDNA1 Cryptosporidium parvu 31 5.2
	emb Z68144 SPAC3H1 S. pombe chromosome I cosmid c3H1. 31 5.2
c	emb AE001422 AE001422 Plasmodium falciparum chromosome 2, sectio 31 5.2
55	emb AE001401 AE001401 Plasmodium falciparum chromosome 2, sectio 31 5.2
	emb AE001380 AE001380 Plasmodium falciparum chromosome 2, sectio 31 5.2
	emb AC004157 AC004157 Plasmodium falciparum chromosome 12 clone 31 5.2
	emb AE001376 AE001376 Plasmodium falciparum chromosome 2, sectio 31 5.2
	emb AQ941118 AQ941118 Sheared DNA-35E12.TF Sheared DNA Trypanoso 31 5.2
60	emb AQ949411 AQ949411 Sheared DNA-38N10.TF Sheared DNA Trypanoso 31 5.2

Query= AL021890.71_at 16298_at /id_source genbank /description emb|caa17152.1| (al021890) putative protein [arabidopsis thaliana] /blast score 1.00e-68 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|al021890|/ncgi http://www.ncgr.org/cgi-bin/ff?al021890 (375 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

10

Score

15 Sequences producing significant alignments: (bits) Value

emb|AW685341|AW685341 NF026D08NR1F1000 Nodulated root Medicago t... 162 1e-39 gb[BE124622]BE124622 EST393657 GVN Medicago truncatula cDNA clon... 162 1e-39 emb|AI943438|AI943438 MF02E10 MF Mesembryanthemum crystallinum c... 158 2e-38 20 gb|BE033541|BE033541 MF02E10 MF Mesembryanthemum crystallinum cD... 158 2e-38 emb|AW667752|AW667752 GA_Ea0010I06 Gossypium arboreum 7-10 dpa ... 155 1e-37 emb|AW747419|AW747419 WSI_68_E10.b1_A002 Water-stressed 1 (WS1) ... 155 2e-37 emb|AW981480|AW981480 EST392633 DSIL Medicago truncatula cDNA cl... 154 4e-37 emb|AW441269|AW441269 EST310665 tomato fruit red ripe, TAMU Lyco... 153 5e-37 25 emb|AW223703|AW223703 EST300514 tomato fruit red ripe, TAMU Lyco... 153 5e-37 emb|AW034892|AW034892 EST279121 tomato callus, TAMU Lycopersicon... 153 5e-37 emb|AW224013|AW224013 EST300824 tomato fruit red ripe, TAMU Lyco... 153 5e-37 emb|AW907232|AW907232 EST343355 potato stolon, Cornell Universit... 153 7e-37 emb|AW747501|AW747501 WS1 68 E10.g1 A002 Water-stressed 1 (WS1) ... 152 9e-37 30 emb|AW760599|AW760599 s152d09.y1 Gm-c1027 Glycine max cDNA clone... 151 2e-36 emb|AI960575|AI960575 sc86c01.yl Gm-c1018 Glycine max cDNA clone... 151 2e-36 emb|AW706639|AW706639 sj62h07.yl Gm-c1033 Glycine max cDNA clone... 151 2e-36 emb|AI166395|AI166395 xylem.est.231 Poplar xylem Lambda ZAPII li... 150 5e-36 35 emb|AI443884|AI443884 sa44f06.yl Gm-c1004 Glycine max cDNA clone... 149 6e-36 emb|AW568285|AW568285 si69g11.yl Gm-r1030 Glycine max cDNA clone... 149 6e-36 emb|AW186193|AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone... 149 6e-36 emb|AI855496|AI855496 sc16h05.yl Gm-c1013 Glycine max cDNA clone... 149 le-35 gb|BE020351|BE020351 sm43b05.yl Gm-c1028 Glycine max cDNA clone ... 148 2e-35 40 emb|AW132618|AW132618 se06f04.y1 Gm-c1013 Glycine max cDNA clone... 148 2e-35 emb|AI777814|AI777814 EST258693 tomato susceptible, Cornell Lyco... 146 8e-35 emb|AV408412|AV408412 AV408412 Lotus japonicus young plants (two... 141 2e-33 emb|AW156084|AW156084 ga24f11.yl Moss EST library PPU Physcomitr... 131 3e-30 emb|AV398027|AV398027 AV398027 Chlamydomonas reinhardtii C9 Chla... 126 7e-29 45 emb|AI965929|AI965929 sc79h07.yl Gm-c1018 Glycine max cDNA clone... 123 6e-28 emb|AV427426|AV427426 AV427426 Lotus japonicus young plants (two... 108 2e-23 emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 102 1e-21 emb|AW738874|AW738874 gb03e09.y1 Moss EST library PPN Physcomitr... 99 2e-20 emb|AW476911|AW476911 ga38h10.y1 Moss EST library PPU Physcomitr... 95 2e-19 emb|AL049558|SPBC216 S.pombe chromosome II cosmid c216. emb|AW335287|AW335287 S45D10 AGS-1 Pneumocystis carinii f. sp. c... 71 3e-19 emb|AI822525|AI822525 LO-1030T3 Ice plant Lambda Uni-Zap XR expr... 95 3e-19 emb|AI730110|AI730110 BNLGHi6160 Six-day Cotton fiber Gossypium ... 94 6e-19 emb|AW933218|AW933218 EST359061 tomato fruit mature green, TAMU ... 90 5e-18 55 emb|AW933878|AW933878 EST359721 tomato fruit mature green, TAMU ... 90 5e-18 emb|AW222361|AW222361 EST299172 tomato fruit red ripe, TAMU Lyco... 90 5e-18 emb|AW617209|AW617209 EST323620 L. hirsutum trichome, Cornell Un... 90 5e-18 emb|AW222638|AW222638 EST299449 tomato fruit red ripe, TAMU Lyco... 90 5e-18 emb|AW094164|AW094164 EST287344 tomato mixed elicitor, BTI Lycop... 90 5e-18 60 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 90 5e-18 emb|AI939238|AI939238 sc68h11.yl Gm-c1016 Glycine max cDNA clone... 90 7e-18

	gb BE060018 BE060018 sn39h09.y1 Gm-c1027 Glycine max cDNA clone 90 7e-18 emb AW775277 AW775277 EST334342 DSIL Medicago truncatula cDNA cl 88 4e-17 emb AW127596 AW127596 M110327 DSLC Medicago truncatula cDNA clon 86 9e-17
_	emb AI026521 AI026521 TENU0733 T. cruzi epimastigote normalized 73 1e-16
5	emb X59720 SCCHRIII S. cerevisiae chromosome III complete DNA seq 85 2e-16
	gb T36700 T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar 79 1e-14
•	emb AW650769 AW650769 EST329223 tomato germinating seedlings, TA 79 1e-14
	emb AW739119 AW739119 gb26a12.yl Moss EST library PPN Physcomitr 79 1e-14 emb AT000681 AT000681 AT000681 Brassica rapa guard cell Brassica 62 4e-14
10	emb AT000681 AT000681 AT000681 Brassica rapa guard cell Brassica 62 4e-14 gb N81594 N81594 TgESTzy60e01.rl TgRH Tachyzoite cDNA Toxoplasma 55 1e-12
10	emb AA740047 AA740047 812 PtIFG2 Pinus taeda cDNA clone 9275M 3' 62 4e-12
	emb AW907238 AW907238 EST343361 potato stolon, Cornell Universit 68 2e-11
	emb AA948748 AA948748 LO-267M13R Ice plant Lambda Uni-Zap XR exp 66 1e-10
	emb AA842826 AA842826 CFB57 Floral bud cDNA library of Hot peppe 63 1e-09
15	emb AW351206 AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA 61 5e-09
•	emb AI495735 AI495735 sb15f07.yl Gm-c1004 Glycine max cDNA clone 61 5e-09
	emb AW597401 AW597401 si92d06.yl Gm-c1031 Glycine max cDNA clone 60 9e-09
	emb AW094112 AW094112 EST287292 tomato mixed elicitor, BTI Lycop 58 2e-08
· ·	emb AV412908 AV412908 AV412908 Lotus japonicus young plants (two 54 6e-07
20	emb AW931744 AW931744 EST357587 tomato fruit mature green, TAMU 46 9e-05
	_emb AW459770 AW459770 sh91h03.y1 Gm-c1016 Glycine max cDNA clone 42 0.002
	emb AI483073 AI483073 EST242396 tomato shoot, Cornell Lycopersic 35 0.19
	emb AW686356 AW686356 NF040G07NR1F1000 Nodulated root Medicago t 35 0.36
25	emb AV389829 AV389829 AV389829 Chlamydomonas reinhardtii C9 Chla 34 0.49
25	emb Z71549 SCYNL273W S.cerevisiae chromosome XIV reading frame O 34 0.68
	emb AQ845543 AQ845543 LMAJFV1_lm26g12.y1 Leishmania major FV1 ra 33 0.93
	emb AW692037 AW692037 NF046H05ST1F1000 Developing stem Medicago 30 1.1
	emb AW329632 AW329632 N200892e rootphos(-) Medicago truncatula c 30 1.2 emb AL136235 SPAC664 S.pombe chromosome I cosmid c664. 32 1.8
30	emb AU013634 AU013634 AU013634 Schizosaccharomyces pombe late lo 32 1.8
50	emb AF152203 AF152203 Metasequoia glyptostroboides maturase (mat 32 1.8
	emb AU013588 AU013588 AU013588 Schizosaccharomyces pombe late lo 32 1.8
	emb X83998 CPEAPB C.parasitica eapB gene. 32 2.4
	gb BE049708 BE049708 NXNV_142_E09_F Nsf Xylem Normal wood Vertic 31 3.3
35	emb AW310022 AW310022 sf28e03.x1 Gm-c1028 Glycine max cDNA clone 31 3.3
	emb AI813025 AI813025 2H4 Pine Lambda Zap Xylem library Pinus ta 31 3.3
	emb AQ399658 AQ399658 mgxb0002B08f CUGI Rice Blast BAC Library P 31 3.3
	emb AW349850 AW349850 GM210005B21F11R Gm-r1021 Glycine max cDNA 31 3.3
40	emb AI440691 AI440691 sa67h01.y1 Gm-c1004 Glycine max cDNA clone 31 3.3
40	emb AW497050 AW497050 ga53b08.y1 Moss EST library PPU Physcomitr 31 3.3 emb AW278010 AW278010 sf89d09.y1 Gm-c1019 Glycine max cDNA clone 30 3.6
	emb AW278010 AW278010 sf89d09.y1 Gm-c1019 Glycine max cDNA clone 30 3.6 emb AW496915 AW496915 ga50a09.y1 Moss EST library PPU Physcomitr 31 4.6
	emb AZ048302 AZ048302 LMAJFV1_lm76d06.x1 Leishmania major FV1 ra 31 4.6
	emb AQ398363 AQ398363 mgxb0014B01f CUGI Rice Blast BAC Library P 31 4.6
45	emb X90948 ANRNAHSP7 A.nodosum mRNA for HSP70 protein. 31 4.6
	emb AW509671 AW509671 ga62c03.yl Moss EST library PPU Physcomitr 31 4.6
	emb AW561529 AW561529 ga81h08.yl Moss EST library PPU Physcomitr 31 4.6
	emb AW738897 AW738897 gb03h02.yl Moss EST library PPN Physcomitr 31 4.6
	emb[X79095]FTPDKG F.trinervia pdk gene for pyruvate,orthophospha 30 6.3
50	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9. 30 6.3
	emb X79192 FBPDK F.brownii pdk gene. 30 6.3
	emb Al164197 Al164197 A056p02u Hybrid aspen plasmid library Popu 30 6.3
	emb AW156147 AW156147 se20b05.yl Gm-c1015 Glycine max cDNA clone 30 6.3
	emb X75516 FPPDK F.pringlei mRNA for pyruvate, orthophosphate di 30 6.3
55	gb U08399 FBU08399 Flaveria brownii cold stable pyruvate, orthop 30 6.3
	Open AT 024496 198 -416900 -4/13
	Query= AL024486.185_at 16299_at /id_source genbank /description emb caa19705.1 (al024486) putative protein [arabidopsis thaliana]
	/blast_score 1.00e-170 /ec number /family /chip nova /gb link
60	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb al024486 /ncgi
	The second of the Post of the

```
http://www.ncgr.org/cgi-bin/ff?al024486
     (844 letters)
```

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching.....

Score E

10

5

Sequences producing significant alignments: (bits) Value emb|AI489421|AI489421 EST247760 tomato ovary, TAMU Lycopersicon ... 336 1e-91 emb|AW329288|AW329288 N200509e rootphos(-) Medicago truncatula c... 307 9e-83 emb|AW733754|AW733754 sk77g11.yl Gm-c1016 Glycine max cDNA clone... 290 9e-78 15 emblAW561007|AW561007 EST316055 DSIR Medicago truncatula cDNA cl... 287 8e-77 emb|AI489189|AI489189 EST247528 tomato ovary, TAMU Lycopersicon ... 273 1e-72 emb|AI488043|AI488043 EST246365 tomato ovary, TAMU Lycopersicon ... 269 2e-71 emb|AW625207|AW625207 EST319114 tomato radicle, 5 d post-imbibit... 258 5e-68 emb|AW559910|AW559910 EST314958 DSIR Medicago truncatula cDNA cl... 258 5e-68 20 emblAW559909lAW559909 EST314957 DSIR Medicago truncatula cDNA cl... 245 4e-64 emb|AI487722|AI487722 EST246044 tomato ovary, TAMU Lycopersicon ... 241 5e-63 emb|AW218466|AW218466 EST303649 tomato radicle, 5 d post-imbibit... 238 3e-62 emb|AW624963|AW624963 EST313792 tomato radicle, 5 d post-imbibit... 234 8e-61 emb[AW774997]AW774997 EST334148 KV3 Medicago truncatula cDNA clo... 217 1e-55 25 emb|AA495616|AA495616 c425 Zhou and Ragan 1993 Gracilaria gracil... 118 3e-52 emb|AW678376|AW678376 WS1_15_G07.g1_A002 Water-stressed 1 (WS1) ... 175_5e-50 emb|AW760767|AW760767 sl36g03.yl Gm-c1027 Glycine max cDNA clone... 194 8e-49 emb|AI416755|AI416755 sa18h08.x1 Gm-c1005 Glycine max cDNA clone... 175 5e-44 gb|BE020624|BE020624 sm51d11.y1 Gm-c1028 Glycine max cDNA clone ... 175 4e-43 30 emb|AW218418|AW218418 EST303601 tomato radicle, 5 d post-imbibit... 174 9e-43 emb|AW684921|AW684921 NF023B02NR1F1000 Nodulated root Medicago t... 138 8e-40 emb|AL035218|SPCC1281 S.pombe chromosome III cosmid c1281. 81 3e-37 emb|AW222782|AW222782 EST299593 tomato fruit red ripe, TAMU Lyco... 149 4e-35 emb|AW098211|AW098211 ga07f10.yl Moss EST library CPU Ceratodon ... 147 9e-35 35 emb|Z48639|SC9920 S.cerevisiae chromosome XIII cosmid 9920. emb|AA660525|AA660525 00411 MtRHE Medicago truncatula cDNA 5', m... 104 1e-33 emb|Z28301|SCYKR076W S.cerevisiae chromosome XI reading frame OR... 77 5e-32 emb|AW931289|AW931289 EST357132 tomato fruit mature green, TAMU ... 123 1e-27 emb|X85807|SCCVIIRA S.cerevisiae chromosome VII 27kbp right arm ... 51 2e-23 40 emb|Z72939|SCYGR154C S.cerevisiae chromosome VII reading frame O... 51 2e-23 emb|AA788015|AA788015 r4b01a1.r1 Aspergillus nidulans 24hr asexu... 90 1e-22 emblAW931288|AW931288 EST357131 tomato fruit mature green, TAMU ... 106 2e-22 emb|AW686971|AW686971 NF004E10RT1F1082 Developing root Medicago ... 104 1e-21 emb|AI416795|AI416795 sa18h08.y1 Gm-c1005 Glycine max cDNA clone... 98 7e-20 45 emb|AI327824|AI327824 j0c06a1 rl Aspergillus nidulans 24hr asexu... 77 le-17 emb|AI212279|AI212279 x1e09a1.rl Aspergillus nidulans 24hr asexu... 90 2e-17 emb|AI165879|AI165879 B002P45U Hybrid aspen plasmid library Popu... 84 2e-15 emb|AA966531|AA966531 w5h12a1.rl Aspergillus nidulans 24hr asexu... 82 5e-15 emb|AW931345|AW931345 EST357188 tomato fruit mature green, TAMU ... 82 7e-15 50 emb|AW442112|AW442112 EST311508 tomato fruit red ripe, TAMU Lyco... 80 2e-14 emb|AW704348|AW704348 sk18b11.y1 Gm-c1028 Glycine max cDNA clone... 77 2e-13 emb|AW221318|AW221318 EST297787 tomato fruit mature green, TAMU ... 68 9e-11 emb|AQ875035|AQ875035 V120D9 mTn-3xHA/lacZ Insertion Library, st... 67 2e-10 emb|AW934230|AW934230 EST360073 tomato fruit mature green, TAMU ... 66 3e-10 55 emb|AA787150|AA787150 m8a03a1.rl Aspergillus nidulans 24hr asexu... 58 1e-07 emb|AQ492097|AQ492097 V111F10 mTn-3xHA/lacZ Insertion Library Sa... 55 9e-07 emb|AA788014|AA788014 r4b01a1.fl Aspergillus nidulans 24hr asexu... 35 4e-04 emb|AA787149|AA787149 m8a03a1.fl Aspergillus nidulans 24hr asexu... 46 5e-04 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 38 0.12 60 emb|AA788490|AA788490 13a06a1.fl Aspergillus nidulans 24hr asexu... 35 0.58 emb|AV420850|AV420850 AV420850 Lotus japonicus young plants (two... 29 1.0

5	emb Z49346 SCYJL071W S.cerevisiae chromosome X reading frame ORF 34 1.5 emb X71362 HVDHN7 H.vulgare gene for dehydrin 7. 34 1.5
	emb[X88851 SCESTGENE S.cerevisiae DNA for hypotetical proteins a 34 1.5
	emb AF043087 AF043087 Hordeum vulgare dehydrin 1 (dhn1) gene, co 34 1.5
	emb AI988341 AI988341 sc99e11.yl Gm-c1020 Glycine max cDNA clone 34 2.1
	emb Y10224 CMAO1 C.melo ao1 gene, partial. 34 2.1
10	emb AI900471 AI900471 sc11b06.yl Gm-c1012 Glycine max cDNA clone 34 2.1
	emb AQ874584 AQ874584 V111B3 mTn-3xHA/lacZ Insertion Library, st 34 2.1
	emb AW279161 AW279161 sf67b09.y1 Gm-c1013 Glycine max cDNA clone 34 2.1
	emb Z99531 SPAC19D5 S.pombe chromosome I cosmid c19D5. 33 2.8
1.5	emb AJ273736 AJ273736 AJ273736 Metarhizium anisopliae ARSEF 2575 33 2.8
15	emb AW730699 AW730699 GA_Ea0027C11 Gossypium arboreum 7-10 dpa 33 3.9
	emb AW982536 AW982536 HVSMEg0003112f Hordeum vulgare pre-anthesi 33 3.9
	emb AJ229614 KLAJ9614 Kluyveromyces lactis DNA fragment for sequ 33 3.9 emb Z49625 SCYJR125C S.cerevisiae chromosome X reading frame ORF 33 3.9
20	emb Z49624 SCYJR124C S.cerevisiae chromosome X reading frame ORF 33 3.9 emb Z98547 PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque 25 5.2
	emb Z35776 SCYBL015W S.cerevisiae chromosome II reading frame OR 32 5.3
·	emb AZ214742 AZ214742 Sheared DNA-68E9.TR Sheared DNA Trypanosom 32 5.3
	emb AW691304 AW691304 NF040B04ST1F1000 Developing stem Medicago 32 5.3
	emb X68577 SC114 S. cerevisiae 11.4kb segment of chromosome II. 32 5.3
25	gb[M31036[YSCACH1A S.cerevisiae acetyl-CoA hydrolase (ACH1) mRNA 32 5.3
	emb AJ243754 SAL243754 Sinapis alba chloroplast rpoB operon (rpo 32 5.3
	emb AL110506 SPBC577 S.pombe chromosome II cosmid c577. 26 5.9
	emb AU010645 AU010645 AU010645 Schizosaccharomyces pombe late lo 32 7.3
20	emb AI966191 AI966191 sc35a11.yl Gm-c1014 Glycine max cDNA clone 32 7.3
30	emb AL022244 SPBC3B8 S.pombe chromosome II cosmid c3B8. 32 7.3
	emb AU012735 AU012735 AU012735 Schizosaccharomyces pombe late lo 32 7.3
	emb AE001394 AE001394 Plasmodium falciparum chromosome 2, sectio 32 7.3
	Ouerv= AF149413 38 at 16357 at /id. source genbank /description
35	Query= AF149413.38_at 16357_at /id_source genbank /description "gblaad40144.1laf149413_25 (af149413) contains similarity to protein
35	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein
35	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien
35	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova
	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-
35 40	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi
	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413
	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi
	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters)
40	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal
	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters)
40	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters
40	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal
40	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfingal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /cc_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching
40 45 50	"gb aad40144.1 af149413_25 (af149413) contains similarity to protein kinase domains (pfam f00069, score=162.6, e=6.8e-45, n=1) and leucien rich repeats (pfam pf00560, score=210.7, e=2.2e-59, n=10) [arabidopsis thaliana]" /blast_score 0 /ec_number /family kinase /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb af149413 /ncgi http://www.ncgr.org/cgi-bin/ff?af149413 (3018 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching

	emb A67429 A67429 Sequence 2 from Patent WO9743429. 145 4e-71
	emb A67428 A67428 Sequence 1 from Patent WO9743429. 145 4e-71
	gb U42444 U42444 Lycopersicon pimpinellifolium leucine rich repe 150 4e-70
	emb A57130 A57130 Sequence 1 from Patent WO9531564. 150 4e-70
5	gb[U42445[U42445 Lycopersicon pimpinellifolium leucine rich repe 150 4e-70
,	
,	
	emb AW034426 AW034426 EST277997 tomato callus, TAMU Lycopersicon 252 1e-65
	emb AW560797 AW560797 EST315845 DSIR Medicago truncatula cDNA cl 240 5e-62
	emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) 144 7e-60
10	emb A67432 A67432 Sequence 5 from Patent WO9743429. 144 7e-60
	emb AW033860 AW033860 EST277431 tomato callus, TAMU Lycopersicon 117 2e-59
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (inr 136 1e-55
	emb AI486612 AI486612 EST244933 tomato ovary, TAMU Lycopersicon 133 2e-53
	emb AW979740 AW979740 EST341365 tomato root deficiency, Cornell 105 5e-53
15	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr 142 2e-52
15	
	emb AW726024 AW726024 GA_Ea0020G24 Gossypium arboreum 7-10 dpa 149 le-51
	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) 139 2e-51
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci 133 9e-51
	emb AW564182 AW564182 LG1_285_D10.b1_A002 Light Grown 1 (LG1) So 193 3e-48
20	emb AW693988 AW693988 NF071C05ST1F1037 Developing stem Medicago 190 6e-47
-	—dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti 84 1e-45
	emb AW650232 AW650232 EST328686 tomato germinating seedlings, TA 96 7e-45
	emb AI895242 AI895242 EST264685 tomato callus, TAMU Lycopersicon 154 1e-44
	gb BE060160 BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis 90 4e-44
25	emb AW621923 AW621923 EST312721 tomato root during/after fruit s 94 2e-43
23	emb AW428824 AW428824 Ljirnpest24-927-c5 Ljirnp Lambda HybriZap 120 8e-43
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds. 85 2e-42
	emb AI484701 AI484701 EST242962 tomato ovary, TAMU Lycopersicon 89 2e-41
20	emb AW621706 AW621706 EST312504 tomato root during/after fruit s 92 3e-41
30	emb AW668493 AW668493 GA_Ea0014C20 Gossypium arboreum 7-10 dpa 92 6e-41
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase 83 7e-41
	emb AW929662 AW929662 EST338450 tomato flower buds 8 mm to pre-a 92 8e-41
•	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR 128 1e-40
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp 82 1e-40
35	emb Z73295 CRPK1 C.roseus mRNA for receptor-like protein kinase. 136 1e-40
	emb AW684304 AW684304 NF015C05NR1F1000 Nodulated root Medicago t 108 1e-40
	emb AW010219 AW010219 ST03E03 Pine TriplEx shoot tip library Pin 144 2e-40
	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1 129 2e-40
	emb AW287714 AW287714 LG1_271_E06.b1_A002 Light Grown 1 (LG1) So 103 2e-40
40	emb AW036763 AW036763 EST252152 tomato ovary, TAMU Lycopersicon 85 2e-40
10	emb AW092144 AW092144 EST285240 tomato mixed elicitor, BTI Lycop 102 3e-40
	emb AW704459 AW704459 sk53c10.y1 Gm-c1019 Glycine max cDNA clone 100 3e-40
	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon 85 4e-40
46	emb AV427160 AV427160 AV427160 Lotus japonicus young plants (two 117 4e-39
45	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine 84 4e-39
	emb AA557073 AA557073 915 Loblolly pine N Pinus taeda cDNA clone 96 4e-39
	emb AW831515 AW831515 sm26h11.yl Gm-c1028 Glycine max cDNA clone 93 6e-39
	emb AW299180 AW299180 EST305990 KV2 Medicago truncatula cDNA clo 122 7e-39
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc 85 3e-38
50	emb AW727470 AW727470 GA_Ea0012H16 Gossypium arboreum 7-10 dpa 93 3e-38
	emb AW039328 AW039328 EST281585 tomato mixed elicitor, BTI Lycop 102 3e-38
	emb AW694732 AW694732 NF079D07ST1F1061 Developing stem Medicago 102 3e-3
	emb A1894931 A1894931 EST264374 tomato callus, TAMU Lycopersicon 97 4e-38
	emb AW686018 AW686018 NF033E02NR1F1000 Nodulated root Medicago t 122 4e-38
55	
J.J	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop 102 4e-38
	emb AI967314 AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two 90 7e-38
	emb AV418863 AV418863 AV418863 Lotus japonicus young plants (two 112 9e-38
	emb AI485090 AI485090 EST243394 tomato ovary, TAMU Lycopersicon 85 3e-37
	gb BE059471 BE059471 sn32d11.yl Gm-c1016 Glycine max cDNA clone 82 3e-37
60	emb AI771841 AI771841 EST252941 tomato ovary, TAMU Lycopersicon 85 3e-37
	embl A 1485862 A 1485862 FST 244183 tomato overs. TAMILIT impression 85 3e-37

emb|AW756743|AW756743 sl26f10.yl Gm-c1027 Glycine max cDNA clone... 92 4e-37 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 78 5e-37 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 78 5e-37 emb|AB030083|AB030083 Populus nigra PnLPK mRNA for lectin-like p... 121 6e-37 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 91 6e-37 emb|AW746575|AW746575 WS1_54_G12.b1_A002 Water-stressed 1 (WS1) ... 150 8e-37 emb|AW756409|AW756409 sl21a08.yl Gm-c1036 Glycine max cDNA clone... 114 1e-36 emb|AI725692|AI725692 BNLGHi12653 Six-day Cotton fiber Gossypium... 101 1e-36 emb|AW458376|AW458376 sh87d06.y1 Gm-c1016 Glycine max cDNA clone... 74 2e-36 10 emb|AW185015|AW185015 se85e10.yl Gm-c1023 Glycine max cDNA clone... 100 2e-36 dbj|D88193|D88193 Brassica rapa DNA for S-receptor kinase, compl... 84 3e-36 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 100 4e-36 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 78 8e-36 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 83 8e-36 15 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 85 8e-36 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 77 1e-35 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 84 2e-35 emb|AW734633|AW734633 sk97d07.y1 Gm-c1035 Glycine max cDNA clone... 101 2e-35 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 82 3e-35 20 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 91 4e-35 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 76 9e-35 emb|AW774582|AW774582 EST333733 KV3 Medicago truncatula cDNA clo... 94 9e-35 emb|AW219672|AW219672 EST302154 tomato root during/after fruit s... 124 1e-34 gb|BE020963|BE020963 sm54a06.yl Gm-c1028 Glycine max cDNA clone ... 80 1e-34 25 emb|AW329560|AW329560 N200811e rootphos(-) Medicago truncatula c... 146 2e-34 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 87 2e-34 emb|AF166121|AF166121 Hordeum vulgare Cf2/Cf5 disease resistance... 103 2e-34 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... I41 3e-34 emb[Y14286]BOY14286 Brassica oleracea SFR3 gene, partial. 82 3e-34 30 Query= AL031187.126_at 16360_at /id_source genbank /description emb|caa20203.1| (al031187) receptor-like serine/threonine protein kinase ark3 [arabidopsis thaliana] /blast_score 0 /ec_number /family kinase/chip nova/gb link 35 http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187| /ncgi http://www.ncgr.org/cgi-bin/ff?al031187 (2553 letters) 40 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 45 Score Sequences producing significant alignments: (bits) Value emb[X98520]BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 820 0.0 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 50 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ... 505 0.0 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 504 0.0 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 501 0.0 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 490 0.0 55 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 489 0.0 dbi|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 488 0.0 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 485 0.0 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 483 0.0 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 461 0.0 60 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds.

gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 455 0.0

dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein... 395 0.0 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 394 0.0 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 374 0.0 emb[Y14286[BOY14286 Brassica oleracea SFR3 gene, partial. emb[Y12530]BOARLKGEN B.oleraceae gene encoding serine/threonine ... 652 0.0 emb|AB000972|AB000972 Brassica campestris pseudogene for SLG-lik... 237 0.0 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 481 0.0 emb|AB024419|AB024419S1 Brassica oleracea SRK13 gene, exon 1. emb|AB024421|AB024421S1 Brassica oleracea SRK13-b gene, exon 1. 10 emb|AB024418|AB024418 Brassica oleracea SLG13-b gene, partial cds. 506 0.0 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 320 e-180 emb[X55275]BOSLG13 B.oleracea SLG-13 gene for S-locus glycoprotein. 499 e-179 emb|AB009680|AB009680 Raphanus sativus SLG(S4) gene for S glycop... 493 e-179 emb|AB024417|AB024417 Brassica oleracea SLG13 gene, partial cds. 15 dbj|D85206|D85206 Brassica oleracea DNA for S blycoprotein, part... 406 e-177 dbj[D85215]D85215 Brassica campestris DNA for S glycoprotein, pa... 295 e-176 dbi|D85224|D85224 Brassica campestris DNA for S glycoprotein, pa... 486 e-176 dbj|D88765|D88765 Brassica oleracea DNA for S glycoprotein, part... 287 e-176 dbj|D85199|D85199 Brassica oleracea DNA for S glycoprotein, part... 485 e-176 20 emb|AB013719|AB013719 Brassica oleracea mRNA for SLG23Bol, compl... 404 e-175 dbj|D85219|D85219 Brassica campestris DNA for S glycoprotein, pa... 405 e-175 dbj|D85203|D85203 Brassica oleracea DNA for S glycoprotein, part... 409 e-175 dbj|D85198|D85198 Brassica oleracea DNA for S glycoprotein, part... 494 e-175 dbi|D85220|D85220 Brassica campestris DNA for S glycoprotein, pa... 410 e-175 25 emb[X55274]BCSLG8 B.campestris SLG-8 gene for S-locus glycoprotein. 482 e-175 emb|AB009682|AB009682 Raphanus sativus SLG(S6) gene for S glycop... 405 e-174 emb|Y00268|BOSLSG Brassica oleracea mRNA for S-locus specific gl... 408 e-174 emb|X03170|BOSLSGR Brassica oleracea mRNA 3' end for S-locus-spe... 408 e-174 dbj|D84468|BNASLG8A Brassica campestris mRNA for S-glycoprotein ... 478 e-173 30 emb|AB009681|AB009681 Raphanus sativus SLG(S5) gene for S glycop... 406 e-173 gb|S70937|S70937 self-incompatibility gene [Brassica campestris,... 283 e-173 dbj|D85218|D85218 Brassica campestris DNA for S glycoprotein, pa... 286 e-173 dbj|D85213|D85213 Brassica campestris DNA for S glycoprotein, pa... 283 e-173 emb|AB009683|AB009683 Raphanus sativus SLG(S8) gene for S glycop... 284 e-173 35 dbj|D85227|D85227 Brassica campestris DNA for S glycoprotein, pa... 293 e-172 dbj|D85211|D85211 Brassica oleracea DNA for S glycoprotein, part... 281 e-172 emb[X16123]BOS292 B. oleracea mRNA for S-locus specific glycopro... 397 e-172 gb]M36301]BNASLSGRA B.campestris S-locus-specific glycoprotein m... 402 e-172 dbj|D85225|D85225 Brassica campestris DNA for S glycoprotein, pa... 281 e-172 40 dbj|D85216|D85216 Brassica campestris DNA for S glycoprotein, pa... 409 e-171 dbj|D85204|D85204 Brassica oleracea DNA for S glycoprotein, part... 283 e-171 dbj[D85201|D85201 Brassica oleracea DNA for S glycoprotein, part... 490 e-171 emb|AB009684|AB009684 Raphanus sativus SLG(S7) gene for S glycop... 397 e-171 emb[X79432]BOSRK3 B.oleracea SRK3 gene. 396 e-171 45 dbj|D85208|D85208 Brassica oleracea DNA for S glycoprotein, part... 282 e-171 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 286 e-170 dbj|D84469|BNASLG12B Brassica campestris mRNA for S-glycoprotein... 287 e-170 emb|AB013717|AB013717S1 Brassica rapa gene for SRK46Bra, exon 1. 269 e-170 dbj|D85209|D85209 Brassica oleracea DNA for S glycoprotein, part... 286 e-170 50 dbj[D85205]D85205 Brassica oleracea DNA for S glycoprotein, part... 395 e-170 dbj|D85221|D85221 Brassica campestris DNA for S glycoprotein, pa... 348 e-170 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. emb|AB032471|AB032471 Brassica oleracea SLG pseudogene for S-loc... 398 e-169 gb L08608 BNASLOCGLY Brassica napus S-locus glycoprotein mRNA, c... 477 e-168 55 emb|Z21608|BNESLOGPA B.napus mRNA for endogenous S-locus glycopr... 477 e-168 gb|L10736|BNASLGGA Brassica napus S-locus related glycoprotein (... 477 e-168 dbj[D85222|D85222 Brassica campestris DNA for S glycoprotein, pa... 243 e-166 dbi|D85229|D85229 Brassica oleracea DNA for S glycoprotein, part... 401 e-166 emb|AB009679|AB009679 Raphanus sativus SLG(S3) gene for S glycop... 285 e-166 60 dbj|D85212|D85212 Brassica oleracea DNA for S glycoprotein, part... 244 e-164 dbj|D85214|D85214 Brassica campestris DNA for S glycoprotein, pa... 395 e-163

-- -WO-02/22675 -- -PCT/US01/28506

	emb AB009677 AB009677 Raphanus sativus SLG(S1) gene for S glycop 266 e-163 dbj D85200 D85200 Brassica oleracea DNA for S glycoprotein, part 204 e-163
	emb AB008190 AB008190 Brassica rapa gene for SLG29, complete cds. 290 e-163
5	emb Y18261 BOY18261 Brassica oleracea SLGB gene, partial. 286 e-163 emb Z19548 BNSLGPII B.napus mRNA for S-locus glycoprotein type II. 286 e-163
	emb Z11724 BNWSLGLP B. napus mRNA for S-locus glycoprotein. 278 e-160
	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco 380 e-160 emb AB024415 AB024415 Brassica oleracea SLG2-b mRNA, complete cds. 282 e-160
	dbj D85226 D85226 Brassica campestris DNA for S glycoprotein, pa 221 e-160
10	dbj D85223 D85223 Brassica campestris DNA for S glycoprotein, pa 224 e-160
	emb AB032472 AB032472 Brassica oleracea SLG60 pseudogene for S60 160 e-159 emb Z18921 BOSRKL B.oleracea gene for S-receptor kinase-like pro 198 e-158
	emb AB012105 AB012105 Brassica rapa mRNA for SLG45, complete cds. 221 e-158
15	dbj D88193 D88193 Brassica rapa DNA for S-receptor kinase, compl 160 e-158 emb X51637 BOSLSGA B.oleracea SLSG mRNA for self-incompatibility 263 e-155
13	dbj[D88192]D88192 Brassica rapa DNA for S-locus glycoprotein, co 148 e-153
	dbj D30050 BOLSRKB Turnip mRNA for S-glycoprotein SLG9, complete 148 e-153
	emb AF161333 AF161333 Raphanus raphanistrum subsp. raphanistrum 310 e-150 emb AF162908 AF162908 Hirschfeldia incana S-locus related (SLR) 261 e-150
20	emb[Y12321]BOY12321 Brassica oleracea SLG-Sc and SLA-Sc genes an 285 e-149
· - · · · - · ·	emb AB009872 AB009872 Orychophragmus violaceus gene for SLR1, pa 413 e-149
	emb X57673 BOSLR2RNA B.oleroceae RNA for S-locus-related glycopr 167 e-149 emb AB009873 AB009873 Cheiranthus cheiri gene for SLR1, partial 163 e-147
	emb X58440 BCNS1 B.campestris NS1 mRNA for NS1 glycoprotein. 273 e-145
25	emb X52089 BOSLRG Brassica gene for S locus related glycoprotein. 272 e-143
	Query= AC003974.136_at 16365_at /id_source genbank /description
	gb aac04495.1 (ac003974) putative disease resistance protein [arabidopsis thaliana] /blast score 0 /ec number /family disease
30	/chip nova/gb link
	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac003974 /ncgi http://www.ncgr.org/cgi-bin/ff?ac003974
25	(2673 letters)
35	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
40	Searchingdone
40	Score E
	Sequences producing significant alignments: (bits) Value
÷	emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) 148 4e-74
45	emb A67434 A67434 Sequence 7 from Patent WO9743429. 148 4e-74
	emb AF053993 AF053993 Lycopersicon esculentum disease resistance 148 4e-74 emb A67429 A67429 Sequence 2 from Patent WO9743429. 148 4e-74
	emb A67428 A67428 Sequence 1 from Patent WO9743429. 148 4e-74
50	emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) 150 4e-74 emb AF053997 AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) 146 1e-72
50	emb A67432 A67432 Sequence 5 from Patent WO9743429. 146 1e-72
	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe 150 3e-71
	emb[A57133]A57133 Sequence 4 from Patent WO9531564. 150 3e-71 gb[U42444[U42444 Lycopersicon pimpinellifolium leucine rich repe 150 8e-71
55	emb A57130 A57130 Sequence 1 from Patent WO9531564. 150 8e-71
	emb AB029327 AB029327 Nicotiana tabacum mRNA for elicitor-induci 97 4e-65
	emb AF053994 AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) 149 6e-37 emb AF119040 AF119040 Lycopersicon esculentum haplotype Northern 143 3e-36
60	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr 144 3e-35
60	emb AF119041 AF119041 Lycopersicon esculentum haplotype Southern 139 2e-33 emb AJ002235 LHJ002235 Lycopersicon hirsutum Cf-4 resistance gen 139 3e-33
	and mooned lengthoread photolession impuriting C1.4 (constance Retire 198, 36-3)

emb|AJ002236|LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist... 140 4e-33 emb|AJ002237|LEJ002237 Lycopersicon esculentum haplotype of the ... 138 1e-32 emb[Y12640]LECF4A L.esculentum Cf-4A gene. 137 1e-32 emb|A58270|A58270 Sequence 1 from Patent WO9635790. 138 2e-31 5 gb[U15936|LPU15936 Lycopersicon pimpinellifolium Cf-9 precursor ... 138 2e-31 emb|AI778581|AI778581 EST259460 tomato susceptible, Cornell Lyco... 92 1e-29 emb|AW458587|AW458587 sh11a09.y1 Gm-c1016 Glycine max cDNA clone... 131 3e-29 emb|AW306725|AW306725 sf47e12.yl Gm-c1009 Glycine max cDNA clone... 129 1e-28 emb|AF215729|AF215729 Glycine max RFLP clone A 45-10 sequence; a... 123 5e-27 10 emb[X81370]TAAWJL236 T.aestivumn (subclone pAWJL236) AWJL236 gene. 115 8e-27 emb|AF140552|AF140552 Lycopersicon esculentum plant disease resi... 121 2e-26 emb|A1895949|A1895949 EST265392 tomato callus, TAMU Lycopersicon... 70 5e-25 emb|AW624314|AW624314 EST322175 tomato flower buds 3-8 mm, Corne... 113 5e-24 emb[X81369]TAAWJL218 T.aestivumn (subclone pAWJL218) AWJL218 gene. 104 1e-23 15 emb[X81367]TAAWJL172 T.aestivumn (subclone pAWJL172) AWJL172 gene. emb|X81368|TAAWJL175 T.aestivumn (subclone pAWJL175) AWJL175 gene. emb[AW705275]AW705275 sk59a10.yl Gm-c1019 Glycine max cDNA clone... 108 2e-22 emb|AF166121|AF166121 Hordeum vulgare Cf2/Cf5 disease resistance... 94 3e-22 emblAI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 100 1e-21 20 emb|AW888094|AW888094 NXNV_108_E11_F Nsf Xylem Normal wood Verti... 105 2e-21 emblAQ917191|AQ917191 T233043b Medicago truncatula BAC library M... 93 1e-20 gb|U77888|INU77888 Ipomoea nil receptor-like protein kinase (inr... 79 2e-20 emb|AQ367638|AQ367638 toxb0002D20f CUGI Tomato BAC Library Lycop... 101 3e-20 emb|AZ044600|AZ044600 Gm_UMb001_116_G01.R UMN Soybean BAC Librar... 73 2e-19 25 emblAW064561|AW064561 ST33A08 Pine TriplEx shoot tip library Pin... 98 3e-19 emb|AI484441|AI484441 EST242451 tomato ovary, TAMU Lycopersicon ... 98 3e-19 emb|AW279193|AW279193 sf67g09.yl Gm-c1013 Glycine max cDNA clone... 98 4e-19 emb|AI900597|AI900597 sc13d11.yl Gm-c1013 Glycine max cDNA clone... 97 5e-19 emb|AF197946|AF197946 Glycine max receptor protein kinase-like p... 82 1e-18 30 emb|AW032163|AW032163 EST275617 tomato callus, TAMU Lycopersicon... emb|AW979663|AW979663 EST341269 tomato root deficiency, Cornell ... 61 1e-18 emblAW650508lAW650508 EST328962 tomato germinating seedlings, TA... 91 1e-18 emb|AI488023|AI488023 EST246345 tomato ovary, TAMU Lycopersicon ... 91 le-18 emb|AI896676|AI896676 EST266119 tomato callus, TAMU Lycopersicon... 91 1e-18 35 emb[AW307311]AW307311 sf55d03.y1 Gm-c1009 Glycine max cDNA clone... 66 2e-18 emb|AV415568|AV415568 AV415568 Lotus japonicus young plants (two... 85 2e-18 emb|AI895309|AI895309 EST264752 tomato callus, TAMU Lycopersicon... 95 2e-18 emb|AI727073|AI727073 BNLGHi7256 Six-day Cotton fiber Gossypium ... 95 2e-18 emb|AW306675|AW306675 se53h08.y1 Gm-c1017 Glycine max cDNA clone... 95 3e-18 40 emb[X79130|TSLRRR Triticum sp. (pAWJL3) leucine rich repeat regi... 84 4e-18 emb|AW031498|AW031498 EST274952 tomato callus, TAMU Lycopersicon... 94 5e-18 emb|AW775087|AW775087 EST334238 KV3 Medicago truncatula cDNA clo... 94 6e-18 emb|AW690301|AW690301 NF029C05ST1F1000 Developing stem Medicago ... 81 7e-18 emb|AW267958|AW267958 EST306300 DSIR Medicago truncatula cDNA cl... 80 7e-18 45 emb|AI895893|AI895893 EST265336 tomato callus, TAMU Lycopersicon... 61 9e-18 emb|AW647847|AW647847 EST326301 tomato germinating seedlings, TA... 91 1e-17 emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 92 2e-17 emb|AW689506|AW689506 NF021E06ST1F1000 Developing stem Medicago ... 92 2e-17 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 82 2e-17 50 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 91 4e-17 emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 91 4e-17 emb|AW031218|AW031218 EST274756 tomato callus, TAMU Lycopersicon... 91 4e-17 emblAW033367|AW033367 EST276938 tomato callus, TAMU Lycopersicon... 89 1e-16 emb|AI443128|AI443128 sa84f10.yl Gm-c1004 Glycine max cDNA clone... 89 1e-16 55 emb|AI896313|AI896313 EST265756 tomato callus, TAMU Lycopersicon... 60 le-16 emb|AW735867|AW735867 EST336635 tomato flower buds 0-3 mm, Corne... 89 2e-16 emb|AW980804|AW980804 EST391957 GVN Medicago truncatula cDNA clo... emb[AI488443]AI488443 EST246782 tomato ovary, TAMU Lycopersicon ... 88 3e-16 emb|AW033129|AW033129 EST276688 tomato callus, TAMU Lycopersicon... 78 3e-16 60 emb|AW127035|AW127035 ga20c02.y1 Moss EST library PPU Physcomitr... 88 4e-16 emb|AI895669|AI895669 EST265112 tomato callus, TAMU Lycopersicon... 88 4e-16

WO 02/22675 -----PCT/US01/28506

emb|AW618685|AW618685 EST320671 L. pennellii trichome, Cornell U... 88 4e-16 emb|AI894989|AI894989 EST264432 tomato callus, TAMU Lycopersicon... 88 4e-16 emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 87 5e-16 emb|AW648795|AW648795 EST327249 tomato germinating seedlings, TA... 87 5e-16 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... 78 6e-16 emb|AV415057|AV415057 AV415057 Lotus japonicus young plants (two... 87 7e-16 emb|AW399097|AW399097 EST309597 L. pennellii trichome, Cornell U... 63 8e-16 emb|AW761367|AW761367 sl66e07.yl Gm-c1027 Glycine max cDNA clone... 86 1e-15 emb|AW649208|AW649208 EST327662 tomato germinating seedlings, TA... 86 1e-15 10 emb|AV428126|AV428126 AV428126 Lotus japonicus young plants (two... 85 2e-15 emb|AW290705|AW290705 NXNV045C11F Nsf Xylem Normal wood Vertical... 85 2e-15 emb|AI352869|AI352869 MB70-4A PZ204.BNlib Brassica napus cDNA cl... 85 2e-15 emb|AA661049|AA661049 00946 MtRHE Medicago truncatula cDNA 5' si... 85 2e-15 emb|AW455303|AW455303 EST311841 tomato root during/after fruit s... 85 3e-15 15 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 85_3e-15 emb|AW398651|AW398651 EST309151 L. pennellii trichome, Cornell U... 84 4e-15 emb|AW398661|AW398661 EST309161 L. pennellii trichome, Cornell U... 84 4e-15 emb|AF049920|AF049920 Petunia x hybrida PGPS/D4 (PGPS/D4) mRNA, ... 84 4e-15 emb|AW624634|AW624634 EST322579 tomato flower buds 3-8 mm, Corne... 59 4e-15 20 emb|AW618879|AW618879 EST320865 L. pennellii trichome, Cornell U... 62 4e-15 gb|BE035885|BE035885 MO11F02 MO Mesembryanthemum crystallinum cD..._84 5e-15 Query= AL096882.91_s_at 16817_s_at /id_source genbank /description emb|cab51412.1| (al096882) acc synthase (atacs-6) [arabidopsis 25 thaliana] /blast score 0 /ec number /family /chip nova /gb link /ncgi (1488 letters) Database: plantfungal 30 661,018 sequences; 426,114,510 total letters Searching..... Score E 35 Sequences producing significant alignments: (bits) Value emb[X82273]BOACCS B.oleracea mRNA for ACC synthase. 986 0.0 emb[X72676]BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo... 875 0.0 emb|AF057563|AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-... 765 0.0 40 emb|AJ005002|NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro... 761 0.0 emb|AB034992|AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc... 754 0.0 emb|AB034993|AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc... 755 0.0 gb|U72389|LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1... 756 0.0 gb[U72390]LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1... 753 0.0 45 emb|AB033503|AB033503 Populus euramericana peacs-2 mRNA for 1-am... 741 0.0 gb|U68216|CPU68216 Carica papaya ACC synthase mRNA, complete cds. 461 0.0 emblAF061605|AF061605 Nicotiana glutinosa ACC synthase mRNA, com... 742 0.0 emb|AB013100|AB013100 Lycopersicon esculentum LE-ACS6 mRNA for 1... 741 0.0 emb|AJ012551|CSI012551 Citrus sinensis mRNA for ACC synthase. 50 emb|AB013346|AB013346 Lycopersicon esculentum mRNA for 1-aminocy... 739 0.0 emb|AB033502|AB033502 Populus euphratica peacs-1 mRNA for 1-amin... 620 0.0 gb|U88971|PHU88971 Pelargonium hortorum 1-aminocyclopropane-1-ca... 455 0.0 emb|Z11613|VRACCSYNM V.radiata mRNA for ACC synthase. 456 0.0 emb|X98492|NTACCS Nicotiana tabacum mRNA for ACC-synthase (clone... 455 0.0 55 emb[X67100]GMCACCS1 G.max mRNA for ACC synthase. 454 0.0 emb|Z18952|DCAMCRBSY D.caryophyllus mRNA for 1-aminocyclopropane... 716 0.0 emb|AJ012696|CSI012696 Citrus sinensis mRNA for ACC synthase (AC... 449 0.0 emb|AJ011095|CSI011095 Citrus sinensis mRNA for ACC synthase (ac... 452 0.0

emb|Z18953|PHAMCRBSY P.hybrida mRNA for 1-aminocyclopropane 1-ca... 450 0.0

emb|AB006804|AB006804 Cucumis sativus CS-ACS2 mRNA for ACC synth... 451 0.0 emb|AF080258|AF080258 Musa acuminata 1-aminocyclopropane-1-carbo... 711 0.0

60

emb|AF016459|AF016459 Pisum sativum 1-aminocyclopropane-1-carbox... 445 0.0 emb|AF109927|AF109927 Musa acuminata 1-aminocyclopropane-1-carbo... 707 0.0 dbj|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 705 0.0 emb|AB021906|AB021906 Musa acuminata MA-ACS1 mRNA for ACC syntha... 703 0.0 5 emb|AB006803|AB006803 Cucumis sativus CS-ACS1 mRNA for ACC synth... 703 0.0 emb|AF129508|AF129508 Musa acuminata 1-aminocyclopropane-1-carbo... 702 0.0 emb[X65982[NTXACCSYN N.tabacum mRNA for 1-aminocyclopropane-1-ca... 438 0.0 emb|AB031026|AB031026 Prunus mume PM-ACS1 mRNA for ACC synthase,... 434 0.0 emb|AB015625|AB015625 Pyrus pyrifolia pPPACS3 mRNA for 1-aminocy... 418 0.0 10 dbj[D01032|CUCACCW Cucurbita maxima mRNA for 1-aminocyclopropane... 695 0.0 dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 695 0.0 gb|M58323|CUCACCSYN Cucurbita pepo 1-aminocyclopropane-1-carboxy... 692 0.0 emb[Y11357|CP1A1CS C.papaya mRNA for 1-aminocyclopropane-1-carbo... 430 0.0 emb|X62536|LEACC L.esculentum mRNA for ACC synthase. 15 emb|AF057562|AF057562 Nicotiana glutinosa 1-aminocyclopropane-1-... 437 0.0 emb[X59145]LEACC2MR Lycopersicon esculentum LE-ASCC2 mRNA (ptACC... 326 0.0) gb/U79999/MAU79999 Musa acuminata ACC synthase (acs3) mRNA, comp... 687 0.0 emb[Y15739]MAACSYNTH Musa acuminata mRNA for 1-aminocyclopropane... 687 0.0 gb|M34289|TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha... 327 0.0 20 gb|M63490|TOMACCS Tomato 1-aminocyclopropane-1-carboxylate synth... 682 0.0 emb[X59146]LEACC4MR Lycopersicon esculentum LE-ACC4 mRNA (ptACC4... 681 0.0 gb[U17229]PHU17229 Pelargonium hortorum clone pGAC-1 1-aminocycl... 438 0.0 gb[U17231]PHU17231 Pelargonium hortorum clone pGAC-2 1-aminocycl... 423 0.0 emb|AF038945|AF038945 Rumex palustris 1-aminocyclopropane-1-carb... 407 0.0 25 gb|L20634|POTACCSYN Solanum tuberosum 1-aminocyclopropane-1-carb... 403 0.0 emb|AJ276295|CSI276295 Citrus sinensis partial mRNA for ACC synt... 446 0.0 emb|AF239987|AF239987 Prunus persica ACC synthase ACS1 mRNA, par... 662 0.0 emb|AF178076|AF178076 Carica papaya 1-aminocyclopropane-1-carbox... 395 0.0 emb[X82265]CAACC1 C.anuum mRNA for 1-aminocylopropane-1-carboxyl... 639 0.0 30 gb|U70842|STU70842 Solanum tuberosum 1-aminocyclopropane-1-carbo... 637 0.0 emblAF144746lAF144746 Solanum melongena 1-aminocyclopropane-1-ca... 636 0.0 emblAJ012577|CPA012577 Carica papaya mRNA for 1-aminocyclopropan... 387 e-180 gb[U73815]MDU73815 Malus domestica ACC synthase (MdACS-2) mRNA, ... 623 e-178 dbj|D37937|D37937 Cucumis melo mRNA for l-aminocyclopropane-1-ca... 380 e-177 35 emb|Z11562|VRACCSYN V.radiata mRNA for 1-aminocyclopropane-1-car... 375 e-176 emb|AF177769|AF177769 Carica papaya 1-aminocyclopropane-1-carbox... 369 e-175 emb|AF083814|AF083814 Antirrhinum majus ACC synthase 1 (ACS1) mR... 605 e-172 emb|AF178077|AF178077 Carica papaya 1-aminocyclopropane-1-carbox... 316 e-172 emb|AF239989|AF239989 Prunus persica ACC synthase ACS25 mRNA, pa... 597 e-170 40 gb[U22523]MIU22523 Mangifera indica 1-aminocyclopropane-carboxyl... 359 e-169 emb[X66605]DCACCS D.caryophyllus mRNA for 1-aminocyclopropane-1-... 396 e-168 gb|L31347|MAUACCSYN Malus domestica 1-aminocyclopropane-1-carbox... 378 e-168 emb|AB015624|AB015624 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 377 e-168 emb|AF049137|AF049137 Dianthus caryophyllus 1-aminocyclopropane-... 338 e-167 45 emb|AF170705|AF170705 Mangifera indica 1-aminocyclopropane-1-car... 290 e-167 gb[U03294]MSU03294 Malus sylvestris 1-aminocyclopropane-1-carbox... 372 e-166 emb|Z77854|PSPACS1 Phalaenopsis species mRNA for 1-aminocyclopro... 513 e-166 emb|AJ277160|CPA277160 Carica papaya partial paccs1A gene for 1-... 266 e-165 gb[U73816]MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ... 505 e-164 50 emb|AB007449|AB007449 Actinidia deliciosa mRNA for 1-aminocyclop... 355 e-164 emb|AB007639|AB007639 Pyrus pyrifolia mRNA for 1-aminocyclopropa... 502 e-164 dbj|D01033|CUCACCA Cucurbita maxima mRNA for 1-aminocyclopropane... 366 e-164 emb[X87112]PCPCACS1G P.communis mRNA for 1-aminocyclopropane-1-c... 363 e-163 gb|U17972|LEU17972 Lycopersicon esculentum 1-aminocyclopropane-1... 362 e-163 55 emb|AB015495|AB015495 Passiflora edulis PE-ACS2 mRNA for ACC syn... 368 e-162 emb|AB006805|AB006805 Cucumis sativus CS-ACS3 mRNA for ACC synth... 360 e-160 emb|AB000679|AB000679 Vigna radiata mRNA for 1-aminocyclopropane... 365 e-158 gb|U34987|VRU34987 Vigna radiata 1-aminocyclopropane-1-carboxyli... 325 e-157 gb[M66619]DINCARACC D.caryophyllus 1-aminocyclopropane-1-carboxy... 496 e-156 60 gb[U34986[VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli... 362 e-156 gb[U64031]DCU64031 Dendrobium crumenatum ACC synthase gene, comp... 259 e-154

-WO 02/22675

emb|AF016458|AF016458 Pisum sativum 1-aminocyclopropane-1-carbox... 355 e-154 emb|Z27233|STACCAS1 S.tuberosum (STAC1) gene for amino cycloprop... 237 e-152 emb|Z27234|STACCAS2 S.tuberosum STACS2 gene for 1-Aminocycloprop... 232 e-152 emb|AF043122|AF043122 Lycopersicon esculentum ACC synthase (LE-A... 236 e-150 gb|U37774|CMU37774 Cucurbita maxima 1-aminocyclopropane-1-carbox... 234 e-150 gb|L34171|TOMACS3A Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149 gb|U18055|LEU18055 Lycopersicon esculentum 1-aminocyclopropane-1... 235 e-149 emb|AF151961|AF151961 Vigna radiata 1-aminocyclopropane-1-carbox... 232 e-146 emb|Z12135|VRACCSYN4 V.radiata gene for ACC synthase (pMAC-4). 10 gb|L07883|DORAMICARB Moth orchid 1-aminocyclopropane-1-carboxyla... 243 e-144 emb|AF074927|AF074927 Sinapis arvensis 1-aminocyclopropane-1-car... 330 e-142 emb|AF083815|AF083815 Antirrhinum majus ACC synthase 2 (ACS2) mR... 482 e-141 emb|AB021907|AB021907 Musa acuminata MA-ACS2 mRNA for ACC syntha... 310 e-140 emb|AB021908|AB021908 Musa acuminata MA-ACS3 mRNA for ACC syntha... 298 e-138 15 Query= AC000107.5_at 17278_at /id_source genbank /description gb|aad36959.1|ac000107_5 (ac000107) f17f8.5 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000107|/ncgi 20 http://www.ncgr.org/cgi-bin/ff?ac000107 (1950 letters)

Database: plantfungal

25

30

35

661,018 sequences; 426,114,510 total letters

Searching.....done

Score

Sequences producing significant alignments:

(bits) Value

gb/U79958PSU79958 Pisum sativum BP-80 vacuolar sorting receptor... 630 0.0 emb|AB006809|AB006809 Cucurbita sp. mRNA for PV72, complete cds. emb|AW267745|AW267745 EST305873 DSIR Medicago truncatula cDNA cl... 350 e-124 emb|AW931583|AW931583 EST357426 tomato fruit mature green, TAMU ... 165 e-112 emb|AW309187|AW309187 sg05d06.yl Gm-c1019 Glycine max cDNA clone... 326 e-108

emb|AW622833|AW622833 EST306903 tomato flower buds 3-8 mm, Corne... 387 e-106 emb|AW774434|AW774434 EST333585 KV3 Medicago truncatula cDNA clo... 294 e-100 emb|AW689392|AW689392 NF018F12ST1F1000 Developing stem Medicago ... 338 e-100 emb|AI782787|AI782787 EST263666 tomato susceptible, Cornell Lyco... 332 6e-90

emb|AW737948|AW737948 EST339375 tomato flower buds, anthesis, Co... 225 1e-89 emb|AW615949|AW615949 EST325315 tomato flower buds 0-3 mm, Corne... 217 3e-86 emb|AW932529|AW932529 EST358372 tomato fruit mature green, TAMU ... 303 1e-83 emb[AW685785]AW685785 NF030C07NR1F1000 Nodulated root Medicago t... 157 2e-81

45 emb|AW747297|AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ... 286 4e-76 emb|AI443067|AI443067 sa47a01.yl Gm-c1004 Glycine max cDNA clone... 265 6e-76 emb|AI728635|AI728635 BNLGHi11276 Six-day Cotton fiber Gossypium... 135 1e-75 emb|AI484571|AI484571 EST242801 tomato ovary, TAMU Lycopersicon ... 278 1e-73 emb|AI727826|AI727826 BNLGHi9195 Six-day Cotton fiber Gossypium ... 135 9e-71

50 emb[AW695542]AW695542 NF096C05ST1F1037 Developing stem Medicago ... 153 2e-65 emb|AV406766|AV406766 AV406766 Lotus japonicus young plants (two... 170 5e-65 emb|AW509740|AW509740 ga63h11.yl Moss EST library PPU Physcomitr... 226 6e-63 emb|AW256542|AW256542 EST304679 KV2 Medicago truncatula cDNA clo... 181 8e-60 emb|AW397829|AW397829 sg68h03.yl Gm-c1007 Glycine max cDNA clone... 225 1e-57

55 emb|AW289687|AW289687 NXNV004E04F Nsf Xylem Normal wood Vertical... 182 7e-55 emb|AW690002|AW690002 NF026G04ST1F1000 Developing stem Medicago ... 143 4e-54 emb|AA660289|AA660289 00158 MtRHE Medicago truncatula cDNA 5', m... 138 2e-53 emb|AW064744|AW064744 ST35C06 Pine TriplEx shoot tip library Pin... 141 6e-53 emb|AV428420|AV428420 AV428420 Lotus japonicus young plants (two... 134 le-51

60 emb|AW623959|AW623959 EST321904 tomato flower buds 3-8 mm, Corne... 74 1e-49 emb|AW568619|AW568619 si60a11.yl Gm-r1030 Glycine max cDNA clone... 165 2e-47

emb|AI967865|AI967865 Ljirnpest14-100-f3 Ljirnp Lambda HybriZap ... 180 5e-47 emb|AW309191|AW309191 sg05d10.y1 Gm-c1019 Glycine max cDNA clone... 105 2e-46 emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 132 2e-45 emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 182 6e-45 emb|AW096632|AW096632 EST289812 tomato mixed elicitor, BTI Lycop... 81 7e-45 emb|AF209910|AF209910 Prumus dulcis vacuolar sorting receptor pr... 76 8e-44 emb|AW056624|AW056624 ST53G07 Pine TriplEx shoot tip library Pin... 178 1e-43 emb|AW680054|AW680054 WS1 3 A01.gl A002 Water-stressed 1 (WS1) S... 77 1e-41 emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 170 4e-41 10 gb|BE125908|BE125908 DG1 59 E01.bl A002 Dark Grown 1 (DG1) Sorgh... 164 2e-39 emb|AI161766|AI161766 A006P54U Hybrid aspen plasmid library Popu... 76 3e-39 emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 130 2e-37 gb|BE049814|BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic... 156 4e-37 emb|AW508719|AW508719 si35f03.yl Gm-r1030 Glycine max cDNA clone... 155 8e-37 15 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 153 4e-36 emb|AW616461|AW616461 EST322872 L. hirsutum trichome, Cornell Un... 102 4e-33 emb|AA660955|AA660955 00852 MtRHE Medicago truncatula cDNA 5' si... 72 4e-31 emb|AW774190|AW774190 EST333273 KV3 Medicago truncatula cDNA clo... 134 2e-30 emb|AW201441|AW201441 sf03b09.yl Gm-c1027 Glycine max cDNA clone... 73 5e-30 20 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 78 2e-27 emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 73 9e-27 emb|AW620693|AW620693 sj08d10.yl Gm-c1032 Glycine max cDNA clone... 77 1e-26 emb|AW317388|AW317388 sg48g10.yl Gm-c1025 Glycine max cDNA clone... 72 2e-26 emb|AW706755|AW706755 sk02f10.yl Gm-c1023 Glycine max cDNA clone... 117 3e-25 25 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 71 1e-23 emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 69 1e-22 emb|AW348825|AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3... 66 2e-22 emb|AW093844|AW093844 EST287024 tomato mixed elicitor, BTI Lycop... 98 3e-19 emb|AW691052|AW691052 NF037B05ST1F1000 Developing stem Medicago ... 79 6e-17 30 emb|AW119909|AW119909 sd54d08.yl Gm-c1016 Glycine max cDNA clone... 88 2e-16 emb[AW685952]AW685952 NF036G09NR1F1000 Nodulated root Medicago t... 50 1e-15 emb|AW774852|AW774852 EST334003 KV3 Medicago truncatula cDNA clo... 83 9e-15 emb|AI794754|AI794754 sb68f11.yl Gm-c1019 Glycine max cDNA clone... 82 1e-14 gbBE060808BE060808 HVSMEg0013H06f Hordeum vulgare pre-anthesis... 78 6e-14 35 emb|AW760128|AW760128 sl58d09.yl Gm-c1027 Glycine max cDNA clone... 66 8e-14 emb|AW037563|AW037563 EST278890 tomato mixed elicitor, BTI Lycop... 77 6e-13 emb|AW256398|AW256398 EST304465 KV2 Medicago truncatula cDNA clo... 72 7e-13 emb|AW686287|AW686287 NF040A08NR1F1000 Nodulated root Medicago t... 67 6e-10 emblAW443352|AW443352 EST308282 tomato mixed elicitor, BTI Lycop... 65 2e-09 40 emb|AW747372|AW747372 WS1_67_G06.g1_A002 Water-stressed 1 (WS1) ... 64 4e-09 emb|AW127457|AW127457 M110648 DSIL Medicago truncatula cDNA clon... 63 6e-09 emb|AI939286|AI939286 sc69h02.yl Gm-c1016 Glycine max cDNA clone... 48 2e-04 emb|AQ652964|AQ652964 Sheared DNA-1M1.TR Sheared DNA Trypanosoma... 39 0.16 gb|C95899|C95899 C95899 Marchantia polymorpha immature sex organ... 38 0.31 45 gbB67199B67199 CpG0015B CpIOWAgDNA1 Cryptosporidium parvum gen... 38 0.31 emb|AW692657|AW692657 NF057H03ST1F1000 Developing stem Medicago ... 37 0.42 emb|AF083502|AF083502 Plasmodium vivax ookinete surface protein ... 37 0.42 emb|AW626172|AW626172 EST320079 tomato radicle, 5 d post-imbibit... 37 0.42 emb|AC008054|AC008054 Leishmania major chromosome 35 clone L8453... 36 0.55 50 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 35 1.5 emb|AB033343|AB033343 Plasmodium vivax gene for ookinete surface... 35 1.5 emb|AB033342|AB033342 Plasmodium vivax gene for ookinete surface... 35 1.5 emb|AB033341|AB033341 Plasmodium vivax gene for ookinete surface... 35 1.5 emb|AB033340|AB033340 Plasmodium vivax gene for ookinete surface... 35 1.5 55 emb|AB033339|AB033339 Plasmodium vivax gene for ookinete surface... 35 1.5 emb|AV410215|AV410215 AV410215 Lotus japonicus young plants (two... 35 2.1 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 35 2.8 emb|AQ649743|AQ649743 Sheared DNA-17O2.TR Sheared DNA Trypanosom... 35 2.8 emb|AW982863|AW982863 HVSMEg0004G15f Hordeum vulgare pre-anthesi... 35 2.8 60 emb|AZ216543|AZ216543 Sheared DNA-116G5.TR Sheared DNA Trypanoso... 35 2.8 emb|AC004157|AC004157 Plasmodium falciparum chromosome 12 clone ... 35 2.8

gb|U18916|SCE9781 Saccharomyces cerevisiae chromosome V cosmids ... dbj|D13340|CHL58S25S Chlorella ellipsoidea genes for 5.8S rRNA a... 35 2.8 emb|AW648383|AW648383 EST326837 tomato germinating seedlings, TA... 33 3.3 emb|AI778616|AI778616 EST259495 tomato susceptible, Cornell Lyco... 33 3.3 emb|AA749476|AA749476 L30-23M13T3 Ice plant Lambda Uni-Zap XR ex... emb|AA938798|AA938798 L0-249M13R Ice plant Lambda Uni-Zap XR exp... emblAI822187|AI822187 L0-664T3 Ice plant Lambda Uni-Zap XR expre... 31 3.3 emb|AI822671|AI822671 L0-1192T3 Ice plant Lambda Uni-Zap XR expr... 31 3.3 10 Query= AC004684.168 s at 17744 s at /id_source genbank /description gb|aac23646.1| (ac004684) putative alcohol dehydrogenase [arabidopsis thaliana] /blast score 1.00e-170 /ec number /family /chip nova /gb link /ncgi (885 letters) 15 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 20 Score E Sequences producing significant alignments: (bits) Value emb[X97606]MSRNAAAA M.sativa mRNA translated from abscisic activ... 306 e-115 25 emb[AW666569]AW666569 GA __Ea0005J12 Gossypium arboreum 7-10 dpa ... 310 6e-91 emb|AW692860|AW692860 NF056E06ST1F1000 Developing stem Medicago ... 309 2e-89 gb|BE123903|BE123903 EST394028 DSIL Medicago truncatula cDNA clo... 304 7e-88 emb|AW774316|AW774316 EST333467 KV3 Medicago truncatula cDNA clo... 308 5e-83 emb[AW728361]AW728361 GA Ea0016H09 Gossypium arboreum 7-10 dpa ... 306 2e-82 30 emb|AW267789|AW267789 EST305917 DSIR Medicago truncatula cDNA cl... 169 4e-81 emb|AW329160|AW329160 N200369e rootphos(-) Medicago truncatula c... 224 2e-80 emb|AW696127|AW696127 NF102F09ST1F1078 Developing stem Medicago ... 298 4e-80 emb|AI794650|AI794650 sb67a05.y1 Gm-c1019 Glycine max cDNA clone... 286 2e-76 gb|BE037103|BE037103 MP15A03 MP Mesembryanthemum crystallinum cD... 139 8e-76 35 emb|AW399617|AW399617 EST310117 L. pennellii trichome, Cornell U... 281 5e-75 emb|AW564270|AW564270 LG1 289 E10.b1 A002 Light Grown 1 (LG1) So... 162 6e-72 emb|AW756208|AW756208 s117d10.yl Gm-c1036 Glycine max cDNA clone... 264 5e-70 emb|AW760494|AW760494 sl51a09.yl Gm-c1027 Glycine max cDNA clone... 178 1e-69 emb|AW831516|AW831516 sm27a02.y1 Gm-c1028 Glycine max cDNA clone... 261 4e-69 40 emb|AJ223291|SRAJ3291 Sesbania rostrata mRNA for putative chalco... 115 2e-64 emb|AW830327|AW830327 sm25f04.yl Gm-c1028 Glycine max cDNA clone... 242 2e-63 emb|AW688330|AW688330 NF006B06ST1F1000 Developing stem Medicago ... 169 6e-63 gb|BE020597|BE020597 sm51b07.yl Gm-c1028 Glycine max cDNA clone ... 239 2e-62 emb[X82368]MSCHR2A M.sativa mRNA for chalcone reductase (1134 bp). 117 6e-61 45 gb[U13925]MSU13925 Medicago sativa Apollo clone CHR7 chalcone re... 117 6e-61 emb|X57526|HVALREDR H.vulgare gene for aldose reductase-related ... 92 1e-60 emb[X82367]MSCHR1B M.sativa mRNA for chalcone reductase (1115 bp). 116 1e-60 emb[X82366]MSCHR1A M.sativa mRNA for chalcone reductase (1202 bp). 116 2e-60 emb[AF133841]AF133841 Xerophyta viscosa aldose reductase ALDRXV4... 97 2e-60 50 gb[U13924]MSU13924 Medicago sativa Apollo clone CHR12 chalcone r... 114 8e-60 emb[X55730]GMREDUC Soybean mRNA for reductase involved in deoxyc... 111 le-59 emb|AF108438|AF108438 Papaver somniferum putative NADPH-dependen... 154 le-59 gb|L12042|BMUSUSCUL Bromus inermis aldose reductase-related prot... 86 2e-59

emb|AW694657|AW694657 NF078G04ST1F1035 Developing stem Medicago ... 164 3e-59
emb|X59465|PSXYL1RE P.stipitis XYL1-gene for NAD(P)H-dependent X... 125 2e-58
emb|AF020040|AF020040 Pichia guilliermondii xylose reductase mRN... 121 2e-58
emb|AF039182|AF039182 Fragaria x ananassa probable aldo-keto red... 105 5e-58
emb|AB002105|AB002105 Candida tropicalis DNA for D-xylose reduct... 127 6e-58
emb|AW991001|AW991001 SsS0116 Suaeda salsa ZAP cDNA library Suae... 184 1e-57
emb|AB002106|AB002106 Candida tropicalis DNA for D-xylose reduct... 124 2e-57
emb|AW830449|AW830449 sm27b05.yl Gm-c1028 Glycine max cDNA clone... 223 2e-57

	dbj D83718 GYCPKR Glycyrrhiza echinata mRNA for polyketide reduc 111 6e-57
	gb U40706 PTU40706 Pachysolen tannophilus aldose reductase gene, 123 8e-57
	dbj D86559 D86559 Glycyrrhiza glabra mRNA for polyketide reducta 110 1e-56
	dbj D86558 D86558 Glycyrrhiza glabra mRNA for polyketide reducta 110 1e-56
5	emb AF074484 AF074484 Candida tenuis xylose reductase (xylr) gen 127 2e-54
•	gb[L36993[YSKXYL Kluyveromyces lactis xylose reductase (XYL1) ge 120 5e-53
	emb Z73100 SPAC26F1 S.pombe chromosome I cosmid c26F1. 92 1e-51
	emb AW730093 AW730093 GA Ea0027M16 Gossypium arboreum 7-10 dpa 128 1e-51
	emb AW186336 AW186336 se66e01.yl Gm-c1019 Glycine max cDNA clone 127 2e-51
10	
10	gb U83687 AGU83687 Apium graveolens NADPH-dependent mannose 6-ph 80 2e-51
	emb AF108432 AF108432 Papaver somniferum NADPH-dependent codeino 141 4e-51
•	gb[U00059]YSCH8263 Saccharomyces cerevisiae chromosome VIII cosm 116 2e-50
	dbj D11080 MAUS6PDH Apple S6PDH mRNA for NADP-dependent D-sorbit 78 2e-49
	emb AF219625 AF219625 Aspergillus niger D-xylose reductase (xyrA 86 6e-49
15	emb AF108435 AF108435 Papaver somniferum NADPH-dependent codeino 85 1e-48
	emb AF108434 AF108434 Papaver somniferum NADPH-dependent codeino 83 1e-48
	emb AW773597 AW773597 EST332583 KV3 Medicago truncatula cDNA clo 161 2e-48
	emb AF108433 AF108433 Papaver somniferum NADPH-dependent codeino 85 2e-47
	emb AW982655 AW982655 HVSMEg0003N17f Hordeum vulgare pre-anthesi 156 2e-47
20	emblAL021815 SPBC8E4 S.pombe chromosome I cosmid c8E4. 84 3e-47
	gb J04483 LEIP10011E Leishmania major reductase (P100/11E) mRNA, 83 5e-47
	emb AW266162 AW266162 L30-2855T3 Ice plant Lambda Uni-Zap XR exp 185 7e-47
	emb AW351113 AW351113 GM210010B20E10R Gm-r1021 Glycine max cDNA 122 2e-46
	emb AW267703 AW267703 EST305831 DSIR Medicago truncatula cDNA cl 114 3e-46
25	emb AL110661 CNS018Q6 Botrytis cinerea strain T4 cDNA library un 108 2e-45
	emb AB014493 AB014493 Gibberella zeae gene for reductase, partia 91 5e-45
	emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo 57 2e-44
	emb[X90518]SCXVORFS S.cerevisiae DNA of 51 Kb from chromosome XV 57 2e-44
	emb Z75028 SCYOR120W S.cerevisiae chromosome XV reading frame OR 57 2e-44
30	emb X13228 SCGCY Yeast GCY gene (homologous to vertebrate eye le 57 2e-44'
50	emb X96740 SCGCY1 S. cerevisiae GCY1 gene. 57 2e-44
	emb AW775175 AW775175 EST334326 KV3 Medicago truncatula cDNA clo 101 5e-44
	emb AW776733 AW776733 EST335798 DSIL Medicago truncatula cDNA cl 177 9e-44
	gb BE036780 BE036780 MP05F01 MP Mesembryanthemum crystallinum cD 84 9e-43
35	- · · · · ·
33	
	emb AW706251 AW706251 sj54a08.yl Gm-c1033 Glycine max cDNA clone 106 2e-42
	emb AW564750 AW564750 LG1_301_D05.b1_A002 Light Grown 1 (LG1) So 155 3e-42 gb BE123887 BE123887 EST394012 DSIL Medicago truncatula cDNA clo 114 3e-42
40	emb AW686854 AW686854 NF003B10RT1F1000 Developing root Medicago 114 4e-42
40	gb U21747 AFU21747 Avena fatua aldose reductase-related protein 91 4e-41
	emb AW981220 AW981220 EST392310 DSIL Medicago truncatula cDNA cl 83 5e-41
	emb AW685322 AW685322 NF027B04NR1F1000 Nodulated root Medicago t 93 6e-41
	emb AW091709 AW091709 EST284805 tomato mixed elicitor, BTI Lycop 166 2e-40
4-	emb AW041447 AW041447 EST284311 tomato mixed elicitor, BTI Lycop 166 2e-40
45	emb AW568008 AW568008 si56c03.yl Gm-r1030 Glycine max cDNA clone 166 3e-40
	emb AW567986 AW567986 si56a03.yl Gm-r1030 Glycine max cDNA clone 166 3e-40
	emb AW310318 AW310318 sf34d05.x1 Gm-c1028 Glycine max cDNA clone 124 1e-38
	emb AL115070 CNS01C4M Botrytis cinerea strain T4 cDNA library un 90 2e-38
	emb AW704367 AW704367 sk30b12.yl Gm-c1028 Glycine max cDNA clone 109 2e-38
50	emb AW306925 AW306925 sf50e02.yl Gm-c1009 Glycine max cDNA clone 93 2e-38
	emb AW564756 AW564756 LG1_301_B12.b1_A002 Light Grown 1 (LG1) So 147 6e-38
	emblAW560687 AW560687 EST315735 DSIR Medicago truncatula cDNA cl 93 3e-37
	emb AW775758 AW775758 EST334823 DSIL Medicago truncatula cDNA cl 89 1e-36
	emb AA825062 AA825062 ETN380 Trypanosoma brucei rhodesiense ZAP 85 2e-36
55	emb AW728632 AW728632 GA Ea0017G17 Gossypium arboreum 7-10 dpa 80 3e-36
-	emb AI441520 AI441520 sa87d08.yl Gm-c1004 Glycine max cDNA clone 126 3e-36
	emb AW761087 AW761087 sl63a04.yl Gm-c1027 Glycine max cDNA clone 74 5e-36
	emb AI939278 AI939278 sc69f11.y1 Gm-c1016 Glycine max cDNA clone 150 1e-35
	emb AW831528 AW831528 sm27e03.yl Gm-c1028 Glycine max cDNA clone 125 2e-35
60	emb AW756704 AW756704 sl26b12.yl Gm-c1027 Glycine max cDNA clone 79 2e-35
. .	gblU26463 SSU26463 Sporidiobolus salmonicolor NADPH-dependent al 86 3e-35
	EVINEY IVANDO VEVINA DIVININIVANIA BUHUNHANDI IVALA IIPUDDENGIN AL ON -XC-3.5

emb|AW234076|AW234076 sf34a01 yl Gm-c1028 Glycine max cDNA clone... 111 7e-35

Query= AC004392.2_at 17775_at /id_source genbank /description gb|aac28500.1| (ac004392) similar to glucose-6-phosphate/phosphate-translocator (gpt) gb|af020814 from pisum sativum. [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004392| /ncgi

http://www.ncgr.org/cgi-bin/ff?ac004392 (1233 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

25

Searching.....done

Score E

emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 626 e-179

Sequences producing significant alignments:

(bits) Value

20

emb|AF020816|AF020816 Solanum tuberosum glucose-6-phosphate/phos... 359 e-167 emb|AW761153|AW761153 sl63h08.y1 Gm-c1027 Glycine max cDNA clone... 403 e-111 emb|AI973973|AI973973 sd14e11.y1 Gm-c1020 Glycine max cDNA clone... 387 e-106 emb|AW832261|AW832261 sm21g08.y1 Gm-c1027 Glycine max cDNA clone... 372 e-102 emb|AW507609|AW507609 si42a06.y1 Gm-r1030 Glycine max cDNA clone... 365 e-100 emb|AI974103|AI974103 sd16e09.y1 Gm-c1020 Glycine max cDNA clone... 202 9e-91 emb|AV421952|AV421952 AV421952 Lotus japonicus young plants (two... 304 1e-81

emb|AW509448|AW509448 si37c07.yl Gm-r1030 Glycine max cDNA clone... 297 4e-81
30 emb|AW985263|AW985263 NXNV_135_B02_F Nsf Xylem Normal wood Verti... 209 5e-73
emb|AI352923|AI352923 MB73-9C PZ204.BNlib Brassica napus cDNA cl... 226 1e-70
gb|U13630|BOU13630 Brassica oleracea var. botrytis chloroplast p... 189 2e-69
emb|X75088|NTRNPHTR Nicotiana tabacum mRNA for phosphate translo... 185 8e-69

emb|X13754|SOPHTRAN Spinach mRNA for chloroplast phosphate trans... 186 8e-69
emb|X67045|STTPTMR S.tuberosum mRNA TPT for triose phosphate tra... 183 1e-67
emb|AW234628|AW234628 sf17d12.yl Gm-c1028 Glycine max cDNA clone... 254 1e-66
gb|BE060177|BE060177 HVSMEg0011C12f Hordeum vulgare pre-anthesis... 249 3e-65
emb|AV413897|AV413897 AV413897 Lotus japonicus young plants (two... 229 3e-59
emb|AI894606|AI894606 EST264049 tomato callus, TAMU Lycopersicon... 228 6e-59

40 emb|AW926251|AW926251 HVSMEg0006L14 Hordeum vulgare pre-anthesis... 226 2e-58 emb|AW472436|AW472436 si25b11.yl Gm-c1029 Glycine max cDNA clone... 221 2e-57 emb|AF173679|AF173679 Beta vulgaris phophate translocator (pt) m... 135 2e-53 emb|AW560889|AW560889 EST315937 DSIR Medicago truncatula cDNA cl... 205 2e-53 emb|AI939281|AI939281 sc69g06.yl Gm-c1016 Glycine max cDNA clone... 204 1e-51

emb|AW688995|AW688995 NF014B11ST1F1000 Developing stem Medicago ... 150 2e-50 emb|AW034833|AW034833 EST278941 tomato callus, TAMU Lycopersicon... 196 3e-49 emb|X54639|PSCIRP36 P. sativum mRNA for chloroplast import recep... 193 2e-48 emb|X68077|PSPTCPA P. sativum mRNA for phosphate translocator. 193 2e-48 emb|AW760040|AW760040 sl57c08.yl Gm-c1027 Glycine max cDNA clone... 193 3e-48

emb|AW691966|AW691966 NF051A06ST1F1000 Developing stem Medicago ... 166 3e-47 emb|AI772801|AI772801 EST253901 tomato resistant, Cornell Lycope... 188 8e-47 emb|AW217547|AW217547 EST296261 tomato flower buds 3-8 mm, Corne... 188 8e-47 emb|X92656|LETPT L.esculentum mRNA for triose phosphate transloc... 188 8e-47 emb|Z26633|CHFPCPT F.pringlei fpcpt mRNA for triose phosphate/ph... 188 1e-46

55 emb|AW758970|AW758970 sl33a11.yl Gm-c1027 Glycine max cDNA clone... 187 2e-46 emb|Z26632|CHFTCPT F.trinervia flcpt mRNA for triose phosphate/p... 184 1e-45 emb|AW031949|AW031949 EST275403 tomato callus, TAMU Lycopersicon... 184 1e-45 emb|AW564653|AW564653 LG1_297_C06.bl_A002 Light Grown 1 (LG1) So... 182 3e-45 emb|AI773418|AI773418 EST254518 tomato resistant, Cornell Lycope... 182 3e-45

60 emb|AI812950|AI812950 22G7 Pine Lambda Zap Xylem library Pinus t... 176 3e-43 emb|AI774019|AI774019 EST255119 tomato resistant, Cornell Lycope... 175 6e-43

```
emb|AW689300|AW689300 NF017F08ST1F1000 Developing stem Medicago ... 172 7e-43
      emb|AW933284|AW933284 EST359127 tomato fruit mature green, TAMU ... 175 8e-43
      emb|AW399333|AW399333 EST309833 L. pennellii trichome, Cornell U... 175 8e-43
      emblAW626582|AW626582 NXNV067A01 Nsf Xylem Normal wood Vertical ... 107 2e-42
      emb|AW671381|AW671381 LG1_335_G10.b1_A002 Light Grown 1 (LG1) So... 173 3e-42
      emb|AW671933|AW671933 LG1 353 E03.b1 A002 Light Grown 1 (LG1) So... 173 3e-42
      emb|AW559735|AW559735 EST314727 DSIR Medicago truncatula cDNA cl... 167 3e-42
      gb|BE034606|BE034606 MK02F02 MK Mesembryanthemum crystallinum cD... 170 2e-41
      emb|AW690541|AW690541 NF035G02ST1F1000 Developing stem Medicago ... 166 5e-41
10
      gb|U13632|BOU13632 Brassica oleracea var. botrytis non-green pla... 166 2e-40
      emb|A93887|A93887 Sequence 1 from Patent WO9725346.
                                                                   166 2e-40
      emb|AW782182|AW782182 sm02e11.yl Gm-c1027 Glycine max cDNA clone... 166 3e-40
      gb U66402 NTU66402 Nicotiana tabacum plastid phosphate/phosphoen... 165 6e-40
      emb|AW666055|AW666055 sk31e07.yl Gm-c1028 Glycine max cDNA clone... 160 2e-39
15
      emb|AW776623|AW776623 EST335688 DSIL Medicago truncatula cDNA cl... 162 4e-39
      gb|U66401|NTU66401 Nicotiana tabacum plastid phosphate/phosphoen... 162 4e-39
      emb|AF173656|AF173656 Beta vulgaris clone GPTII109UNI glucose-6-... 161 1e-38
      emb|AW736423|AW736423 EST332437 KV3 Medicago truncatula cDNA clo... 153 6e-38
      emb|AW038916|AW038916 EST280872 tomato mixed elicitor, BTI Lycop... 158 1e-37
20
      emb|AW930290|AW930290 EST340747 tomato fruit mature green, TAMU ... 157 2e-37
      emb|AV415709|AV415709 AV415709 Lotus japonicus young plants (two... 153 2e-36
      emb|AW201212|AW201212 se99c01.yl Gm-c1027 Glycine max cDNA clone... 93 3e-36
      emb|AI736196|AI736196 sb24f10.y1 Gm-c1008 Glycine max cDNA clone... 151 8e-36
      emb|AV426398|AV426398 AV426398 Lotus japonicus young plants (two... 149 6e-35
25
      emb|AV422882|AV422882 AV422882 Lotus japonicus young plants (two... 147 2e-34
      emb|AF173660|AF173660 Beta vulgaris clone GPTI109UNI glucose-6-p... 146 4e-34
      emblA1822397|A1822397 L0-856T3 Ice plant Lambda Uni-Zap XR expre... 125 7e-34
      emb|AW040008|AW040008 EST282499 tomato mixed elicitor, BTI Lycop... 144 1e-33
      emb|AW039997|AW039997 EST282488 tomato mixed elicitor, BTI Lycop... 144 1e-33
30
      gb|BE059998|BE059998 sn39f10.yl Gm-c1027 Glycine max cDNA clone ... 143 3e-33
      emb|AW671168|AW671168 LG1_330_E06.b1_A002 Light Grown 1 (LG1) So... 142 5e-33
      emb|AW667825|AW667825 GA_Ea0010N10 Gossypium arboreum 7-10 dpa ... 141 9e-33
      emb|AW760961|AW760961 sl61c01.yl Gm-c1027 Glycine max cDNA clone... 138 8e-32
      emb|AW832362|AW832362 sm08e01.yl Gm-c1027 Glycine max cDNA clone... 138 8e-32
35
      emb|AW781979|AW781979 sl99a06.yl Gm-c1027 Glycine max cDNA clone... 138 8e-32
      emb[AV426209]AV426209 AV426209 Lotus japonicus young plants (two... 135 6e-31
      emb|AW287694|AW287694 LG1_271_C05.b1 A002 Light Grown 1 (LG1) So... 135 8e-31
      emb|AW041671|AW041671 EST284535 tomato mixed elicitor, BTI Lycop... 135 8e-31
      emb|AW564618|AW564618 LG1_297_G09.b1_A002 Light Grown 1 (LG1) So... 134 1e-30
40
      emb|AW924990|AW924990 WS1_74_A05.b1_A002 Water-stressed 1 (WS1) ... 134 1e-30
      emb|AW888070|AW888070 NXNV_126_H09_F Nsf Xylem Normal wood Verti... 134 1e-30
      emb|AW694653|AW694653 NF078G03ST1F1023 Developing stem Medicago ... 108 2e-30
      emb|AV425340|AV425340 AV425340 Lotus japonicus young plants (two... 132 5e-30
      emb|AW030490|AW030490 EST273745 tomato callus, TAMU Lycopersicon... 132 7e-30
45
      emb|AW738715|AW738715 EST340142 tomato flower buds, anthesis, Co... 132 7e-30
      emb|AW040512|AW040512 EST283472 tomato mixed elicitor, BTI Lycop... 131 1e-29
      emb|AW780617|AW780617 sl73c03.yl Gm-c1027 Glycine max cDNA clone... 131 1e-29
      emb|AW287232|AW287232 LG1 268 C02.b1 A002 Light Grown 1 (LG1) So... 130 2e-29
      emb|AV410940|AV410940 AV410940 Lotus japonicus young plants (two... 130 2e-29
50
      emb|AW286886|AW286886 LG1 222 F11.b1 A002 Light Grown 1 (LG1) So... 129 3e-29
      emb|AW399232|AW399232 EST309732 L. pennellii trichome, Cornell U... 129 5e-29
      emb|AW287673|AW287673 LG1 271_A05.b1_A002 Light Grown 1 (LG1) So... 129 5e-29
      emb|AV412063|AV412063 AV412063 Lotus japonicus young plants (two... 128 7e-29
      emb|AV421682|AV421682 AV421682 Lotus japonicus young plants (two... 128 7e-29
55
      emb|AW759175|AW759175 sl38a01.yl Gm-c1027 Glycine max cDNA clone... 128 7e-29
      emb|AW672543|AW672543 LG1 360 B12.b1 A002 Light Grown 1 (LG1) So... 128 7e-29
      emb|AW596590|AW596590 sj14c04.yl Gm-c1032 Glycine max cDNA clone... 128 9e-29
      emb|AW694511|AW694511 NF077A11ST1F1084 Developing stem Medicago ... 128 9e-29
      emb|AV415908|AV415908 AV415908 Lotus japonicus young plants (two... 127 2e-28
60
```

Query= AC002333.223 s at 17840 s at /id source genbank /description

gblaab64049.1 (ac002333) putative endochitinase [arabidopsis thaliana] /blast_score 1.00e-161 /ec_number /family /chip nova /gb_link /ncgi (834 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 10 Ε Score Sequences producing significant alignments: (bits) Value gb[U21848]BNU21848 Brassica napus chitinase class IV (LSC222) mR... 225 e-134 15 emb|X61488|BNCHITIN B.napus mRNA for chitinase. gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 173 3e-77 gb[U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 174 2e-76 emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 149 2e-74 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 157 5e-70 20 dbi|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 100 5e-67 gb[U52845]DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 114 7e-67 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 111 9e-66 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 129 1e-65 gb[U52847]DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 110 8e-65 25 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 111 2e-64 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 125 2e-64 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 123 2e-63 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 120 6e-63 dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ... 96 1e-62 30 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 100 3e-62 dbi|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 100 4e-60 emb[X75945]BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 92 6e-60 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 92 6e-60 emb[X88803]VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p... 118 3e-59 emblAI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 110 1e-58 35 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 105 2e-58 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 158 3e-58 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 89 8e-58 gb|LA2467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 93 2e-57 40 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 166 2e-57 emb|A1897843|A1897843 EST267286 tomato ovary, TAMU Lycopersicon ... 103 1e-56 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 149 9e-56 gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 162 4e-54 emb[AW680953]AW680953 WS1 9 A06.b1 A002 Water-stressed 1 (WS1) S... 178 3e-52 45 gb|BE033502|BE033502 ME03F10 ME Mesembryanthemum crystallinum cD... 87 4e-50 gb[M94105]ALCCHITIN Allium sativum chitinase mRNA, 3' end. 100 6e-49 emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 83 1e-48 gb[U83592]MSU83592 Medicago sativa class I chitinase mRNA, compl... 109 1e-48 gb[U83591[MSU83591 Medicago sativa class I chitinase mRNA, compl... 109 1e-48 50 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 83 3e-48 emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 83 3e-48 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 83 3e-48 gb|BE034481 |BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 162 5e-48 emb|AW924422|AW924422 WS1 69 C06.b1 A002 Water-stressed 1 (WS1) ... 140 7e-48 55 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 83 1e-47 emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 99 1e-47 emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 83 3e-47 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 109 3e-47 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 87 5e-47 emb[X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). emb[X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 95 6e-47

gb[M13968]PHVCHM P.vulgaris chitinase mRNA, complete cds. 106 1e-46 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 161 2e-46 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 106 5e-46 emb[X88800]VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 105 1e-45 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 108 6e-45 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... emb[Y10373]MTCHITIN1 M.truncatula mRNA for chitinase. 109 8e-45 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 83 2e-44 gb M94106 ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 10 emb|AW746018|AW746018 WS1 38 H11.g1 A002 Water-stressed 1 (WS1) ... 170 3e-44 emb|AW922735|AW922735 DG1 45 B06.g1 A002 Dark Grown 1 (DG1) Sorg... 178 4e-44 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 178 4e-44 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 95 5e-44 15 emb|AF061806|AF061806 Elaeagnus umbellata basic chitinase mRNA, ... 105 1e-43 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 98 1e-43 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 95 2e-43 emb[X16939]NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 95 2e-43 emb[X76041 [TACHIG T.aestivum (Chinese spring) chi gene for endoc... 93 4e-43 20 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 97 6e-43 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 104 2e-42 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 95 3e-42 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 95 4e-42 emb|Z46950|SNCHJET19 S.nigra mRNA chitinase class II, pathogenes... 104 6e-42 25 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 102 1e-41 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 81 3e-41 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 95 6e-41 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 95 6e-41 30 emblAF034566lAF034566 Gossypium hirsutum class I chitinase mRNA,... 100 6e-41 gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 165 7e-41 gb|M25337|POPCHIB Populus sp. chitinase (win8) mRNA, complete cds. 89 8e-41 gb|BE034267|BE034267 MH02D06 MH Mesembryanthemum crystallinum cD... 66 2e-40 emb|A1897217|A1897217 EST266756 tomato ovary, TAMU Lycopersicon ... 110 4e-40 35 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 91 4e-40 emb|X95610|CSHITIB C.sativa mRNA for chitinase Ib. 88 9e-40 gb|U48687|CSU48687 Castanea sativa endochitinase mRNA, complete ... 88 9e-40 emb|AW676775|AW676775 DG1_14_C09.g1_A002 Dark Grown 1 (DG1) Sorg... 161_2e-39 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 40 emblAW745819|AW745819 WS1 37 H11.g1 A002 Water-stressed 1 (WS1) ... 163 2e-39 emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 94 2e-39 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 77 5e-39 gb|L22032|ULMCHITIN Ulmus americana chitinase (pHS2) mRNA, compl... 106 6e-39 emb|AW924229|AW924229 WS1_51_H04.b1_A002 Water-stressed 1 (WS1) ... 161 7e-39 emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 109 7e-39 emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 109 7e-39 emblAW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 78 3e-38 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 96 4e-38 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 101 1e-37 50 emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 106 1e-37 emb|AW746429|AW746429 WS1_53_G09.b1_A002 Water-stressed 1 (WS1) ... 97 4e-37 emb[X74919[PVGEC9 P.vulgaris gene for endochitinase. 149 6e-37

Query= AC002391.150_s_at 17843_s_at /id_source genbank /description gb|aab87109.1| (ac002391) putative cytochrome p450 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi

(1548 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Score E 5 Sequences producing significant alignments: (bits) Value emb|AB001379|AB001379 Glycyrrhiza echinata CYP81E1 mRNA for cyto... 323 e-137 emb|AJ238439|CAR238439 Cicer arietinum mRNA for a cytochrome P45... 328 e-136 emb|AB022732|AB022732 Glycyrrhiza echinata CYP Ge-31 mRNA for cy... 322 e-136 10 emb|AB025016|AB025016 Lotus japonicus mRNA for cytochrome P450, ... 291 e-134 emb|AJ012581|CAR012581 Cicer arietinum mRNA for cytochrome P450. 324 e-134 emb|AJ000478|HTCYP81L Helianthus tuberosus mRNA for cytochrome P... 227 e-124 emb|AJ000477|HTCYP81C Helianthus tuberosus mRNA for cytochrome P... 227 e-124 emb|AJ239051|CAR239051 Cicer arietinum mRNA for cytochrome P450 ... 237 3e-82 15 emb|AJ249800|CAR249800 Cicer arietinum partial mRNA for cytochro... 290 3e-79 emb|AW185361|AW185361 se90e02.yl Gm-c1027 Glycine max cDNA clone... 280 3e-74 emb|AW775904|AW775904 EST334969 DSIL Medicago truncatula cDNA cl... 228 1e-70 emb|AF082028|AF082028 Hemerocallis hybrid cultivar senescence-as... 189 2e-70 emb|AW234443|AW234443 sf25c03.yl Gm-c1028 Glycine max cDNA clone... 264 1e-69 20 emb|AW307234|AW307234 sf54d12.yl Gm-c1009 Glycine max cDNA clone... 258 1e-67 emb|AW733691|AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone... 253 3e-66 emb|AW171738|AW171738 N100632e rootphos(-) Medicago truncatula c... 251 1e-65 emb|AJ249801|CAR249801 Cicer arietinum partial mRNA for cytochro... 242 5e-63 emb|AI729126|AI729126 BNLGHi12694 Six-day Cotton fiber Gossypium... 180 4e-58 25 emb|AW329224|AW329224 N200436e rootphos(-) Medicago truncatula c... 224 1e-57 emb|AI725744|AI725744 BNLGHi12803 Six-day Cotton fiber Gossypium... 180 4e-57 emb|AI495626|AI495626 sb11c08.yl Gm-c1004 Glycine max cDNA clone... 222 6e-57 emb[AW100311]AW100311 sd22g12.y2 Gm-c1012 Glycine max cDNA clone... 206 5e-56 emb|AW257188|AW257188 EST305325 KV2 Medicago truncatula cDNA clo... 177 6e-56 30 emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycope... 144 Se-54 emb|AW171672|AW171672 N100566e rootphos(-) Medicago truncatula c... 212 7e-54 emb|AW932147|AW932147 EST357990 tomato fruit mature green, TAMU ... 211 1e-53 emb|AI731481|AI731481 BNLGHi9879 Six-day Cotton fiber Gossypium ... 168 3e-51 emb|AI731081|AI731081 BNLGHi8648 Six-day Cotton fiber Gossypium ... 200 2e-50 35 emb|AI728374|AI728374 BNLGHi10609 Six-day Cotton fiber Gossypium... 163 9e-50 emb|AF014802|AF014802 Eschscholzia californica (S)-N-methylcocla... 173 3e-48 emb|AV412147|AV412147 AV412147 Lotus japonicus young plants (two... 185 7e-46 emb|AF156976|AF156976 Gerbera hybrida flavone synthase II (CYP93... 100 8e-46 dbj[E13663]E13663 cDNA encoding cytochrome P450 which is induced... 104 1e-45 40 dbj[D83968]SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 104 1e-45 emb[Y10492]GMC450CP5 G.max mRNA for putative cytochrome P450, cl... 106 6e-44 emblAW695923|AW695923 NF100G02ST1F1018 Developing stem Medicago ... 170 9e-44 emb|AW684707|AW684707 NF020A02NR1F1000 Nodulated root Medicago t... 178 1e-43 emb|AB015762|AB015762 Nicotiana tabacum mRNA for cytochrome P450... 160 2e-43 45 emb|AI973839|AI973839 sd11c06.y1 Gm-c1020 Glycine max cDNA clone... 104 2e-43 emb|AF155332|AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... 158 2e-43 emb|AW734404|AW734404 sk19f09.yl Gm-c1028 Glycine max cDNA clone... 157 2e-43 gb[U29333]PSU29333 Pisum sativum novel wound-inducible cytochrom... 160 5e-43 emb|AF124372|AF124372 Nicotiana tabacum NT7 mRNA, partial cds. 134 6e-43 50 gb|U72654|EGU72654 Eustoma grandiflorum flavonoid 3'5'-hydroxyla... 149 2e-42 dbj|D86351|D86351 Glycine max CYP93A2 mRNA for cytochrome P-450,... 102 2e-42 emb|AW688601|AW688601 NF009D12ST1F1000 Developing stem Medicago ... 173 4e-42 emb|AW616170|AW616170 EST307209 L. hirsutum trichome, Cornell Un... 148 5e-42 dbj D14589 D14589 Eustoma russellianum mRNA for flavonoid 3',5'-... 148 6e-42 55 emb|AJ011862|CRO011862 Catharanthus roseus mRNA for flavonoid 3'... 155 6e-42 emb|Z22545|PHFLAHYDB P.hybrida flavonoid 3',5'-hydroxylase mRNA. dbi|D14588|PETHF1 Petunia hybrida Hf1 mRNA for flavonoid-3',5'-h... 148 8e-42 emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 148 1e-41 emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 148 1e-41 .60 emb|AW309826|AW309826 sf25c03.x1 Gm-c1028 Glycine max cDNA clone... 166 1e-41 emb|AB024931|AB024931 Lotus japonicus mRNA for cytochrome P450, ... 100 2e-41

	•
	emb AW299084 AW299084 EST305758 KV2 Medicago truncatula cDNA clo 171 2e-41
	emb AW728587 AW728587 GA
	emb Z22544 PHFLAHYDA P.hybrida flavonoid 3',5'-hydroxylase mRNA. 146 3e-41
	emb AW616075 AW616075 EST296834 L. hirsutum trichome, Cornell Un 148 3e-41
5	emb AF195800 AF195800 Medicago sativa isoflavone synthase 1 (ifs 99 4e-41
•	emb AW255096 AW255096 ML139 peppermint glandular trichome Mentha 157 5e-41
	emb AI776121 AI776121 EST257209 tomato resistant, Cornell Lycope 111 5e-41
	emb AF135484 AF135484 Glycine max cytochrome P450 monooxygenase 98 6e-41
	emb AF195811 AF195811 Trifolium pratense isoflavone synthase 2 (98 6e-41
10	
10	emb AF195810 AF195810 Trifolium pratense isoflavone synthase 1 (98 6e-41
	emb AF195809 AF195809 Vigna radiata isoflavone synthase 4 (ifs4) 98 6e-41
	emb AF195808 AF195808 Vigna radiata isoflavone synthase 3 (ifs3) 98 6e-41
	emb AF195807 AF195807 Vigna radiata isoflavone synthase 2 (ifs2) 98 6e-41
16	emb AF195802 AF195802 Medicago sativa isoflavone synthase 3 (ifs 98 6e-41
15	emb Y10982 GMP450CP6 Glycine max mRNA for cytochrome P450-like p 149 7e-41
	emb AF255014 AF255014 Citrus sinensis cinnamate 4-hydroxylase CY 145 7e-41
	emb AW651341 AW651341 EST329795 tomato germinating seedlings, TA 148 7e-41
	emb AF195798 AF195798 Glycine max isoflavone synthase 1 (ifs1) m 98 8e-41
	dbj D14590 D14590 Campanula medium mRNA for flavonoid 3',5'-hydr 151 1e-40
20	emb AI782402 AI782402 EST263281 tomato susceptible, Cornell Lyco 144 2e-40
•	emb AF195799 AF195799 Glycine max isoflavone synthase 2 (ifs2) m 96 2e-40
	emb AF022462 AF022462 Glycine max cytochrome P450 monooxygenase 96 2e-40
	emb AF195806 AF195806 Vigna radiata isoflavone synthase 1 (ifs1) 96 2e-40
	emb AF195812 AF195812 Pisum sativum isoflavone synthase 1 (ifs1) 98 2e-40
25	emb AF195817 AF195817 Beta vulgaris isoflavone synthase 2 (ifs2) 97 2e-40
	emb AW687247 AW687247 NF007E11RT1F1086 Developing root Medicago 167 2e-40
	emb AF096998 AF096998 Pinus taeda trans-cinnamate 4-hydroxylase 143 2e-40
	emb AF195815 AF195815 Trifolium repens isoflavone synthase 2 (if 96 3e-40
	emb AW278589 AW278589 sf46e01.yl Gm-c1009 Glycine max cDNA clone 97 3e-40
['] 30	emb AW034115 AW034115 EST277610 tomato callus, TAMU Lycopersicon 147 4e-40
	emb AF081575 AF081575 Petunia x hybrida flavonoid 3',5'-hydroxyl 142 5e-40
	emb Z17369 HTTC4MMR H.tuberosus mRNA for trans-cinnamate 4-monoo 143 5e-40
	emb A74279 A74279 Sequence 1 from Patent WO9401564. 143 5e-40
	emb AF195813 AF195813 Lupinus albus isoflavone synthase 1 (ifs1) 96 5e-40
35	emb AW616066 AW616066 EST296823 L. hirsutum trichome, Cornell Un 145 5e-40
	emb AW728802 AW728802 GA_Ea0028I12 Gossypium arboreum 7-10 dpa 148 6e-40
	emb AF195801 AF195801 Medicago sativa isoflavone synthase 2 (ifs 98 7e-40
	gb[U47293]PTU47293 Populus tremuloides trans-cinnamate 4-hydroxy 141 9e-40
	dbj D87520 D87520 Glycyrrhiza echinata suspension-cultured cells 141 9e-40
40	gb L07634 PHVC4HYDRO Phaseolus aureus cinnamate 4-hydroxylase mR 141 9e-40
	emb AF195814 AF195814 Trifolium repens isoflavone synthase 1 (if 98 1e-39
	dbj D82815 POPPCYP73D Populus kitakamiensis cyp73a mRNA for cinn 140 1e-39
	emb AJ243804 CAR243804 Cicer arietinum mRNA for cytochrome P450 96 1e-39
	emb AF195803 AF195803 Vicia villosa isoflavone synthase 1 (ifs1) 96 1e-39
45	emb AF195816 AF195816 Beta vulgaris isoflavone synthase 1 (ifs1) 97 1e-39
	•
	Query= AC005315.131_at 18844_at /id_source genbank /description
	gb aac33239.1 (ac005315) putative ligand-gated ion channel protein
	[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
50	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb ac005315 /ncgi
	http://www.ncgr.org/cgi-bin/ff?ac005315
	(2805 letters)
55	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
60	Score E
	Sequences producing significant alignments: (bits) Value

```
emb|AF109392|AF109392 Brassica napus ligand gated channel-like p... 142 3e-57
      emb|AW034636|AW034636 EST278320 tomato callus, TAMU Lycopersicon... 100 2e-26
      emb|AI054890|AI054890 coau0002H02 Cotton Boll Abscission Zone cD... 90 1e-23
      emb|AI759920|AI759920 sb66c06.yl Gm-c1017 Glycine max cDNA clone... 84 4e-15
      gb[BE022401]BE022401 sm85d03.y1 Gm-c1015 Glycine max cDNA clone ... 55 3e-13
      emb|AW773978|AW773978 EST332964 KV3 Medicago truncatula cDNA clo... 53 le-12
      emb|AW982953|AW982953 HVSMEg0004K11f Hordeum vulgare pre-anthesi... 73 8e-12
      gb|BE059628|BE059628 sn34g08.y1 Gm-c1016 Glycine max cDNA clone ... 58 5e-10
10
      emb|AW928584|AW928584 EST337372 tomato flower buds 8 mm to pre-a... 66 1e-09
      emb|AW622410|AW622410 EST313197 tomato root during/after fruit s... 40 3e-06
      emb|AW160184|AW160184 EST290041 L. pennellii trichome, Cornell U... 40 4e-06
      emb|AW933376|AW933376 EST359219 tomato fruit mature green, TAMU ... 52 2e-05
      emb|AI441698|AI441698 sa60b02.yl Gm-c1004 Glycine max cDNA clone... 49 2e-04
15
      emb|AW925534|AW925534 HVSMEg0002H02 Hordeum vulgare pre-anthesis... 48 3e-04
      emb|AW284671|AW284671 LG1 214 A11.g1 A002 Light Grown 1 (LG1) So... 47 8e-04
      emb|AI054607|AI054607 coan0001I04 Cotton Boll Abscission Zone cD... 46 0.001
      emb|AW933855|AW933855 EST359698 tomato fruit mature green, TAMU ... 31 0.42
      emb|AW931421|AW931421 EST357264 tomato fruit mature green, TAMU ... 31 0.42
      emb|AW034378|AW034378 EST277949 tomato callus, TAMU Lycopersicon... 31 0.42
20
      emb|AW030398|AW030398 EST273653 tomato callus, TAMU Lycopersicon... 31 0.42
      emb|AW625904|AW625904 EST319799 tomato radicle, 5 d post-imbibit... 31 0.42
      emb|AI781375|AI781375 EST262242 tomato susceptible, Cornell Lyco... 31 0.42
      emb|AW031815|AW031815 EST275269 tomato callus, TAMU Lycopersicon... 31 0.42
25
      emb|AW443041|AW443041 EST307971 tomato mixed elicitor, BTI Lycop... 31 0.42
      emb|AI489138|AI489138 EST247477 tomato ovary, TAMU Lycopersicon ... 31 0.42
      emb|AW931241|AW931241 EST357084 tomato fruit mature green, TAMU ... 31 0.42
      emb|AW931511|AW931511 EST357354 tomato fruit mature green, TAMU ... 31 0.42
      emb|AW218030|AW218030 EST296745 tomato flower buds, anthesis, Co... 31 0.42
30
      emb|AW224605|AW224605 EST303048 tomato root, plants pre-anthesis... 31 0.42
      emb|AW441557|AW441557 EST310953 tomato fruit red ripe, TAMU Lyco... 31 0.42
      emb|AI485565|AI485565 EST243886 tomato ovary, TAMU Lycopersicon ... 31 0.42
      emb|AI490454|AI490454 EST248780 tomato ovary, TAMU Lycopersicon ... 31 0.42
      emb|AW221704|AW221704 EST298515 tomato fruit red ripe, TAMU Lyco... 31 0.42
35
      emb|AW455351|AW455351 EST311889 tomato root during/after fruit s... 31 0.42
      emb|AW034104|AW034104 EST277599 tomato callus, TAMU Lycopersicon... 31 0.43
      emb|AW038338|AW038338 EST280021 tomato mixed elicitor, BTI Lycop... 31 0.43
      emb|AW222646|AW222646 EST299457 tomato fruit red ripe, TAMU Lyco... 31 0.43
      emb|AW933318|AW933318 EST359161 tomato fruit mature green, TAMU ... 31 0.43
40
      emb|AI487939|AI487939 EST246261 tomato ovary, TAMU Lycopersicon ... 31 0.43
      emb|AW032107|AW032107 EST275561 tomato callus, TAMU Lycopersicon... 31 0.43
      emb|AW221841|AW221841 EST298652 tomato fruit red ripe, TAMU Lyco... 31 0.43
      emb|AW932038|AW932038 EST357881 tomato fruit mature green, TAMU ... 31 0.43
      emblAW039616lAW039616 EST282064 tomato mixed elicitor, BTI Lycop... 31 0.43
      emb|AW222971|AW222971 EST299782 tomato fruit red ripe, TAMU Lyco... 31 0.59
      emb|AW931586|AW931586 EST357429 tomato fruit mature green, TAMU ... 37 0.62
      emb|AI812461|AI812461 11D11 Pine Lambda Zap Xylem library Pinus ... 26 0.73
      emb|AI774678|AI774678 EST255778 tomato resistant, Cornell Lycope... 37 0.85
      emb|AW982678|AW982678 HVSMEg0003O16f Hordeum vulgare pre-anthesi... 35 1.0
50
      emb|AW933175|AW933175 EST359018 tomato fruit mature green, TAMU ... 36 1.6
      emb|Z50171|TBBSLARNA T.brucei brucei SLA RNA gene.
                                                                     36 1.6
      emb|AI484282|AI484282 EST248834 tomato susceptible, Cornell Lyco... 31 2.0
      emb|AW925473|AW925473 HVSMEg0001O11 Hordeum vulgare pre-anthesis...
      emb|Z69727|SPAC4G9 S.pombe chromosome I cosmid c4G9.
55
      emb[AB008750]AB008750 Schizosaccharomyces pombe gene for Alp11, ... 35 2.2
      emb|AW983412|AW983412 HVSMEg0010I20f Hordeum vulgare pre-anthesi... 33 2.5
      emb|AF110134|AF110134 Volvox carteri f. nagariensis GlsA (glsA) ... 35 3.0
      emb|AJ011856|SCE011856 Saccharomyces cerevisiae complete mitocho... 35 3.0
      emb[V00694]MISC13 Saccharomyces cerevisiae mitochondrion COX/OXI... 35 3.0
      gb|L36897|YSCMTCG13 Saccharomyces cerevisiae mitochondrion oxi3 ... 35 3.0
      emb|AW933203|AW933203 EST359046 tomato fruit mature green, TAMU ... 35 3.0
```

	emb Z46869 KLEXG1 K.lactis gene for exo-1,3-beta-glucanase/1,3-b 35 3.0 emb AA415065 AA415065 Mg0012 RCW Lambda Zap Express Library Pyri 35 3.0 emb AL122012 LMFL8342 Leishmania major Friedlin chromosome 23 co 35 4.2
5	emb AW257203 AW257203 EST305340 KV2 Medicago truncatula cDNA clo 35 4.2
S	emb AC005504 AC005504 Plasmodium falciparum chromosome 12, *** S 35 4.2
	emb AI784905 AI784905 1268 PtIFG2 Pinus taeda cDNA clone 8876r, 35 4.2
	emb AA739776 AA739776 541 PtIFG2 Pinus taeda cDNA clone 8876M 3' 35 4.2
	emb AI965479 AI965479 sc72e01.y1 Gm-c1018 Glycine max cDNA clone 35 4.2 emb AW932343 AW932343 EST358186 tomato fruit mature green, TAMU 35 4.2
10	emb[AC004710]AC004710 Plasmodium falciparum chromosome 12, *** S 35 4.2
10	emb[AC005507]AC005507 Plasmodium falciparum chromosome 12 clone 35 4.2
	emb AF236108 AF236108 Glycine max putative purple acid phosphata 35 4.2
	emb AA739843 AA739843 608 PtIFG2 Pinus taeda cDNA clone 8988M 3' 35 4.2
	emb AQ849884 AQ849884 LMAJFV1_lm51b04.x1 Leishmania major FV1 ra 34 5.7
15	emb AV406712 AV406712 AV406712 Lotus japonicus young plants (two 34 5.7
	emb Z49212 SC9952X S.cerevisiae chromosome XIII cosmid 9952. 34 5.7
	emb AW735973 AW735973 EST336741 tomato flower buds 0-3 mm, Corne 34 5.7
	emb AW668487 AW668487 GA
	emb AL110295 SPBC106 S.pombe chromosome II cosmid c106. 34 5.7
20	gb[U08622 SPU08622 Schizosaccharomyces pombe cAMP-dependent prot 34 5.7
	emb AV411500 AV411500 AV411500 Lotus japonicus young plants (two 34 5.7
	emb AQ649646 AQ649646 Sheared DNA-16E6.TF Sheared DNA Trypanosom 34 5.7
	emb AV407948 AV407948 AV407948 Lotus japonicus young plants (two 34 5.7
	dbj D23667 YSPPKA1 Fission yeast pka1 gene for catalytic subunit 34 5.7
25	emb AW719775 AW719775 LjNEST9G5r Lotus japonicus nodule library 34 5.7
	gb BE052571 BE052571 GA_Ea0035M21f Gossypium arboreum 7-10 dpa 32 6.1
	emb AQ852061 AQ852061 LMAJFV1 lm60f08.y1 Leishmania major FV1 ra 34 6.4
	emb AL132675 SPAC144 S.pombe chromosome I cosmid c144. 34 7.8
20	emb AJ223818 LEAJ3818 Lycopersicon esculentum cv Red River unkno 34 7.8
30	gb B07277 B07277 G267T3 MVAT4 sheared genomic library Trypanosom 34 7.8
	emb AW982385 AW982385 HVSMEg0003C03f Hordeum vulgare pre-anthesi 34 7.8
	emb AW442327 AW442327 EST311723 tomato fruit red ripe, TAMU Lyco 34 7.8 emb X13486 CHCMPSBA C. moewusii chloroplast psbA gene for photos 34 7.8
	emb[X15601]CMCHPSBA C.moewusii chloroplast psbA gene. 34 7.8
35	517.0
•	Query= AF071527.44_at 19247_at /id source genbank /description
	gb aad11587.1 aad11587 (af071527) hypothetical protein [arabidopsis
	thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
	http://www3.ncbi.nlm.nih.gov/htbin-
40	post/entrez/query?db=n&form=6&dopt=g&uid=gb af071527 /ncgi
	http://www.ncgr.org/cgi-bin/ff?af071527
	(1926 letters)
45	Database: plantfungal
43	661,018 sequences; 426,114,510 total letters
	Searchingdone
	0000 mg
	Score E
50	Sequences producing significant alignments: (bits) Value
	emb AI894928 AI894928 EST264371 tomato callus, TAMU Lycopersicon 58 2e-07
	gb BE033853 BE033853 MG01B02 MG Mesembryanthemum crystallinum cD 55 2e-06
	emb AW621748 AW621748 EST312546 tomato root during/after fruit s 53 8e-06
55	emb AI729861 AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium 52 2e-05
	emb AW035961 AW035961 EST282820 tomato callus, TAMU Lycopersicon 51 3e-05
	emb AV420300 AV420300 AV420300 Lotus japonicus young plants (two 49 1e-04
	emb AZ124241 AZ124241 T223105b Medicago truncatula BAC library M 49 1e-04
۲0	emb AW694103 AW694103 NF072D04ST1F1041 Developing stem Medicago 48 3e-04
60	emb AI896054 AI896054 EST265497 tomato callus, TAMU Lycopersicon 47 4e-04
	emb AI729969 AI729969 BNLGHi5823 Six-day Cotton fiber Gossypium 34 0.002

- WO 02/22675 - ___ PCT/US01/28506

emb|AZ124239|AZ124239 T223103b Medicago truncatula BAC library M... 43 0.003 emb|AV414054|AV414054 AV414054 Lotus japonicus young plants (two... 44 0.004 emb|AI487562|AI487562 EST245884 tomato ovary, TAMU Lycopersicon ... 44 0.005 emb|Z69731|SPAC6C3 S.pombe chromosome I cosmid c6C3. emb|AW164678|AW164678 se76b06.y1 Gm-c1023 Glycine max cDNA clone... 43 0.007 emb|AI489135|AI489135 EST247474 tomato ovary, TAMU Lycopersicon ... 43 0.007 emb|AI736949|AI736949 sb35a01.yl Gm-c1013 Glycine max cDNA clone... 42 0.017 emb|AW736367|AW736367 EST332286 KV3 Medicago truncatula cDNA clo... 42 0.017 emb|AI164848|AI164848 A069p65u Hybrid aspen plasmid library Popu... 41 0.033 10 emb|AQ638202|AQ638202 927P1-9H10.TP 927P1 Trypanosoma brucei gen... 41 0.033 emb|AW040703|AW040703 EST283567 tomato mixed elicitor, BTI Lycop... 41 0.033 emb]AI054990|AI054990 coau0002L09 Cotton Boll Abscission Zone cD... 41 0.033 emb|AI166315|AI166315 xylem.est.16 Poplar xylem Lambda ZAPII lib... 37 0.035 emb|AI055156|AI055156 coau0003D05 Cotton Boll Abscission Zone cD... 40 0.045 15 emb|AW256577|AW256577 EST304714 KV2 Medicago truncatula cDNA clo... 30 0.064 emb|AA783893|AA783893 c8g07a1.rl Aspergillus nidulans 24hr asexu... 30 0.16 emb|AW053754|AW053754 L30-1647T3 Ice plant Lambda Uni-Zap XR exp... 38 0.30 emb|AI054715|AI054715 coau0001M19 Cotton Boll Abscission Zone cD... 37 0.41 gb|BE035556|BE035556 MO09B06 MO Mesembryanthemum crystallinum cD... 29 0.69 20 gb|BE036920|BE036920 MP09B06 MP Mesembryanthemum crystallinum cD... 29 0.71 emb|AL033534|SPBC215 S.pombe chromosome II cosmid c215. emb|AW932897|AW932897 EST358740 tomato fruit mature green, TAMU ... 36 1.1 emb|AW596694|AW596694 sj15e12.y1 Gm-c1032 Glycine max cDNA clone... 35 1.5 emb[X02390]ANTRPC1 Aspergillus nidulans trpC gene. 35 2.0 25 emb|X52152|SCIME S. cerevisiae IME1 gene for Ime1, a meiosis ind... 35 2.0 emb|Z49595|SCYJR095W S.cerevisiae chromosome X reading frame ORF... gb|L47610|PIAEMB4R Picea glauca EMB4 mRNA. emb|Z49594|SCYJR094C S.cerevisiae chromosome X reading frame ORF... 35 2.0 emb|AI622956|AI622956 TENG0590 T. Cruzi epimastigote normalised ... 35 2.0 30 gb|M37188|YSCIME1 S.cerevisiae meiosis-inducing protein (IME1) g... 35 2.0 gb|BE034285|BE034285 MH02G01 MH Mesembryanthemum crystallinum cD... 35 2.8 emb|AW256576|AW256576 EST304713 KV2 Medicago truncatula cDNA clo... 35 2.8 emb|AI167045|AI167045 xylem.est.817 Poplar xylem Lambda ZAPII li... 35 2.8 emb|AW696259|AW696259 NF104F08ST1F1074 Developing stem Medicago ... 29 3.2 35 emb|AI974296|AI974296 T110298e KV0 Medicago truncatula cDNA clon... 34 3.8 emb|AI756377|AI756377 EtESTea12b12.yl Eimeria M5-6 Merozoite sta... 34 3.8 emb|AZ217340|AZ217340 Sheared DNA-117G6.TF Sheared DNA Trypanoso... 34 3.8 emb|AQ988815|AQ988815 11E1D03NE.R1 C. parvum Lambda Zap Express ... 34 3.8 emb|AW565712|AW565712 LG1 348 C03.g1 A002 Light Grown 1 (LG1) So... 34 3.8 40 gb|L20566|ASNACDP Aspergillus niger acid phospatase complete cds. emb|AW869952|AW869952 NXNV_120_C10_F Nsf Xylem Normal wood Verti... 34 5.3 emb|AW691961|AW691961 NF046B02ST1F1000 Developing stem Medicago ... 34 5.3 emb|AF007946|AF007946 Trautvetteria carolinensis maturase (matK)... 34 5.3 emb|AW185605|AW185605 se79h09.v1 Gm-c1023 Glycine max cDNA clone... 33 7.2 45 emb|AQ639089|AQ639089 927P1-1D11.TP 927P1 Trypanosoma brucei gen... 33 7.2 emb|AW731466|AW731466 GA_Ea0030J17 Gossypium arboreum 7-10 dpa ... 33 7.2 emb|AW623353|AW623353 EST321298 tomato flower buds 3-8 mm, Corne... 33 7.2 emb|AI781323|AI781323 EST262202 tomato susceptible, Cornell Lyco... 33 7.2 emb|AZ214634|AZ214634 Sheared DNA-68B12.TR Sheared DNA Trypanoso... 33 7.2 50 emb|AQ656501|AQ656501 Sheared DNA-12B14.TF Sheared DNA Trypanoso... 33 7.2 emb|AW932874|AW932874 EST358717 tomato fruit mature green, TAMU ... 33 7.2 emb|AW926434|AW926434 HVSMEg0007D10 Hordeum vulgare pre-anthesis... 33 7.2 emblAQ945431|AQ945431 Sheared DNA-44E8.TR Sheared DNA Trypanosom... 33 7.2 emb|AQ945478|AQ945478 Sheared DNA-45J6.TF Sheared DNA Trypanosom... 33 7.2 55 emb|AL116771|CNS01DFV Botrytis cinerea strain T4 cDNA library un... 33 7.2 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 7.2 emb|AW776850|AW776850 EST335915 DSIL Medicago truncatula cDNA cl... 33 7.2 emb|AZ219905|AZ219905 Sheared DNA-61D10.TF Sheared DNA Trypanoso... 33 7.2 emb|AZ216687|AZ216687 Sheared DNA-84G10.TR Sheared DNA Trypanoso... 33 7.2 60 emb|X87941|SCDNAGENS S.cerevisiae CRM1, YML9, PET54, SM11, PHO81... 28 7.5 emb|AZ124240|AZ124240 T223104b Medicago truncatula BAC library M... 31 7.9

emb|AI213023|AI213023 y6e12a1.fl Aspergillus nidulans 24hr asexu... 33 9.9 emb|AA556848|AA556848 690 Loblolly pine C Pinus taeda cDNA clone... 33 9.9 emb|AA965673|AA965673 m2g10a1.fl Aspergillus nidulans 24hr asexu... 33 9.9 emb|AI212224|AI212224 w9h05a1.fl Aspergillus nidulans 24hr asexu... 33 9.9 emb|AW924917|AW924917 WS1 73 B03.b1 A002 Water-stressed 1 (WS1) ... 33 9.9 emb|AW127359|AW127359 M110532 DSIL Medicago truncatula cDNA clon... 33 9.9 emb[Y15418]CCY15418 Coprinus cinereus acs-1 gene. emb|AW694961|AW694961 NF081H09ST1F1079 Developing stem Medicago ... 33 9.9 emb|AW991081|AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae... 33 9.9 10 emb|AW399343|AW399343 EST309843 L. pennellii trichome, Cornell U... 33 9.9 emb|AA784746|AA784746 g2a12a1.fl Aspergillus nidulans 24hr asexu... 33 9.9 emb|Z73017|SCYGR232W S.cerevisiae chromosome VII reading frame O... 28 10.0 Query= AC003028.196_at 19284_at /id_source genbank /description 15 gb|aac27173.1| (ac003028) putative anthocyanidin synthase [arabidopsis thaliana] /blast score 0 /ec number /family /chip nova /gb link http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac003028|/ncgi http://www.ncgr.org/cgi-bin/ff?ac003028 20 (1062 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 25 Searching......done Score E Sequences producing significant alignments: (bits) Value 30 emb|AI486803|AI486803 EST245125 tomato ovary, TAMU Lycopersicon ... 358 6e-98 emb|AI486879|AI486879 EST245201 tomato ovary, TAMU Lycopersicon ... 314 8e-85 emb|AW574302|AW574302 EST316893 GVN Medicago truncatula cDNA clo... 255 1e-76 emb|AW459665|AW459665 sh90c10.yl Gm-c1016 Glycine max cDNA clone... 285 5e-76 emb|AI898341|AI898341 EST267784 tomato ovary, TAMU Lycopersicon ... 282 3e-75 35 gb|L42466|PIAEFE Picea glauca ethylene-forming enzyme (EFE) mRNA... 156 4e-75 emb|AW981190|AW981190 EST392384 DSIL Medicago truncatula cDNA cl... 262 2e-73 emb|AI777799|AI777799 EST258678 tomato susceptible, Cornell Lyco... 267 1e-70 emb|AW574101|AW574101 EST316692 GVN Medicago truncatula cDNA clo... 198 2e-67 emb|AW268031|AW268031 EST306309 DSIR Medicago truncatula cDNA cl... 126 6e-65 40 emb|AW775553|AW775553 EST334618 DSIL Medicago truncatula cDNA cl... 210 3e-63 emb|AW509400|AW509400 si22f08.yl Gm-c1029 Glycine max cDNA clone... 237 8e-62 emb|AB003779|AB003779 Perilla frutescens mRNA for leucoanthocyan... 115 5e-59 emb|AW349732|AW349732 GM210006A11F12R Gm-r1021 Glycine max cDNA ... 228 6e-59 gb|U97530|PAU97530 Prunus armeniaca ethylene-forming-enzyme-like... 143 1e-58 45 emb|AF082862|AF082862 Pisum sativum unknown mRNA, partial cds. 220 2e-56 emb|Z22543|PHFLASYNA P.hybrida flavonol synthase mRNA. 99 1e-55 emb|X83229|NTRNA1A1C N.tabacum mRNA for 1-aminocyclopropane-1-ca... 176 1e-54 emb|AF184273|AF184273 Daucus carota leucoanthocyanidin dioxygena... 110 9e-54 emb|AW030000|AW030000 EST273255 tomato callus, TAMU Lycopersicon... 186 1e-53 emb|AF026058|AF026058 Matthiola incana anthocyanidin synthase mR... 116 2e-53 50 emb|AF184274|AF184274 Daucus carota leucoanthocyanidin dioxygena... 110 2e-53 emb|AF117269|AF117269 Malus domestica anthocyanidin synthase (AN... 114 3e-53 emb[X71360]MSPANTHHY Malus sp. mRNA for anthocyanidin hydroxylase. 114 3e-53 emb|AW686531|AW686531 NF042D05NR1F1000 Nodulated root Medicago t... 166 2e-52 55 gb|U54566|NGU54566 Nicotiana glutinosa 1-aminocyclopropane-1-car... 174 2e-52 emb|AF001391|AF001391 Matthiola incana putative flavonol synthas... 118 3e-52 emb|AF119095|AF119095 Malus domestica flavonol synthase (FLS) mR... 91 2e-51 emb|X70786|PHFLV3HDX P.hybrida mRNA for putative flavanone 3-hyd... 112 5e-51 emb|AB012205|AB012205 Lactuca sativa Ls3h1 mRNA for gibberelin 3... 137 9e-51 60 emb|AF028602|AF028602 Ipomoea purpurea anthocyanidin synthase (A... 108 1e-50 emb[AB013101]AB013101 Lycopersicon esculentum LE-ACO4 mRNA for 1... 157 2e-50

emb|AB023786|AB023786 Ipomoea batatas ans I mRNA for anthocyanid... 111 4e-50 emb[X75966]VVLDOX V.vinifera LDOX mRNA for leucoanthocyanidin di... 105 6e-50 emb[X04792]LEETHYBR Tomato mRNA expressed during fruit ripening ... 159 1e-49 emb|AB023787|AB023787 Ipomoea batatas ans II mRNA for anthocyani... 110 1e-49 emb[A35021]A35021 L.esculentum pTOM13. 159 1e-49 emb|AF053354|AF053354 Phaseolus vulgaris 1-aminocyclopropane-1-c... 159 2e-49 gb[U06046[VRU06046 Vigna radiata clone pVR-ACO1 1-aminocycloprop... 157 3e-49 emb[X58885]LEEFEMR L.esculentum mRNA for ethylene-forming enzyme... 157 3e-49 emb|AB003514|AB003514 Actinidia deliciosa mRNA for 1-aminocyclop... 157 4e-49 10 gb[U68215]CPU68215 Carica papaya ACC oxidase mRNA, complete cds. emb|AF117270|AF117270 Malus domestica flavanone 3-hydroxylase (F... 100 5e-49 emb[X69664]MSF3HA Malus sp. mRNA for naringenin,2-oxoglutarate,3... 100 5e-49 gb[M97961]ACTACCOXI Actinidia deliciosa ACC oxidase homologue pr... 154 7e-49 emb|AB010991|AB010991 Lycopersicon esculentum Le3OH-1 mRNA for 3... 133 7e-49 15 emb|AF115262|AF115262 Trifolium repens mature green leaf 1-amino... 158 7e-49 gb[U19856]PHU19856 Pelargonium hortorum 1-aminocyclopropane-1-ca... 153 1e-48 gb|U07953|PHU07953 Pelargonium hortorum 1-aminocyclopropane-1-ca... 159 1e-48 gb|U54565|NGU54565 Nicotiana glutinosa 1-aminocyclopropane-1-car... 156 1e-48 emb|AW459318|AW459318 sh23e02.y1 Gm-c1016 Glycine max cDNA clone... 165 1e-48 20 gb|U74081|IPU74081 Ipomoea purpurea flavanone 3-hydroxylase (F3H... 99 2e-48 emb|AF254125|AF254125 Carica papaya ACC oxidase mRNA, complete cds. 150 2e-48 emb|AB012857|AB012857 Nicotiana tabacum mRNA for ACC oxidase, co... 155 2e-48 emb|AB002667|AB002667 Vigna angularis mRNA for ACC-oxidase, comp... 158 2e-48 emblAB023789|AB023789 Ipomoea batatas f3h II mRNA for flavanone ... 96 2e-48 25 emb|AB023790|AB023790 Ipomoea batatas f3h III mRNA for flavanone... 96 2e-48 gb[U06047|VRU06047 Vigna radiata clone pVR-ACO2 1-aminocycloprop... 157 3e-48 gb|BE058138|BE058138 sn11h05.yl Gm-c1016 Glycine max cDNA clone ... 193 3e-48 emb[Y10749]BPACORNA B.pendula ACO mRNA. 150 3e-48 gb|U67861|PHU67861 Pelargonium hortorum 1-aminocyclopropane-1-ca... 154 5e-48 30 emblX87097|PCPCACO1G P.communis mRNA for 1-aminocyclopropane-1-c... 155 5e-48 emb|AF115263|AF115263 Trifolium repens senescent leaf 1-aminocyc... 162 5e-48 emb|AW685998|AW685998 NF032F07NR1F1000 Nodulated root Medicago t... 159 5e-48 emb|AI440611|AI440611 sa68d07.yl Gm-c1004 Glycine max cDNA clone... 192 5e-48 emb|AB023788|AB023788 Ipomoea batatas f3h I mRNA for fravanone 3... 95 6e-48 35 gb[U23066]PAU23066 Persea americana flavanone 3-hydroxylase mRNA... 100 6e-48 gblM98357|PEAAMINCAR Pea 1-aminocyclopropane-1-carboxylate oxida... 155 6e-48 emb|X98493|NTACCO Nicotiana tabacum mRNA for ACC-oxidase (clone ... 154 9e-48 emb[X81628]BOACCOX1 B.oleracea mRNA for ACC oxidase (ACC0x1). 148 le-47 gb[L35152]DINACCA Dianthus caryophyllus amino-cyclopropane carbo... 158 le-47 40 emb|AW685110|AW685110 NF025C04NR1F1000 Nodulated root Medicago t... 158 1e-47 emblAB032198|AB032198 Nicotiana tabacum mRNA for gibberellin 3be... 135 2e-47 gb|L37103|DORCAROXI Doritaenopsis sp. 1-aminocyclopropane-1-carb... 125 2e-47 emb|AB012206|AB012206 Lactuca sativa Ls3h2 mRNA for gibberellin ... 118 2e-47 dbi|D67038|D67038 Pyrus pyrifolia mRNA for ACC oxidase, complete... 152 2e-47 45 emb[Y10034]PP1AMCSYN R.palustris mRNA for 1-aminocyclopropane-1-... 159 2e-47 gb[M62380]DINCARSR Carnation senescence related protein RNA, com... 157 2e-47 gb[M81794]MAURRP Malus sylvestris ripening-related protein mRNA,. 153 2e-47 emb[X61390]MDETR M.domestica ethylene-related mRNA. 153 2e-47 emb|AB011796|AB011796 Citrus unshiu CitFLS mRNA for flavonol syn... 104 3e-47 50 emb|AJ001646|MDACCOXI2 Malus domestica mRNA for ACC oxidase. dbj|D83041|D83041 Ipomoea nil mRNA for 2-oxogulutarate 3-dioxyge... 95 4e-47 gb|L29405|HNNACC Helianthus annuus 1-1-aminocyclopropane-1-carbo... 152 4e-47 emb|AF115261|AF115261 Trifolium repens stolon apex 1-aminocyclop... 156 4e-47 emb|AF240764|AF240764 Eustoma russellianum flavonol synthase (fl... 100 6e-47 55 emb|Z46349|NTACCDEAM N.tabacum mRNA for 1-aminocyclopropane-1-ca... 150 8e-47 gb|L07912|DORACCOXID Moth orchid ACC oxidase mRNA, complete cds. emb[X77232]PPPAO1 P.persica PAO1 mRNA for 1-aminocyclopropane-1-... 156 1e-46 emb|Z11750|BJEFEMR B.juncea mRNA for ethylene-forming enzyme. 146 le-46 emb|AF026793|AF026793 Prunus armeniaca 1-aminocyclopropane-1-car... 156 1e-46 60 emb[X72594]MIFHT M.incana mRNA for flavanone 3-beta-hydroxylase. 94 2e-46 gb|M90294|PETEFE Petunia hybrida L. ethylene forming enzyme mRNA... 152 2e-46

emb|AB010992|AB010992 Lycopersicon esculentum Le3OH-2 mRNA for 3... 133 2e-46 emb|X75965|VVF3H V.vinifera F3H mRNA for flavanone 3-hydroxylase. 95 3e-46 emb|AB031027|AB031027 Prunus mume PM-ACO1 mRNA for ACC oxidase, ... 155 4e-46 emb|AW775815|AW775815 EST334880 DSIL Medicago truncatula cDNA cl... 154 4e-46 emb|AF041479|AF041479 Rumex palustris 1-aminocyclopropane-1-carb... 154 7e-46 emb|X81629|BOACCOX2 B.oleracea mRNA for ACC oxidase (ACC0x2). 149 7e-46 emb|AW775355|AW775355 EST334420 DSIL Medicago truncatula cDNA cl... 162 8e-46

Query= AL035527.204_at 19762_at /id_source genbank /description emb|cab36812.1| (al035527) peptide transporter-like protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035527| /ncgi http://www.ncgr.org/cgi-bin/ff?al035527

15 (1731 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters

20 Searching done

Ε Score Sequences producing significant alignments: (bits) Value 25 emb|AF023472|AF023472 Hordeum vulgare peptide transporter (ptr1)... 162 e-119 emb|AW929517|AW929517 EST338305 tomato flower buds 8 mm to pre-a... 162 3e-90 emb|AF016713|AF016713 Lycopersicon esculentum oligopeptide trans... 138 3e-89 emb|AF213936|AF213936 Prunus dulcis amino acid/peptide transport... 132 2e-87 emb[Y13862]NTENRT1 Nicotiana tabacum enr-T1 gene. 30 emb|X92852|LENIT2 L.esculentum exon 1 of NIT2 gene. 140 le-80 emb|AW773639|AW773639 EST332625 KV3 Medicago truncatula cDNA clo... 298 9e-80 emb[X92853|LEMIT1 L.esculentum exon 1 of NIT1 gene. 150 9e-74 gb|U17987|BNU17987 Brassica napus RCH2 protein mRNA, complete cds. 80 5e-73 emb|AW929740|AW929740 EST354010 tomato flower buds 8 mm to pre-a... 163 3e-58 35 emb|AW278758|AW278758 sf97b05.yl Gm-c1019 Glycine max cDNA clone... 127 2e-47 emb|AW186088|AW186088 se63e01.yl Gm-c1019 Glycine max cDNA clone... 176 4e-43 emb|AQ917114|AQ917114 T233143b Medicago truncatula BAC library M... 112 6e-42 emb|AF080545|AF080545 Nepenthes alata peptide transporter (PTR1)... 111 1e-41 emblAW677489|AW677489 DG1 8 A08.b1 A002 Dark Grown 1 (DG1) Sorgh... 126 2e-35 40 emb|AW219289|AW219289 EST301771 tomato root during/after fruit s... 144 3e-34 emb|Z69370|CSNITR1 C.sativus mRNA for nitrite transporter. 76 3e-34 emb|AW310175|AW310175 sf32c04.x1 Gm-c1028 Glycine max cDNA clone... 146 5e-34 emb|AW931623|AW931623 EST357466 tomato fruit mature green, TAMU ... 76 8e-34 emb|AW455271|AW455271 EST311931 tomato root during/after fruit s... 144 3e-33 45 emb|AW202366|AW202366 sf14b11.yl Gm-c1027 Glycine max cDNA clone... 144 3e-33 emb|AW694006|AW694006 NF071D12ST1F1101 Developing stem Medicago ... 79 7e-33 emb|AW691380|AW691380 NF040G02ST1F1000 Developing stem Medicago ... 142 1e-32 emb|AW233936|AW233936 sf32c04.y1 Gm-c1028 Glycine max cDNA clone... 82 4e-32 emb|AW774447|AW774447 EST333598 KV3 Medicago truncatula cDNA clo... 85 8e-32 50 emb|AI488938|AI488938 EST247277 tomato ovary, TAMU Lycopersicon ... 85 2e-31

emb|AW14441|AW14447 ES 1333598 KV3 Medicago fruncatula cDNA clo... 85 8e-32 emb|AI488938|AI488938 EST247277 tomato ovary, TAMU Lycopersicon ... 85 2e-31 emb|AF000392|AF000392 Lotus japonicus peptide transporter (LjNOD... 91 7e-31 emb|AW186021|AW186021 se62f04.y1 Gm-c1019 Glycine max cDNA clone... 134 2e-30 emb|AW649721|AW649721 EST328175 tomato germinating seedlings, TA... 109 6e-30 emb|AI485754|AI485754 EST244075 tomato ovary, TAMU Lycopersicon ... 107 9e-30

55 emb|AI812586|AI812586 13F10 Pine Lambda Zap Xylem library Pinus ... 132 1e-29 emb|AW649001|AW649001 EST327455 tomato germinating seedlings, TA... 109 2e-28 emb|AW980440|AW980440 EST391593 GVN Medicago truncatula cDNA clo... 127 3e-28 emb|AW678754|AW678754 WS1_1 E06.b2 A002 Water-stressed 1 (WS1) S... 67 4e-28 emb|AW037664|AW037664 EST279267 tomato mixed elicitor, BTI Lycop... 126 5e-28

60 emb|AW707240|AW707240 sk22e06.yl Gm-c1028 Glycine max cDNA clone... 111 7e-28 emb|AW694862|AW694862 NF080H12ST1F1103 Developing stem Medicago ... 125 9e-28

emb|AW688241|AW688241 NF005B02ST1F1000 Developing stem Medicago ... 77 9e-28 emblAV423709lAV423709 AV423709 Lotus japonicus young plants (two... 83 9e-28 emb|AI899562|AI899562 EST269005 tomato susceptible, Cornell Lyco... 124 2e-27 emblAW201920lAW201920 sf08g07.yl Gm-c1027 Glycine max cDNA clone... 105 4e-27 emb|A43603|A43603 Sequence 28 from Patent WO9507357. 122 6e-27 emb|AW931044|AW931044 EST356887 tomato fruit mature green, TAMU ... 122 6e-27 emb|AW433292|AW433292 sh55b06.yl Gm-c1015 Glycine max cDNA clone... 105 7e-27 emb|AW310283|AW310283 sf33g09.x1 Gm-c1028 Glycine max cDNA clone... 121 2e-26 emb|AW692300|AW692300 NF054C11ST1F1000 Developing stem Medicago ... 77 1e-25 10 emb|AW185746|AW185746 se59b06.y1 Gm-c1019 Glycine max cDNA clone... 105 1e-25 emb|AI930829|AI930829 sc47g08.y1 Gm-c1015 Glycine max cDNA clone... 76 1e-25 emb|AW234064|AW234064 sf33g09.yl Gm-c1028 Glycine max cDNA clone... 93 1e-25 emb|AW758971|AW758971 sl33a12.yl Gm-c1027 Glycine max cDNA clone... 103 2e-25 emb|AW203699|AW203699 sf37c04.yl Gm-c1028 Glycine max cDNA clone... 61 2e-25 **15** . . emb|AI736700|AI736700 sb32d07.yl Gm-c1012 Glycine max cDNA clone... 102 3e-25 emb|AW348589|AW348589 GM210002B22D1R Gm-r1021 Glycine max cDNA 3... emb|AW398957|AW398957 EST309457 L. pennellii trichome, Cornell U... 87 5e-25 emb|AW350656|AW350656 GM210008B20D6R Gm-r1021 Glycine max cDNA 3... 116 7e-20 emb|AA739757|AA739757 522 PtIFG2 Pinus taeda cDNA clone 8840M 3'... 115 1e-24 emb|AW773596|AW773596 EST332582 KV3 Medicago truncatula cDNA clo... 89 2e-24 emb|AW040857|AW040857 EST283721 tomato mixed elicitor, BTI Lycop... 113 5e-24 emb|AW756588|AW756588 sl24c08.yl Gm-c1036 Glycine max cDNA clone... 75 5e-24 emb|AW695244|AW695244 NF093A09ST1F1068 Developing stem Medicago ... 111 2e-23 25 emb|AW256423|AW256423 EST304490 KV2 Medicago truncatula cDNA clo... 46 4e-23 emb|AW929518|AW929518 EST338306 tomato flower buds 8 mm to pre-a... 69 4e-23 emb|AI773875|AI773875 EST254975 tomato resistant, Cornell Lycope... 87 1e-22 emb|AW684249|AW684249 NF014F01NR1F1000 Nodulated root Medicago t... 102 2e-22 emb|AW924370|AW924370 WS1 69 G04.b1 A002 Water-stressed 1 (WS1) ... 86 5e-22 30 emb|AW424380|AW424380 sh64h05.y1 Gm-c1015 Glycine max cDNA clone... 105 8e-22 emb|AW648348|AW648348 EST326802 tomato germinating seedlings, TA... 89 1e-21 emb|AW037585|AW037585 EST279043 tomato mixed elicitor, BTI Lycop... 55 1e-21 emb|AW983508|AW983508 HVSMEg0010N22f Hordeum vulgare pre-anthesi... 57 3e-21 emb|AW929899|AW929899 EST354169 tomato flower buds 8 mm to pre-a... 73 3e-21 35 emb|AW563695|AW563695 LG1 248 G02.g1 A002 Light Grown 1 (LG1) So... 70 6e-21 emb|AW598676|AW598676 si94d11.yl Gm-c1023 Glycine max cDNA clone... 71 9e-21 emb|AW696009|AW696009 NF100H07ST1F1063 Developing stem Medicago ... 58 1e-20 emb|AV409553|AV409553 AV409553 Lotus japonicus young plants (two... 100 3e-20 emb|AW219938|AW219938 EST302421 tomato root during/after fruit s... 48 4e-20 40 emb|AW623831|AW623831 EST321776 tomato flower buds 3-8 mm, Corne... 85 4e-20 emb|AW623819|AW623819 EST321764 tomato flower buds 3-8 mm, Corne... 85 4e-20 emb|AV407359|AV407359 AV407359 Lotus japonicus young plants (two... 84 4e-20 gb|BE058256|BE058256 sn13f01.y1 Gm-c1016 Glycine max cDNA clone ... 100 5e-20 emb|AW688046|AW688046 NF003G03ST1F1000 Developing stem Medicago ... 62 8e-20 45 emb|AW257541|AW257541 EST305678 KV2 Medicago truncatula cDNA clo... 58 1e-19 emb|AW040724|AW040724 EST283588 tomato mixed elicitor, BTI Lycop... 84 1e-19 emb|AW623981|AW623981 EST321926 tomato flower buds 3-8 mm, Corne... 84 1e-19 emb|AW219784|AW219784 EST302266 tomato root during/after fruit s... 73 4e-19 emb[AI494943]AI494943 sa92h11.yl Gm-c1004 Glycine max cDNA clone... 75 5e-19 50 emb|AV418625|AV418625 AV418625 Lotus japonicus young plants (two... 83 5e-19 emb|AI726936|AI726936 BNLGHi6888 Six-day Cotton fiber Gossypium ... 67 7e-19 emb|AW037577|AW037577 EST279035 tomato mixed elicitor, BTI Lycop... 51 7e-19 emb|AW719494|AW719494 LjNEST5b12r Lotus japonicus nodule library... 96 8e-19 emb|AW621680|AW621680 EST312478 tomato root during/after fruit s... 61 1e-18 55 emblAW219076|AW219076 EST301558 tomato root during/after fruit s... 72 1e-18 emb|AW219778|AW219778 EST302260 tomato root during/after fruit s... 72 1e-18 emb|AI779186|AI779186 EST260065 tomato susceptible, Cornell Lyco... 95 2e-18 emb|AW666093|AW666093 sk32b02.yl Gm-c1028 Glycine max cDNA clone... 49 2e-18 emb|AW574204|AW574204 EST316795 GVN Medicago truncatula cDNA clo... 93 5e-18 60 emb|AV426308|AV426308 AV426308 Lotus japonicus young plants (two... 76 6e-18 emb|AW458625|AW458625 sh11e08.yl Gm-c1016 Glycine max cDNA clone... 93 8e-18

```
emb|AW257391|AW257391 EST305528 KV2 Medicago truncatula cDNA clo... 93 8e-18
      emb|A1899409|A1899409 EST268852 tomato ovary, TAMU Lycopersicon ... 48 8e-18
      emb|AW720047|AW720047 LjNEST15g6r Lotus japonicus nodule library... 83 9e-18
      Query= AC006580.8 at 13381_at /id_source genbank /description
 5
      gb|aad22369.1|ac006580 1 (ac006580) nam (no apical meristem)-like
      protein [arabidopsis thaliana] /blast_score 1.00e-169 /ec_number
      /family /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006580| /ncgi
10
      http://www.ncgr.org/cgi-bin/ff?ac006580
           (828 letters)
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
15
      Searching.....done
                                          Score
                                                 E
                                                          (bits) Value
      Sequences producing significant alignments:
20
      emb|AW684737|AW684737 NF021E06NR1F1000 Nodulated root Medicago t... 189 6e-56
      emb|AW032396|AW032396 EST275935 tomato callus, TAMU Lycopersicon... 214 5e-55
      emb|AW934046|AW934046 EST359889 tomato fruit mature green, TAMU ... 214 5e-55
      emb|AW931430|AW931430 EST357273 tomato fruit mature green, TAMU ... 214 5e-55
25
      emb|AF011555|AF011555 Lycopersicon esculentum jasmonic acid 2 (L... 214 5e-55
      emb|AI896441|AI896441 EST265872 tomato callus, TAMU Lycopersicon... 206 2e-52
      emb|AW756289|AW756289 s118e05.y1 Gm-c1036 Glycine max cDNA clone... 157 8e-52
      gb|BE034140|BE034140 MG05E02 MG Mesembryanthemum crystallinum cD... 196 7e-51
      emb|AI488099|AI488099 EST246421 tomato ovary, TAMU Lycopersicon ... 200 7e-51
30
      emb|AI488758|AI488758 EST247097 tomato ovary, TAMU Lycopersicon ... 200 1e-50
      emb|AW220879|AW220879 EST297348 tomato fruit mature green, TAMU ... 200 1e-50
      emb[AI487693]AI487693 EST246015 tomato ovary, TAMU Lycopersicon ... 200 1e-50
      emb|AW775926|AW775926 EST334991 DSIL Medicago truncatula cDNA cl... 195 1e-50
      emb|AW683672|AW683672 NF017D07LF1F1061 Developing leaf Medicago ... 165 4e-50
35
      emb|AI487552|AI487552 EST245874 tomato ovary, TAMU Lycopersicon ... 193 5e-50
      emb[AI488773]AI488773 EST247112 tomato ovary, TAMU Lycopersicon ... 193 5e-50
      emb|AW032532|AW032532 EST276091 tomato callus, TAMU Lycopersicon... 193 5e-50
      emb|AI490551|AI490551 EST249105 tomato ovary, TAMU Lycopersicon ... 193 5e-50
      emb|AI898058|AI898058 EST267501 tomato ovary, TAMU Lycopersicon ... 193 5e-50
40
      emb|AI898890|AI898890 EST268333 tomato ovary, TAMU Lycopersicon ... 193 5e-50
      emb|AI488959|AI488959 EST247298 tomato ovary, TAMU Lycopersicon ... 193 5e-50
      emb|AW035679|AW035679 EST281698 tomato callus, TAMU Lycopersicon... 191 2e-49
      emb|AW443857|AW443857 EST308787 tomato mixed elicitor, BTI Lycop... 192 3e-49
      emb|AI488673|AI488673 EST247012 tomato ovary, TAMU Lycopersicon ... 193 4e-49
45
      emb|AI899016|AI899016 EST268459 tomato ovary, TAMU Lycopersicon ... 195 4e-49
      emb|AW650556|AW650556 EST329010 tomato germinating seedlings, TA... 193 8e-49
      gb|BE020071|BE020071 sm38f07.yl Gm-c1028 Glycine max cDNA clone ... 193 2e-48
      emb|AI771859|AI771859 EST252959 tomato ovary, TAMU Lycopersicon ... 193 2e-48
      emb|AI487093|AI487093 EST245415 tomato ovary, TAMU Lycopersicon ... 193 2e-48
50
      emb|AW032194|AW032194 EST275648 tomato callus, TAMU Lycopersicon... 193 2e-48
      emb|AI897442|AI897442 EST266885 tomato ovary, TAMU Lycopersicon ... 193 2e-48
      emb|AW035194|AW035194 EST280456 tomato callus, TAMU Lycopersicon... 193 2e-48
      emb|AI897257|AI897257 EST266616 tomato ovary, TAMU Lycopersicon ... 193 2e-48
      emb|AI490061|AI490061 EST248400 tomato ovary, TAMU Lycopersicon ... 192 2e-48
55
      emb|AW040320|AW040320 EST283184 tomato mixed elicitor, BTI Lycop... 191 6e-48
      emb|AV410710|AV410710 AV410710 Lotus japonicus young plants (two... 190 1e-47
      emb|AW041100|AW041100 EST283964 tomato mixed elicitor, BTI Lycop... 190 1e-47
      emb|AI484813|AI484813 EST243074 tomato ovary, TAMU Lycopersicon ... 183 4e-47
      emb|AW650475|AW650475 EST328929 tomato germinating seedlings, TA... 187 1e-46
60
      emb|AW668121|AW668121 GA_ Ea0012N05 Gossypium arboreum 7-10 dpa ... 154 1e-46
      emb|AI773440|AI773440 EST254540 tomato resistant, Cornell Lycope... 150 3e-46
```

```
emb|AI898263|AI898263 EST267706 tomato ovary, TAMU Lycopersicon ... 185 5e-46
      emb|AW696936|AW696936 NF110E07ST1F1054 Developing stem Medicago ... 149 9e-46
      emb|AI896058|AI896058 EST265501 tomato callus, TAMU Lycopersicon... 150 1e-45
      emb|AI485389|AI485389 EST243710 tomato ovary, TAMU Lycopersicon ... 183 1e-45
      emb|AI895235|AI895235 EST264678 tomato callus, TAMU Lycopersicon... 150 2e-45
      emb|AW932278|AW932278 EST358121 tomato fruit mature green, TAMU ... 150 2e-45
      emb|A1897596|A1897596 EST267039 tomato ovary, TAMU Lycopersicon ... 183 2e-45
      emb|AW034429|AW034429 EST278000 tomato callus, TAMU Lycopersicon... 146 2e-45
      emb|AW443468|AW443468 EST308398 tomato mixed elicitor, BTI Lycop... 116 2e-45
10
      emb|AW442290|AW442290 EST311686 tomato fruit red ripe, TAMU Lyco... 147 3e-45
      emb|AW442348|AW442348 EST311744 tomato fruit red ripe, TAMU Lyco... 150 3e-45
      emb|AW625882|AW625882 EST319789 tomato radicle, 5 d post-imbibit... 150 3e-45
      emb|AW775866|AW775866 EST334931 DSIL Medicago truncatula cDNA cl... 149 4e-45
      emb|AW736371|AW736371 EST332290 KV3 Medicago truncatula cDNA clo... 149 4e-45
15
      emb|AI856667|AI856667 sb42d09.yl Gm-c1014 Glycine max cDNA clone... 151 4e-45
      emb|AW687506|AW687506 NF010C12RT1F1097 Developing root Medicago ... 149 4e-45
      emb|AW686733|AW686733 NF041H04NR1F1000 Nodulated root Medicago t... 149 4e-45
      emb|AW690801|AW690801 NF035B09ST1F1000 Developing stem Medicago ... 149 4e-45
      gb|BE124309|BE124309 EST394434 DSIL Medicago truncatula cDNA clo... 149 5e-45
20
      emb|AW775409|AW775409 EST334474 DSIL Medicago truncatula cDNA cl... 149 5e-45
      emb|AW559397|AW559397 EST314445 DSIR Medicago truncatula cDNA cl... 149 5e-45
      emb|AW030038|AW030038 EST273293 tomato callus, TAMU Lycopersicon... 150 6e-45
      emb|AW775964|AW775964 EST335029 DSIL Medicago truncatula cDNA cl... 149 1e-44
      emb|AW185617|AW185617 se80b05.yl Gm-c1023 Glycine max cDNA clone... 180 1e-44
25
      emb|AJ010830|TSP010830 Triticum sp. mRNA for GRAB2 protein.
                                                                      133 3e-44
      emb|A82386|A82386 Sequence 11 from Patent WO9856811.
                                                                    133 3e-44
      emb[AW092910]AW092910 EST286090 tomato mixed elicitor, BTI Lycop... 148 3e-44
      emb|AI487779|AI487779 EST246101 tomato ovary, TAMU Lycopersicon ... 148 3e-44
      emb|AW442068|AW442068 EST311464 tomato fruit red ripe, TAMU Lyco... 148 3e-44
30
      emb|AI773092|AI773092 EST254192 tomato resistant, Cornell Lycope... 148 3e-44
      emb|AI489361|AI489361 EST247700 tomato ovary, TAMU Lycopersicon ... 148 4e-44
      emb|AI488314|AI488314 EST246636 tomato ovary, TAMU Lycopersicon ... 148 5e-44
      emb|AI489164|AI489164 EST247503 tomato ovary, TAMU Lycopersicon ... 176 5e-44
      emb|AI898478|AI898478 EST267921 tomato ovary, TAMU Lycopersicon ... 176 5e-44
35
      emb|AW680754|AW680754 WS1 7 A09.b1 A002 Water-stressed I (WS1) S... 149 7e-44
      emb|AI896316|AI896316 EST265759 tomato callus, TAMU Lycopersicon... 145 7e-44
      gb|BE126167|BE126167 DG1 66 F07.b1 A002 Dark Grown 1 (DG1) Sorgh... 149 7e-44
      emb|AW931009|AW931009 EST356852 tomato fruit mature green, TAMU ... 147 7e-44
      emb|AW035978|AW035978 EST282837 tomato callus, TAMU Lycopersicon... 146 1e-43
40
      emb|AW932996|AW932996 EST358839 tomato fruit mature green, TAMU ... 146 1e-43
      emb|AW278088|AW278088 sf39e10.y1 Gm-c1009 Glycine max cDNA clone... 149 2e-43
      emb|AW203537|AW203537 sf35d02.yl Gm-c1028 Glycine max cDNA clone... 143 2e-43
      emb|AW220707|AW220707 EST297176 tomato fruit mature green, TAMU ... 148 3e-43
      emb|A82380|A82380 Sequence 5 from Patent WO9856811.
                                                                   175 4e-43
45
      emb|AJ010829|TSP010829 Triticum sp. mRNA for GRAB1 protein.
                                                                      175 4e-43
      emb|A82384|A82384 Sequence 9 from Patent WO9856811.
                                                                   175 4e-43
      emb|AW737167|AW737167 EST338594 tomato flower buds, anthesis, Co... 148 4e-43
      emb|AW560823|AW560823 EST315871 DSIR Medicago truncatula cDNA cl... 146 6e-43
      emb|AI486492|AI486492 EST244813 tomato ovary, TAMU Lycopersicon ... 144 9e-43
50
      emb|AI486833|AI486833 EST245155 tomato ovary, TAMU Lycopersicon ... 144 9e-43
      emb|AW222093|AW222093 EST298904 tomato fruit red ripe, TAMU Lyco... 104 1e-42
      emb|AW560904|AW560904 EST315952 DSIR Medicago truncatula cDNA cl... 146 2e-42
      emb|AW223963|AW223963 EST300774 tomato fruit red ripe, TAMU Lyco... 147 2e-42
      emb|A82382|A82382 Sequence 7 from Patent WO9856811.
55
      emb|AW164307|AW164307 se70g05.yl Gm-c1023 Glycine max cDNA clone... 143 5e-41
      emb|AW560434|AW560434 EST315482 DSIR Medicago truncatula cDNA cl... 110 1e-40
      emb|AW030017|AW030017 EST273272 tomato callus, TAMU Lycopersicon... 146 1e-40
      emb|AW306698|AW306698 sf47c01.y1 Gm-c1009 Glycine max cDNA clone... 151 1e-40
      emb|AI729055|AI729055 BNLGHi12472 Six-day Cotton fiber Gossypium... 135 1e-40
60
```

Query= AC006218.175 s at 13818 s at /id source genbank /description

gb|aad15433.1| (ac006218) putative aspartate aminotransferase
[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
/gb_link /ncgi
(1290 letters)

5

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

10

Score E

Sequences producing significant alignments:

(bits) Value

gb|BE052217|BE052217 GA __Ea0033E06f Gossypium arboreum 7-10 dpa ... 358 4e-98 15. emb|AI941267|AI941267 sb86g03.y1 Gm-c1010 Glycine max cDNA clone... 317 1e-85 emb|AW472288|AW472288 si23c10.y1 Gm-c1029 Glycine max cDNA clone... 297 2e-79 emb|AW720283|AW720283 LjNEST20a9r Lotus japonicus nodule library... 295 4e-79 emb|AW234168|AW234168 sf22a07.y1 Gm-c1028 Glycine max cDNA clone... 288 7e-77 gb|BE021080|BE021080 sm55b08.y1 Gm-c1028 Glycine max cDNA clone ... 282 3e-75 20 emb|AW509358|AW509358 si22a10.yl Gm-c1029 Glycine max cDNA clone... 272 3e-72 emblAW622811|AW622811 EST306797 tomato flower buds 3-8 mm, Corne... 252 4e-66 emb|AV390505|AV390505 AV390505 Chlamydomonas reinhardtii C9 Chla... 147 4e-58 emb|AW234504|AW234504 sf15a07.yl Gm-c1028 Glycine max cDNA clone... 225 7e-58 emb|AI773174|AI773174 EST254274 tomato resistant, Cornell Lycope... 218 9e-56 25 emb|AI774300|AI774300 EST255316 tomato resistant, Cornell Lycope... 210 1e-53 gb|BE024350|BE024350 894002D06.yl C. reinhardtii CC-1690, normal... 192 5e-48 gb[BE056488]BE056488 894009G03.yl C. reinhardtii CC-1690, normal... 189 3e-47 emb|AW691828|AW691828 NF044F04ST1F1000 Developing stem Medicago ... 179 2e-44 emb|AW719571|AW719571 LjNEST6g3r Lotus japonicus nodule library,... 175 6e-43 30 emb|AW981392|AW981392 EST392545 DSIL Medicago truncatula cDNA cl... 162 4e-39 emb|AW720570|AW720570 LjNEST8h11rc Lotus japonicus nodule librar... 156 4e-37 gb|L46457|L46457 BNAF1543 Mustard flower buds Brassica rapa cDNA... 152 6e-36 emb|AT000069|AT000069 AT000069 Apple young fruit cDNA library Ma... 118 9e-36 emb|AW309618|AW309618 sf22a07.x1 Gm-c1028 Glycine max cDNA clone... 150 2e-35 35 emb|AW830423|AW830423 sm26e11.yl Gm-c1028 Glycine max cDNA clone... 140 2e-32 emb|AW218448|AW218448 EST303631 tomato radicle, 5 d post-imbibit... 133 3e-30 emb|AW428992|AW428992 EST306532 tomato flower buds 0-3 mm, Corne... 132 5e-30 emb|AV390398|AV390398 AV390398 Chlamydomonas reinhardtii C9 Chla... 123 2e-27 emb[AW830756]AW830756 sm29a08.y1 Gm-c1028 Glycine max cDNA clone... 114 2e-24 40 emb|AV389740|AV389740 AV389740 Chlamydomonas reinhardtii C9 Chla... 113 3e-24 emb|AV410690|AV410690 AV410690 Lotus japonicus young plants (two... 89 9e-17 emb|AW217350|AW217350 EST296173 tomato flower buds 0-3 mm, Corne... 62 2e-15 emb|AW477177|AW477177 ga42h10.yl Moss EST library PPU Physcomitr... 66 7e-10 emb|AW559640|AW559640 EST314752 DSIR Medicago truncatula cDNA cl... 60 5e-08 45 emb|AW691076|AW691076 NF041A07ST1F1000 Developing stem Medicago ... 56 6e-07 emb|AI773775|AI773775 EST254875 tomato resistant, Cornell Lycope... 54 3e-06 emb|AW727211|AW727211 GA Ea0023N19 Gossypium arboreum 7-10 dpa ... 49 1e-04 emb|AI729480|AI729480 BNLGHil3474 Six-day Cotton fiber Gossypium... 35 0.001 emb|AI068927|AI068927 mgae0004dB02f Magnaporthe grisea Appressor... 38 0.003 emb|AW043088|AW043088 ST29B11 Pine TriplEx shoot tip library Pin... 43 0.006 emb|AL034356|LMFL7610 Leishmania major Friedlin chromosome 4 cos... 41 0.015 emb|AW568631|AW568631 si60b11.yl Gm-r1030 Glycine max cDNA clone... 40 0.055 emb|AW690226|AW690226 NF030F01ST1F1000 Developing stem Medicago ... 32 0.057 emb|Z12622|ASALLIIN A.sativum mRNA encoding precursor allimase. 55 gb|S73324|S73324 alliinase [Allium sativum=garlics, bulbs, mRNA,... 39 0.10 emb|AI068628|AI068628 mgae0003cD03f Magnaporthe grisea Appressor... 38 0.14 gb|U34986|VRU34986 Vigna radiata 1-aminocyclopropane-1-carboxyli... 38 0.14 emb|AB018355|AB018355 Vigna radiata gene for 1-aminocyclopropane... 38 0.14 emb|AB000679|AB000679 Vigna radiata mRNA for 1-aminocyclopropane... 38 0.14 60 emb[X74106]NTGRPR N.tabacum gene for glycine-rich protein. emb|AV414385|AV414385 AV414385 Lotus japonicus young plants (two... 38 0.19

emb AF170705 AF170705 Mangifera indica 1-aminocyclopemb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycine matemb AW032260 AW032260 EST275714 tomato callus, TAIemb AF119413 AF119413 Lupinus albus 1-aminocyclopropemb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocyclopropemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheareemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb X87372 LESODCC L.esculentum SodCc;Le;2 gene.emb AW651589 AW651589 EST330043 tomato germinatin	ading frame O 38 0.19
gb U53880 YSCL9449 Saccharomyces cerevisiae chromoso emb AV424265 AV424265 AV424265 Lotus japonicus you emb AI055499 AI055499 coau0004C15 Cotton Boll Abscis: emb AI40609 AI440609 sa68d05.yl Gm-c1004 Glycine m emb AI896625 AI896625 EST266068 tomato callus, TAMU emb AI896781 AI896781 EST266224 tomato callus, TAMU emb AF119412 AF119412 Lupinus albus 1-aminocycloprop emb AV033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Abscis: emb AW032141 AW032141 EST275595 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Abscis: emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grov emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC- emb AW03331 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF016490 AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF119410 AF119410 Lupinus albus 1-aminocycloproj emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF170705 AF170705 Mangifera indica 1-aminocycloproj emb AF1704930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF1704931 AF074930 Sinapis arvensis 1-aminocycloproj emb AF1704930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF0749	NA for ACC syntha 38 0.19
emb AV424265 AV424265 AV424265 Lotus japonicus you emb AI055499 AI055499 coau0004C15 Cotton Boll Absciss emb AI440609 AI440609 sa68d05.y1 Gm-c1004 Glycine m emb AI896625 AI896625 EST266068 tomato callus, TAMU emb AI896781 AI8966781 EST266224 tomato callus, TAMU emb AV391798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupimus albus 1-aminocycloprop emb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Abscis emb AW0332141 AW0332141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U172229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocyclopro emb AF016458 AF016458 Pisum sativum 1-aminocyclopro emb AF016458 AF016458 Pisum sativum 1-aminocyclopro emb AF016458 AF016458 Pisum sativum 1-aminocyclopro emb AF074929 AF074929 Sinapis arvensis 1-aminocyclopro emb AF074929 AF074929 Sinapis arvensis 1-aminocyclopro emb AF119414 AF119414 Lupimus albus 1-aminocyclopro emb AF119410 AF119410 Lupimus albus 1-aminocyclopro emb AF119410 AF119410 Lupimus albus 1-aminocyclopro emb AF119410 AF119410 Lupimus albus 1-aminocyclopro emb AF119413 AF119413 Lupimus albus 1-aminocyclopro emb AF119413 AF119413 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF074930 AF074930 Sinapis arvensis 1-aminocyclopro emb AF074930 AF074930 Sinapis arvensis 1-aminocyclopro emb AF07	is, anthesis, Co 38 0.19
emb AV424265 AV424265 AV424265 Lotus japonicus you emb AI055499 AI055499 coau0004C15 Cotton Boll Absciss emb AI440609 AI440609 sa68d05.y1 Gm-c1004 Glycine m emb AI896625 AI896625 EST266068 tomato callus, TAMU emb AI896781 AI8966781 EST266224 tomato callus, TAMU emb AV391798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupimus albus 1-aminocycloprop emb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Abscis emb AW0332141 AW0332141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U172229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocyclopro emb AF016458 AF016458 Pisum sativum 1-aminocyclopro emb AF016458 AF016458 Pisum sativum 1-aminocyclopro emb AF016458 AF016458 Pisum sativum 1-aminocyclopro emb AF074929 AF074929 Sinapis arvensis 1-aminocyclopro emb AF074929 AF074929 Sinapis arvensis 1-aminocyclopro emb AF119414 AF119414 Lupimus albus 1-aminocyclopro emb AF119410 AF119410 Lupimus albus 1-aminocyclopro emb AF119410 AF119410 Lupimus albus 1-aminocyclopro emb AF119410 AF119410 Lupimus albus 1-aminocyclopro emb AF119413 AF119413 Lupimus albus 1-aminocyclopro emb AF119413 AF119413 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF119413 AF119419 Lupimus albus 1-aminocyclopro emb AF074930 AF074930 Sinapis arvensis 1-aminocyclopro emb AF074930 AF074930 Sinapis arvensis 1-aminocyclopro emb AF07	ome XII cosmi 38 0.19
emb AI055499 AI055499 coau0004C15 Cotton Boll Absciss emb AI440609 AI440609 sa68d05.yl Gm-c1004 Glycine m emb AI896625 AI896625 EST266068 tomato callus, TAMU emb AI896781 AI896781 EST266224 tomato callus, TAMU emb AV391798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupinus albus 1-aminocycloprop emb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Absciss emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17228 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloprog emb AF016458 AF016458 Pisum sativum 1-aminocycloprog emb AF014929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF014929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF119414 AF119411 Lupinus albus 1-aminocycloprog emb AF119410 AF119410 Lupinus albus 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 A	mg plants (two 38 0.19
emb A1440609 A1440609 sa68d05.y1 Gm-c1004 Glycine m emb A1896625 A1896625 EST266068 tomato callus, TAMU emb A1896781 A1896781 EST266224 tomato callus, TAMU emb A1991798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupinus albus 1-aminocycloprop emb AW033411 AW033411 EST276982 tomato callus, TAI emb A1054518 A1054518 coau0001D13 Cotton Boll Absciss emb AW032141 AW032141 EST275595 tomato callus, TAI emb A2632 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb A1896469 A1896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016460 Pisum sativum 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074929 AF074921 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF119410 AF119410 Lupinus albus 1-aminocycloproj emb AF119410 AF119410 Lupinus albus 1-aminocycloproj emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930	
emb AI896625 AI896625 EST266068 tomato callus, TAMU emb AI896781 AI896781 EST266224 tomato callus, TAMU emb AV391798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupinus albus 1-aminocycloprop emb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Abscis: emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z66322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grov emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17228 PHU17229 Pelargonium hortorum clone pGAC- emb AL096788 SFBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC- emb AF016460 AF016460 Pisum sativum 1-aminocycloprog emb AF016458 AF016458 Pisum sativum 1-aminocycloprog emb AF016458 AF016458 Pisum sativum 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF119410 AF119410 Lupinus albus 1-aminocycloprog emb AF119410 AF119410 Lupinus albus 1-aminocycloprog emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF170705 Mangifera indica 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb A	
emb AI896781 AI896781 EST266224 tomato callus, TAMU emb AV391798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupinus albus 1-aminocycloprop emb AW03341 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Absciss emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grov emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC- emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC- emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprog emb AF016460 AF016460 Pisum sativum 1-aminocycloprog emb AF016458 AF016458 Pisum sativum 1-aminocycloprog emb AF074929 AF074925 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog em	
emb AV391798 AV391798 AV391798 Chlamydomonas rei emb AF119412 AF119412 Lupinus albus 1-aminocycloprop emb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Abscis emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z6322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs18 emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloprop emb AF016458 AF016458 Pisum sativum 1-aminocycloprop emb AF016458 AF016458 Pisum sativum 1-aminocycloprop emb AF016458 AF016458 Pisum sativum 1-aminocycloprop emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprop emb AF074929 AF074921 Sinapis arvensis 1-aminocycloprop emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprop emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprop emb AF119410 AF119410 Lupinus albus 1-aminocycloprop emb AF119410 AF119410 Lupinus albus 1-aminocycloprop emb AF119410 AF119410 Lupinus albus 1-aminocycloprop emb AF170705 AF170705 Mangifera indica 1-aminocycloprop emb AW333989 AW033989 EST277651 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop emb AF074930 AF07493	
emb AF119412 AF119412 Lupinus albus 1-aminocyclopropemb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Absciss emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1 65 F07.g1 A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit maturemb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC semb AJ277161 CPA277161 Carica papaya partial paccs1B gemb Z69909 SPAC19G10 S.pombe chromosome I cosmid gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SFBC582 S.pombe chromosome II cosmid gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074921 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074921 Sinapis arvensis 1-aminocycloprogemb AF074921 AF016458 Pisum sativum 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Si	inhardtii C9 Chla 37 0.37
emb AW033411 AW033411 EST276982 tomato callus, TAI emb AI054518 AI054518 coau0001D13 Cotton Boll Absciss emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloproemb AF016458 AF016458 Pisum sativum 1-aminocycloproemb AF016458 AF016458 Pisum sativum 1-aminocycloproemb AF016458 AF016458 Pisum sativum 1-aminocycloproemb AF074929 AF074929 Sinapis arvensis 1-aminocycloproemb AF074929 AF074929 Sinapis arvensis 1-aminocycloproemb AF074923 AF074931 Sinapis arvensis 1-aminocycloproemb AF074931 AF074931 Sinapis arvensis 1-aminocycloproemb AF119410 AF119410 Lupinus albus 1-aminocycloproemb AF119410 AF119410 Lupinus albus 1-aminocycloproemb AW032389 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloproemb AF119413 AF119413 Lupinus albus 1-aminocycloproemb AF119413 AF119413 Lupinus albus 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproemb AF074930 AF074930 Sinapis arvensis 1-aminocycloproem	
emb AI054518 AI054518 coau0001D13 Cotton Boll Absciss emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit mature emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paces1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AK096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AK096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AK096788 SPBC682 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016458 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF19410 AF119410 Lupinus albus 1-aminocycloproj emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycim emb AW831752 AW831752 sm16f02.y1 Gm-c1004 Glycine memb AW831752 AW831752 sm16f02.y1 Gm-c1004 Glycine memb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis a	
emb AW032141 AW032141 EST275595 tomato callus, TAI emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grov emb AW934295 AW934295 EST360138 tomato fruit matur emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AE007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AE007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AE007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AE0096788 SPBC582 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC- emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC- emb AF016460 AF016460 Pisum sativum 1-aminocycloprol emb AF016458 AF016458 Pisum sativum 1-aminocycloprol emb AF016458 AF016458 Pisum sativum 1-aminocycloprol emb AF016458 AF016458 Pisum sativum 1-aminocycloprol emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprol emb AF0749231 AF074929 Sinapis arvensis 1-aminocycloprol emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprol emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprol emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprol emb AF119410 AF119410 Lupinus albus 1-aminocycloprol emb AF119410 AF119410 Secryta indica 1-aminocycloprol emb AF074939 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprol emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprol emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprol emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprol emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprol gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AF04949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprol gb U33779 TAU35779 Triticum aestivum 1-aminocycloprol gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprol gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb AF074930 AF0749	
emb Z26322 HVALAAT H.vulgare mRNA for alanine amin gb BE126096 BE126096 DG1_65_F07.g1_A002 Dark Grow emb AW934295 AW934295 EST360138 tomato fruit matur emb A1896469 A1896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC semb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC semb AJ277161 CPA277161 Carica papaya partial paccs1B gemb Z69909 SPAC19G10 S.pombe chromosome I cosmid of gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid of gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprogemb AF10705 AF170705 Mangifera indica 1-aminocycloprogemb AF10705 AF170705 Mangifera indica 1-aminocycloprogemb AF10705 AF170705 Mangifera indica 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF0	sion Zone cD 37 0.37
gb BE126096 BE126096 DG1_65_F07.gl_A002 Dark Grovemb AW934295 AW934295 EST360138 tomato fruit maturemb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC semb AJ277161 CPA277161 Carica papaya partial paccs1B gemb Z69909 SPAC19G10 S.pombe chromosome I cosmid cgb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid cgb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid cgb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930	
emb AW934295 AW934295 EST360138 tomato fruit mature emb AI896469 AI896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC semb AJ277161 CPA277161 Carica papaya partial paccs1B gemb Z69909 SPAC19G10 S.pombe chromosome I cosmid cgb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid cgb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AF016460 AF016460 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine mb AF170705 AF170705 Mangifera indica 1-aminocycloprogemb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF07493	
emb A1896469 A1896469 EST265900 tomato callus, TAMU emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC spemb AJ277161 CPA277161 Carica papaya partial paccs1B gemb Z69909 SPAC19G10 S.pombe chromosome I cosmid cgb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid cgb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprogemb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF07	
emb AF007214 AF007214 Phalaenopsis sp. SM9108 ACC s emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC- emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC- emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprog emb AF016458 AF016458 Pisum sativum 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF119410 AF119410 Lupinus albus 1-aminocycloprog emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine dmb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprog emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprog emb AF119411 AF119411 Lupinus albus 1-aminocycloprog emb AP119411 AF119411 Lupinus albus 1-aminocycloprog gb U31975 CRU31975 Chlamydomonas reinhardtii alanine: emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine: emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
emb AJ277161 CPA277161 Carica papaya partial paccs1B g emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC- emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC- emb AW703931 AW703931 sk25h05.yl Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprog emb AF016458 AF016458 Pisum sativum 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074929 AF074929 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF074931 AF074931 Sinapis arvensis 1-aminocycloprog emb AF119410 AF119410 Lupinus albus 1-aminocycloprog emb AW831752 AW831752 sm16f02.yl Gm-c1027 Glycine dmb AW033989 AW033989 EST277651 tomato callus, TAl emb AF170705 AF170705 Mangifera indica 1-aminocycloprog emb AW032260 AW032260 EST275714 tomato callus, TAl emb AF19413 AF119413 Lupinus albus 1-aminocycloprog emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprog emb AF074930 AF074930 Sinapis arven	
emb Z69909 SPAC19G10 S.pombe chromosome I cosmid c gb U17229 PHU17229 Pelargonium hortorum clone pGAC- emb AL096788 SPBC582 S.pombe chromosome II cosmid c gb U17228 PHU17228 Pelargonium hortorum clone pGAC- emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF119410 AF119410 Lupinus albus 1-aminocycloproj emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycina emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocyclop emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloproj emb AP119411 AF119411 Lupinus albus 1-aminocycloproj gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb AF372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	synthase 3 (AC 36 0.50
gb U17229 PHU17229 Pelargonium hortorum clone pGAC-emb AL096788 SPBC582 S.pombe chromosome II cosmid ogb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprogemb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF014949 AF014949 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprogemb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AW032260 AW032260 EST275714 tomato callus, TAI emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AP119411 AF119411 Lupinus albus 1-aminocycloprogemb AP119411 AF119411 Lupinus albus 1-aminocycloprogemb AW651589 AW651589 EST330043 tomato germinatingemb AW651589 AW651589 EST330043 tomato germinatingemb AW651589 AW651589 EST330043 tomato germinatingemb AW216510 AW216510 EST295224 tomato callus, TAI	gene for 1 35 0.60
emb AL096788 SPBC582 S.pombe chromosome II cosmid of gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprojemb AF016458 AF016458 Pisum sativum 1-aminocycloprojemb AF016458 AF016458 Pisum sativum 1-aminocycloprojemb AF014929 AF074929 Sinapis arvensis 1-aminocycloprojemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprojemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprojemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprojemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprojemb AF119410 AF119410 Lupinus albus 1-aminocycloprojemb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycinemb AW033989 AW033989 EST277651 tomato callus, TAlemb AF170705 AF170705 Mangifera indica 1-aminocycloprojemb AV032260 AW032260 EST275714 tomato callus, TAlemb AF119413 AF119413 Lupinus albus 1-aminocycloprojemb AW032260 AW032260 EST275714 tomato callus, TAlemb AF119413 AF119413 Lupinus albus 1-aminocycloprojemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocycloprojemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheareemb AP119411 AF119411 Lupinus albus 1-aminocycloprojemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheareemb AF119411 AF119411 Lupinus albus 1-aminocycloprojemb AP119411 AF119411 Lupinus albus 1-aminocycloprojemb AW651589 AW651589 EST330043 tomato germinatinemb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato cal	:19G10. 36 0.69
emb AL096788 SPBC582 S.pombe chromosome II cosmid of gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloprojemb AF016458 AF016458 Pisum sativum 1-aminocycloprojemb AF016458 AF016458 Pisum sativum 1-aminocycloprojemb AF014929 AF074929 Sinapis arvensis 1-aminocycloprojemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprojemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprojemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprojemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprojemb AF119410 AF119410 Lupinus albus 1-aminocycloprojemb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycinemb AW033989 AW033989 EST277651 tomato callus, TAlemb AF170705 AF170705 Mangifera indica 1-aminocycloprojemb AV032260 AW032260 EST275714 tomato callus, TAlemb AF119413 AF119413 Lupinus albus 1-aminocycloprojemb AW032260 AW032260 EST275714 tomato callus, TAlemb AF119413 AF119413 Lupinus albus 1-aminocycloprojemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocycloprojemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheareemb AP119411 AF119411 Lupinus albus 1-aminocycloprojemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheareemb AF119411 AF119411 Lupinus albus 1-aminocycloprojemb AP119411 AF119411 Lupinus albus 1-aminocycloprojemb AW651589 AW651589 EST330043 tomato germinatinemb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato cal	1 1-aminocycl 36 0.69
gb U17228 PHU17228 Pelargonium hortorum clone pGAC-emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb AF119410 AF119410 Lupinus albus 1-aminocycloproj emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloproj emb AH60900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloproj emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloproj emb AF119411 AF119411 Lupinus albus 1-aminocycloproj gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
emb AW703931 AW703931 sk25h05.y1 Gm-c1028 Glycine emb AF016460 AF016460 Pisum sativum 1-aminocycloproj emb AF016458 AF016458 Pisum sativum 1-aminocycloproj emb AF019414 AF119414 Lupinus albus 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AF074929 AF074929 Sinapis arvensis 1-aminocycloproj emb AW685223 AW685223 NF027D03NR1F1000 Nodulat emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproj emb Z73199 SCYLR027C S.cerevisiae chromosome XII rea emb AF119410 AF119410 Lupinus albus 1-aminocycloproj emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloproj emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AF074930 AF074930 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AF074930 AF074930 Sinapis arvensis 1-aminocycloproj emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloproj emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloproj emb AF119411 AF119411 Lupinus albus 1-aminocycloproj emb AF119411 AF119411 Lupinus albus 1-aminocycloproj emb AW651589 AW651589 EST330043 tomato germinatin emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
emb AF016460 AF016460 Pisum sativum 1-aminocyclopropemb AF016458 AF016458 Pisum sativum 1-aminocyclopropemb AF014929 AF074929 Sinapis arvensis 1-aminocyclopropemb AF074929 AF074929 Sinapis arvensis 1-aminocyclopropemb AF074929 AF074929 Sinapis arvensis 1-aminocyclopropemb AF074931 AF074931 Sinapis arvensis 1-aminocyclopropemb AF074931 AF074931 Sinapis arvensis 1-aminocyclopropemb AF074931 AF074931 Sinapis arvensis 1-aminocyclopropemb AF119410 AF119410 Lupinus albus 1-aminocyclopropemb AW831752 AW831752 sm16f02.yl Gm-c1027 Glycinemb AW033989 AW033989 EST277651 tomato callus, TAlemb AF170705 AF170705 Mangifera indica 1-aminocyclopropemb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycinemaemb AW032260 AW032260 EST275714 tomato callus, TAlemb AF119413 AF119413 Lupinus albus 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocyclopropemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb AF37372 LESODCC L.esculentum SodCc;Le;2 gene.emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW216510 AW216510 EST295224 tomato callus, TAlemb AW216510 AW21651	
emb AF016458 AF016458 Pisum sativum 1-aminocycloprogemb AF119414 AF119414 Lupinus albus 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074929 AF074929 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF074931 AF074931 Sinapis arvensis 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AF119410 AF119410 Lupinus albus 1-aminocycloprogemb AW831752 AW831752 sm16f02.yl Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprogemb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprogemb AF119411 AF119411 Lupinus albus 1-aminocycloprogemb AF119411 AF119411 Lupinus albus 1-aminocycloprogemb AF119411 AF119411 Lupinus albus 1-aminocycloprogemb AF3772 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	pane-1-carbox 36 0.69
emb AF119414 AF119414 Lupinus albus 1-aminocyclopropemb AF074929 AF074929 Sinapis arvensis 1-aminocyclopropemb AW685223 AW685223 NF027D03NR1F1000 Nodulatemb AF074931 AF074931 Sinapis arvensis 1-aminocyclopropemb Z73199 SCYLR027C S.cerevisiae chromosome XII reaemb AF119410 AF119410 Lupinus albus 1-aminocyclopropemb AW831752 AW831752 sm16f02.yl Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAIemb AF170705 AF170705 Mangifera indica 1-aminocyclopropemb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycine maemb AW032260 AW032260 EST275714 tomato callus, TAIemb AF119413 AF119413 Lupinus albus 1-aminocyclopropemb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocyclopropemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheareemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb X87372 LESODCC L.esculentum SodCc;Le;2 gene.emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAI	mane-1-carbox 36 0.69
emb AF074929 AF074929 Sinapis arvensis 1-aminocyclopromb AW685223 AW685223 NF027D03NR1F1000 Nodulatemb AF074931 AF074931 Sinapis arvensis 1-aminocyclopromb Z73199 SCYLR027C S.cerevisiae chromosome XII reademb AF119410 AF119410 Lupinus albus 1-aminocyclopromemb AW831752 AW831752 sm16f02.yl Gm-c1027 Glycinomb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocyclopromb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycinomb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocyclopromb AF074930 AF074930 Sinapis arvensis 1-aminocyclopromb AF074930 AF074930 Sinapis arvensis 1-aminocyclopromb AF074930 AF074930 Sinapis arvensis 1-aminocyclopromb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocyclopromb AF119411 AF119411 Lupinus albus 1-aminocyclopromb AF119411 AF119411 Lupinus albus 1-aminocyclopromb AF119411 AF119411 Lupinus albus 1-aminocyclopromb X87372 LESODCC L.esculentum SodCc;Le;2 gene.emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAI	pane-1-carbox 35 0.95
 emb AW685223 AW685223 NF027D03NR1F1000 Nodulat emb AF074931 AF074931 Sinapis arvensis 1-aminocycloproemb Z73199 SCYLR027C S.cerevisiae chromosome XII rea emb AF119410 AF119410 Lupinus albus 1-aminocyclopropemb AW831752 AW831752 sm16f02.yl Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocyclopropemb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocyclopropemb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocyclopropemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAI 	onane-1-car 35 0.95
emb AF074931 AF074931 Sinapis arvensis 1-aminocyclopro emb Z73199 SCYLR027C S.cerevisiae chromosome XII rea emb AF119410 AF119410 Lupinus albus 1-aminocycloprop emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycine emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprop emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
emb Z73199 SCYLR027C S.cerevisiae chromosome XII rea emb AF119410 AF119410 Lupinus albus 1-aminocycloprop emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycinus emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprop emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
emb AF119410 AF119410 Lupinus albus 1-aminocycloprop emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycinus emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocycloprop emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	ading frame O 35 0.95
emb AW831752 AW831752 sm16f02.y1 Gm-c1027 Glycind emb AW033989 AW033989 EST277651 tomato callus, TAI emb AF170705 AF170705 Mangifera indica 1-aminocyclope emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocycloprope emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocyclopropemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocyclopropemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAI	
 emb AW033989 AW033989 EST277651 tomato callus, TAl emb AF170705 AF170705 Mangifera indica 1-aminocyclop emb AI460900 AI460900 sa70f07.yl Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAl emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprop gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl 	
emb AF170705 AF170705 Mangifera indica 1-aminocyclop: emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAI	
emb AI460900 AI460900 sa70f07.y1 Gm-c1004 Glycine material emb AW032260 AW032260 EST275714 tomato callus, TAI emb AF119413 AF119413 Lupinus albus 1-aminocyclopropemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogemb AW650504 AW650504 EST328958 tomato germinatingb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatinemb AW216510 AW216510 EST295224 tomato callus, TAI	MO Lycopersicon 35 1.3
emb AW032260 AW032260 EST275714 tomato callus, TAl emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprog emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropgb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl	ropane-1-car 35 1.3
emb AF119413 AF119413 Lupinus albus 1-aminocycloprop emb X72676 BJMACC B. juncea mRNA for 1-Aminocycloprop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	ax cDNA clone 35 1.3
 emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclop emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropgb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl 	MU Lycopersicon 35 1.3
emb AF074930 AF074930 Sinapis arvensis 1-aminocycloprogb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprogemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropgb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl	pane-1-carbox 35-1.8
gb L00673 TRBANTA Trypanosoma cruzi antigen tyrosine emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocyclopropemb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocyclopropemb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl	propane-1-carbo 35 1.8
emb AW650504 AW650504 EST328958 tomato germinatin gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	opane-1-car 35 1.8
gb U35779 TAU35779 Triticum aestivum 1-aminocycloprop emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
 emb AQ949419 AQ949419 Sheared DNA-31M1.TR Sheare emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl 	
emb AF119411 AF119411 Lupinus albus 1-aminocycloprop gb U31975 CRU31975 Chlamydomonas reinhardtii alanine emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl	
gb U31975 CRU31975 Chlamydomonas reinhardtii alanine e emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	
emb X87372 LESODCC L.esculentum SodCc;Le;2 gene. emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAl	
emb AW651589 AW651589 EST330043 tomato germinatin emb AW216510 AW216510 EST295224 tomato callus, TAI	aminotransf 34 2.5
50 emb AW216510 AW216510 EST295224 tomato callus, TAl	34 3.4
50 emb AW216510 AW216510 EST295224 tomato callus, TAl	ng seedlings, TA 34 3.4
emb Z11613 VRACCSYNM V.radiata mRNA for ACC syn	
Query= AL049480.183 s at 13880 s at /id source genbanl	
emb cab39611.1 (al049480) possible apospory-associated li	
[arabidopsis thaliana] /blast_score 0 /ec_number /family /cl	hip nova

/gb_link /ncgi (990 letters)

Database: plantfungal 661,018 sequences; 426,114,510 total letters 60

Searching......done

Score 5 Sequences producing significant alignments: (bits) Value emb|Z36544|PCAPOSPA1 P.ciliare (Higgins) apospory associated mRN... 150 4e-85 gb[U13148]PCU13148 Pennisetum ciliare possible apospory-associat... 150 4e-85 dbj[D37938]PENPSBCA Pennisetum ciliare apomixis-associated mRNA. 10 emb|AW985256|AW985256 NXNV 135 A07_F Nsf Xylem Normal wood Verti... 139 1e-58 emb|AI731493|AI731493 BNLGHi9967 Six-day Cotton fiber Gossypium ... 167 1e-58 emb|AI729163|AI729163 BNLGHi12827 Six-day Cotton fiber Gossypium... 170 1e-58 emb|AW257538|AW257538 EST305675 KV2 Medicago truncatula cDNA clo... 140 4e-58 emb|AW398709|AW398709 EST309209 L. pennellii trichome, Cornell U... 173 2e-57 15 emb|AW625795|AW625795 EST319702 tomato radicle, 5 d post-imbibit... 171 4e-57 emb|AW617782|AW617782 EST324181 L. hirsutum trichome, Cornell Un... 172 1e-56 emb|AW399743|AW399743 EST310243 L. pennellii trichome, Cornell U... 173 1e-56 emb|AI489136|AI489136 EST247475 tomato ovary, TAMU Lycopersicon ... 133 1e-55 emb|AW929457|AW929457 EST338245 tomato flower buds 8 mm to pre-a... 171 6e-55 20 emb|AI771804|AI771804 EST252904 tomato ovary, TAMU Lycopersicon ... 133 7e-55 emb|AW649922|AW649922 EST328376 tomato germinating seedlings, TA... 162 1e-54 emb|AW257536|AW257536 EST305673 KV2 Medicago truncatula cDNA clo... 138 9e-54 emb|AV422847|AV422847 AV422847 Lotus japonicus young plants (two... 101 1e-50 emb|AW289757|AW289757 NXNV005C01F Nsf Xylem Normal wood Vertical... 155 le-49 25 emb|AI896074|AI896074 EST265517 tomato callus, TAMU Lycopersicon... 171 4e-49 emb|AW064926|AW064926 ST37E07 Pine TriplEx shoot tip library Pin... 150 6e-48 emb|AW311433|AW311433 sg39c02.yl Gm-c1025 Glycine max cDNA clone... 85 1e-47 emb|AW745200|AW745200 LG1_387_C06.b1_A002 Light Grown 1 (LG1) So... 155 6e-47 emb|AW011598|AW011598 ST22F11 Pine TriplEx shoot tip library Pin... 153 2e-45 30 emb|AW678250|AW678250 WS1_14_G02.b1_A002 Water-stressed 1 (WS1) ... 155 2e-44 emb[AV408421]AV408421 AV408421 Lotus japonicus young plants (two... 101 3e-44 emb[AW216409]AW216409 EST295153 tomato callus, TAMU Lycopersicon... 171 8e-42 emb|AW290828|AW290828 NXNV047D04F Nsf Xylem Normal wood Vertical... 156 9e-42 gb|L38079|L38079 BNAF0477E Mustard flower buds Brassica rapa cDN... 116 1e-41 35 emb|AI896567|AI896567 EST266010 tomato callus, TAMU Lycopersicon... 110 2e-41 emb[AW756192]AW756192 s117c03.y1 Gm-c1036 Glycine max cDNA clone... 161 8e-39 emb|AW707185|AW707185 sk10h04.y1 Gm-c1023 Glycine max cDNA clone... 82 9e-38 emb|AW285821|AW285821 LG1 237 D02.b1 A002 Light Grown 1 (LG1) So... 154 1e-36 emb|AV422428|AV422428 AV422428 Lotus japonicus young plants (two... 94 1e-36 40 gb|L46551|L46551 BNAF1871 Mustard flower buds Brassica rapa cDNA... 153 2e-36 emb|AA660918|AA660918 00815 MtRHE Medicago truncatula cDNA 5' si... 92 1e-34 emb|AW931737|AW931737 EST357580 tomato fruit mature green, TAMU ... 112 1e-34 emb|AW010913|AW010913 ST12H09 Pine TriplEx shoot tip library Pin... 147 2e-34 emb|AW306296|AW306296 se48h02.yl Gm-c1017 Glycine max cDNA clone... 82 2e-32 emb|AW226128|AW226128 ST77F07 Pine TriplEx shoot tip library Pin... 136 2e-31 emb|AI162924|AI162924 A027P14U Hybrid aspen plasmid library Popu... 132 5e-30 emb]AW692441|AW692441 NF051E02ST1F1000 Developing stem Medicago ... 128 7e-29 emb|AW266636|AW266636 L0-1345T3 Ice plant Lambda Uni-Zap XR expr... 125 5e-28 emb|AW730079|AW730079 GA_Ea0027L09 Gossypium arboreum 7-10 dpa ... 112 2e-27 50 emb|AF195243|AF195243 Chlamydomonas reinhardtii apospory-associa... 71 3e-27 emb|AW038730|AW038730 EST280591 tomato mixed elicitor, BTI Lycop... 72 4e-27 emb|AW668439|AW668439 GA_Ea0013P01 Gossypium arboreum 7-10 dpa ... 117 1e-25 gb|BE060242|BE060242 HVSMEg0011K23f Hordeum vulgare pre-anthesis... 69 3e-24 emb|AV392393|AV392393 AV392393 Chlamydomonas reinhardtii C9 Chla... 59 8e-24 55 gb[H75140]H75140 18 PtIFG1 Pinus taeda cDNA clone 0149e, mRNA se... 106 2e-23 emb|AW226319|AW226319 ST81A06 Pine TriplEx shoot tip library Pin... 106 3e-22 emb|AW678374|AW678374 WS1_15_D11.b1_A002 Water-stressed 1 (WS1) ... 70 5e-22 emb|AW678403|AW678403 WS1_15_D11.g1_A002 Water-stressed 1 (WS1) ... 70 5e-22 emb|AW678308|AW678308 WS1_14_G02.g1_A002 Water-stressed 1 (WS1) ... 62 3e-21 60 emb|AQ946977|AQ946977 Sheared DNA-47C11.TF Sheared DNA Trypanoso... 92 8e-18

emb|AW707360|AW707360 832006H03.yl C. reinhardtii CC-125 nutrien... 71 5e-17

	emb AW697995 AW697995 NXNV_079_C06_F Nsf Xylem Normal wood Verti 87 2e-16 emb AV386805 AV386805 AV386805 Chlamydomonas reinhardtii C9 Chla 71 8e-16
	emb AV427771 AV427771 AV427771 Lotus japonicus young plants (two 78 8e-14 emb AW132277 AW132277 sd98h11.yl Gm-c1013 Glycine max cDNA clone 73 1e-13
5	gb[BE020023]BE020023 sm41b06.yl Gm-c1028 Glycine max cDNA clone 73 1e-13
	emb AW759481 AW759481 sl42b05.y1 Gm-c1027 Glycine max cDNA clone 73 1e-13
	gb BE021423 BE021423 sm48h06.y1 Gm-c1028 Glycine max cDNA clone 73 1e-13
	emb AW776929 AW776929 EST335994 DSIL Medicago truncatula cDNA cl 77 1e-13
	emb AU090159 AU090159 AU090159 Hordeum vulgare subsp. vulgare Up 73 2e-13
10	emb AW428681 AW428681 Ljirnpest22-758-d3 Ljirnp Lambda HybriZap 68 3e-13
	emb AA556516 AA556516 371 Loblolly pine C Pinus taeda cDNA clone 76. 5e-13
	emb AW428777 AW428777 Ljirnpest23-872-f2 Ljirnp Lambda HybriZap 67 1e-12
	emb AV391480 AV391480 AV391480 Chlamydomonas reinhardtii C9 Chla 71 2e-12
15	emb AV387347 AV387347 AV387347 Chlamydomonas reinhardtii C9 Chla 71 2e-12 emb AV397825 AV397825 AV397825 Chlamydomonas reinhardtii C9 Chla 71 2e-12
13	emb AW187436 AW187436 BNLGHi5212 Six-day Cotton fiber Gossypium 74 2e-12
	emb AW569198 AW569198 si64a08.yl Gm-r1030 Glycine max cDNA clone 68 3e-12
•	emb AV414298 AV414298 AV414298 Lotus japonicus young plants (two 68 7e-12
	emb AV389349 AV389349 AV389349 Chlamydomonas reinhardtii C9 Chla 62 1e-11
20	emb AV427840 AV427840 AV427840 Lotus japonicus young plants (two 71 1e-11
	emb AV391742 AV391742 AV391742 Chlamydomonas reinhardtii C9 Chla 55 4e-11
	emb AW620239 AW620239 si93e10.yl Gm-c1031 Glycine max cDNA clone 66 5e-10
	emb AV424492 AV424492 AV424492 Lotus japonicus young plants (two 63 3e-09
25	emb AW981390 AW981390 EST392543 DSIL Medicago truncatula cDNA cl 61 7e-09 emb AW040546 AW040546 EST283326 tomato mixed elicitor, BTI Lycop 43 1e-08
23	emb AW040546 AW040546 EST283326 tomato mixed elicitor, BTI Lycop 43 1e-08 emb AW624837 AW624837 EST313654 tomato radicle, 5 d post-imbibit 43 1e-08
	emb AI491050 AI491050 EST241759 tomato shoot, Cornell Lycopersic 43 1e-08
	emb AW096575 AW096575 EST289755 tomato mixed elicitor, BTI Lycop 43 1e-08
	emb AW217734 AW217734 EST296448 tomato flower buds 8 mm to pre-a 43 1e-08
30	emb AI778221 AI778221 EST259100 tomato susceptible, Cornell Lyco 43 1e-08
	emb AW219376 AW219376 EST301954 tomato root during/after fruit s 43 1e-08
	emb AW399557 AW399557 EST310045 L. pennellii trichome, Cornell U 43 1e-08
•	emb AW755022 AW755022 PC09G01 Pine TriplEx pollen cone library P 60 2e-08
35	emb AW255147 AW255147 ML144 peppermint glandular trichome Mentha 43 4e-08
33	emb AW040573 AW040573 EST283353 tomato mixed elicitor, BTI Lycop 41 4e-08 emb AW933183 AW933183 EST359026 tomato fruit mature green, TAMU 59 5e-08
	emb AW399558 AW399558 EST310046 L, pennellii trichome, Cornell U 42 7e-08
	emb AW266367 AW266367 L30-3121T3 Ice plant Lambda Uni-Zap XR exp 56 6e-07
	emb AI896247 AI896247 EST265690 tomato callus, TAMU Lycopersicon 55 1e-06
40	gb BE059001 BE059001 sn23g06.y1 Gm-c1016 Glycine max cDNA clone 54 2e-06
	emb AW132969 AW132969 se12g02.yl Gm-c1013 Glycine max cDNA clone 53 4e-06
	emb AW704585 AW704585 sk54a04.yl Gm-c1019 Glycine max cDNA clone 52 5e-06
	emb AV388833 AV388833 AV388833 Chlamydomonas reinhardtii C9 Chla 52 5e-06
45	emb AW729558 AW729558 GA_Ea0025G01 Gossypium arboreum 7-10 dpa 51 2e-05
43	emb AW681073 AW681073 WS1_8_H01.b1_A002 Water-stressed 1 (WS1) S 50 4e-05
	Query= AL022373.295_at 14278_at /id_source genbank /description
	emb caa18503.1 (al022373) hypothetical protein [arabidopsis thaliana]
	/blast_score 0 /ec number /family /chip nova /gb link
50	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb al022373 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al022373
	(1518 letters)
55	Databass plantfungel
55	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
60	Score E
	Sequences producing significant alignments: (bits) Value

	gb BE052481 BE052481 GA_Ea0034B15f Gossypium arboreum 7-10 dpa 248 8e-65
	emb AW933316 AW933316 EST359159 tomato fruit mature green, TAMU 127 2e-28
	emb AI897506 AI897506 EST266949 tomato ovary, TAMU Lycopersicon 120 3e-26
5	emb AI055630 AI055630 coau0004J11 Cotton Boll Abscission Zone cD 113 4e-24
	emb AW032891 AW032891 EST276450 tomato callus, TAMU Lycopersicon 103 4e-21
	emb AV427652 AV427652 AV427652 Lotus japonicus young plants (two 88 2e-16
	emb AW307385 AW307385 sf56c11.yl Gm-c1009 Glycine max cDNA clone 72 1e-11
	emb AW726477 AW726477 GA Ea0021M14 Gossypium arboreum 7-10 dpa 60 5e-10
10	emb AW747181 AW747181 WS1 66 B09.b1 A002 Water-stressed 1 (WS1) 59 2e-09
	emb AW091888 AW091888 EST285068 tomato mixed elicitor, BTI Lycop 53 5e-08
	emb AW306935 AW306935 sf50f05.yl Gm-c1009 Glycine max cDNA clone 58 1e-07
	emb AW216365 AW216365 EST295109 tomato callus, TAMU Lycopersicon 58 1e-07
	emb AW306722 AW306722 sf47e06.yl Gm-c1009 Glycine max cDNA clone 58 1e-07
15	emb AW221657 AW221657 EST298468 tomato fruit red ripe, TAMU Lyco 58 2e-07
13	
•	
	emb AW222358 AW222358 EST299169 tomato fruit red ripe, TAMU Lyco 43 0.005
	emb AW738043 AW738043 EST339470 tomato flower buds, anthesis, Co 43 0.005
20	emb AW774865 AW774865 EST334016 KV3 Medicago truncatula cDNA clo 43 0.007
20	emb AW832220 AW832220 sm21a01.yl Gm-c1027 Glycine max cDNA clone 38 0.011
	emb AW931008 AW931008 EST356851 tomato fruit mature green, TAMU 39 0.089
	emb AW396940 AW396940 sg65b05.yl Gm-c1007 Glycine max cDNA clone 39 0.089
•	emb AQ324712 AQ324712 mgxb0019H15r CUGI Rice Blast BAC Library P 37 0.12
	gb[M96818]EUPTBPA Euplotes crassus macronuclear 51 kDa telomere 39 0.12
25	emb AV428867 AV428867 AV428867 Lotus japonicus young plants (two 36 0.60
	gb BE122206 BE122206 894018B07.x1 C. reinhardtii CC-1690, normal 36 0.83
	emb AW757802 AW757802 874003G04.x1 C. reinhardtii CC-1690, Lambd 36 0.83
	emb AW720369 AW720369 LjNEST21g3r Lotus japonicus nodule library 36 0.83
	emb Z75009 SCYOR101W S.cerevisiae chromosome XV reading frame OR 35 1.6
30	gb U32307 SCU32307 Saccharomyces cerevisiae oligosaccharyltransf 35 1.6
•	emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo 35 1.6
	emb Z75010 SCYOR102W S.cerevisiae chromosome XV reading frame OR 35 1.6
	emb AW573717 AW573717 EST316308 GVN Medicago truncatula cDNA clo 35 2.1
	emb AL049769 SPBC9B6 S.pombe chromosome II cosmid c9B6. 34 2.9
35	emb AW395612 AW395612 sg73b12.yl Gm-c1007 Glycine max cDNA clone 34 4.0
	emb Z69380 SPAC4H3 S.pombe chromosome I cosmid c4H3. 34 4.0
	emb AW688677 AW688677 NF010D01ST1F1000 Developing stem Medicago 34 4.0
	emb AV425510 AV425510 AV425510 Lotus japonicus young plants (two 33 5.6
	emb AV424161 AV424161 AV424161 Lotus japonicus young plants (two 33 5.6
40	emb AL354513 LMFL6783 Leishmania major Friedlin cosmid L6783, PR 33 5.6
	emb AQ940380 AQ940380 Sheared DNA-33M12.TF Sheared DNA Trypanoso 33 5.6
	emb AW703257 AW703257 TgESTzz82h11.y1 TgRH*-Tachyzoite cDNA Toxo 33 5.6
	emb AC004688 AC004688 Plasmodium falciparum chromosome 12 clone 33 5.6
	emb AV427411 AV427411 AV427411 Lotus japonicus young plants (two 33 5.6
45	emb A86068 A86068 Sequence 727 from Patent EP0866129. 33 5.6
	emb AW690594 AW690594 NF031E09ST1F1000 Developing stem Medicago 33 5.6
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S 33 5.6
	emb AV423586 AV423586 AV423586 Lotus japonicus young plants (two 33 5.6
	emb AV426453 AV426453 AV426453 Lotus japonicus young plants (two 33 5.6
50	gb BE055549 BE055549 GA_Ea0034M01f Gossypium arboreum 7-10 dpa 33 5.6
	gb U16653 YLU16653 Yarrowia lipolytica Pay2p (PAY2) gene, comple 33 5.6
	emb AW719319 AW719319 LjNEST2f7r Lotus japonicus nodule library, 33 5.6
	emb AW696984 AW696984 NF111A10ST1F1072 Developing stem Medicago 33 7.6
	gb[L07391[NEUNIT6X Neurospora crassa nitrite reductase (nit-6) g 33 7.6
55	emb AQ645907 AQ645907 RPCI93-DpnII-28N21.TV RPCI93-DpnII Trypano 33 7.6
	Query= AC005956.54_at 14320_at /id_source genbank /description
	gb aad23719.1 ac005956_8 (ac005956) putative ring zinc finger protein
	[arabidopsis thaliana] /blast_score 1.00e-110 /ec_number /family
60	/chip nova /gb_link
	http://www3.ncbi.nlm.nih.gov/htbin-

post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005956| /ncgi http://www.ncgr.org/cgi-bin/ff?ac005956 (711 letters)

5 Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

10 Score

Sequences producing significant alignments:

(bits) Value emb|AI895373|AI895373 EST264816 tomato callus, TAMU Lycopersicon... 108 6e-32 emb|AW032769|AW032769 EST276328 tomato callus, TAMU Lycopersicon... 108 6e-32 15 emb|AI731540|AI731540 BNLGHi10032 Six-day Cotton fiber Gossypium... 82 2e-21 emb|AW775221|AW775221 EST331943 GVN Medicago truncatula cDNA clo... 72 2e-19 gb|BE124796|BE124796 EST393831 GVN Medicago truncatula cDNA clon... 72 2e-19 emb|AW399006|AW399006 EST309506 L. pennellii trichome, Cornell U... 77 1e-17 emb|AW442210|AW442210 EST311606 tomato fruit red ripe, TAMU Lyco... 75 2e-17 20 emb|AW703663|AW703663 sk11g09.yl Gm-c1023 Glycine max cDNA clone... 69 2e-16 emb|AI727683|AI727683 BNLGHi8604 Six-day Cotton fiber Gossypium ... 79 3e-14 emb|AI729941|AI729941 BNLGHi5757 Six-day Cotton fiber Gossypium ... 79 3e-14 emb|AW329822|AW329822 N201096e rootphos(-) Medicago truncatula c... 72 5e-14 emb|AI727293|AI727293 BNLGHi7657 Six-day Cotton fiber Gossypium ... 78 5e-14 25 emb|AF150724|AF150724 AF150724 Gossypium hirsutum 24 days postan... 78 5e-14 emb|AW219270|AW219270 EST301752 tomato root during/after fruit s... 74 7e-14 emb|AI730749|AI730749 BNLGHi7802 Six-day Cotton fiber Gossypium ... 78 1e-13 emb|AW219137|AW219137 EST301619 tomato root during/after fruit s... 75 1e-13 gb|BE033932|BE033932 MG02C06 MG Mesembryanthemum crystallinum cD... 77 1e-13 30 emb|AW508608|AW508608 si34c01.yl Gm-r1030 Glycine max cDNA clone... 64 2e-13 emb|AW220356|AW220356 EST302839 tomato root during/after fruit s... 77 2e-13 emb|AW267973|AW267973 EST306195 DSIR Medicago truncatula cDNA cl... 75 2e-13 emb|AV413409|AV413409 AV413409 Lotus japonicus young plants (two... 76 3e-13 emb|AW931758|AW931758 EST357601 tomato fruit mature green, TAMU ... 75 5e-13 35 emb|AI443724|AI443724 sa45b08.yl Gm-c1004 Glycine max cDNA clone... 75 5e-13 emb|AI443646|AI443646 sa42f12.yl Gm-c1004 Glycine max cDNA clone... 75 5e-13 emb|AW682867|AW682867 NF001B05LF1F1044 Developing leaf Medicago ... 75 6e-13 gb|BE059421|BE059421 sn30h03.yl Gm-c1016 Glycine max cDNA clone ... 75 6e-13 40 emb|AW348175|AW348175 GM210001A21E9R Gm-r1021 Glycine max cDNA 3... 75 6e-13 emb|AW279542|AW279542 sf90h11.yl Gm-c1019 Glycine max cDNA clone... 75 6e-13 emb|AW277724|AW277724 sf85g08.yl Gm-c1019 Glycine max cDNA clone... 74 9e-13 emb|AV416001|AV416001 AV416001 Lotus japonicus young plants (two... 74 9e-13 emb|AW223952|AW223952 EST300763 tomato fruit red ripe, TAMU Lyco... 73 2e-12 45 emb|AW622165|AW622165 EST312963 tomato root during/after fruit s... 73 2e-12 emb|AW747694|AW747694 WS1_75_E01.g1_A002 Water-stressed 1 (WS1) ... 73 2e-12 emb[AW185181|AW185181 se88a05.y1 Gm-c1023 Glycine max cDNA clone... 73 2e-12 emb|AW223330|AW223330 EST300141 tomato fruit red ripe, TAMU Lyco... 73 2e-12 emb|AW597455|AW597455 sj85c04.yl Gm-c1034 Glycine max cDNA clone... 69 2e-12 50 emb|AZ044879|AZ044879 Gm_UMb001_030_J12R UMN Soybean BAC Library... 73_3e-12 emb|AW681172|AW681172 WS1_9_C04.g1_A002 Water-stressed 1 (WS1) S... 73 3e-12 emb|AW680957|AW680957 WS1_9_C04.b1_A002 Water-stressed 1 (WS1) S... 73 3e-12 emb|AW622674|AW622674 EST313474 tomato root during/after fruit s... 72 4e-12 emb|AW622457|AW622457 EST313245 tomato root during/after fruit s... 72 4e-12 55 emb|AW568305|AW568305 si58a10.yl Gm-r1030 Glycine max cDNA clone... emb|AW443687|AW443687 EST308617 tomato mixed elicitor, BTI Lycop... 72 6e-12 emb|AV412576|AV412576 AV412576 Lotus japonicus young plants (two... 72 6e-12 emb|AW720382|AW720382 LjNEST22a5r Lotus japonicus nodule library... 72 6e-12 emb|AW351001|AW351001 GM210010B20A4R Gm-r1021 Glycine max cDNA 3... 72 6e-12

emb|AW267780|AW267780 EST305908 DSIR Medicago truncatula cDNA cl... 71 8e-12 emb|AV422284|AV422284 AV422284 Lotus japonicus young plants (two... 56 9e-12

60

```
gb|BE052202|BE052202 GA Ea0034A22f Gossypium arboreum 7-10 dpa ... 71 le-11
      emb|AI782281|AI782281 EST263160 tomato susceptible, Cornell Lyco... 71 1e-11
      gb|BE053763|BE053763 GA Ea0032N22f Gossypium arboreum 7-10 dpa ... 71 1e-11
      emb|AW730444|AW730444 GA Ea0026G01 Gossypium arboreum 7-10 dpa ... 71 1e-11
      gb|BE054849|BE054849 GA Ea0033N22f Gossypium arboreum 7-10 dpa ... 71 1e-11
      emblAA739669|AA739669 434 PtIFG2 Pinus taeda cDNA clone 8721M 3'... 71 1e-11
      10
      emb|AI484163|AI484163 EST248970 tomato resistant, Cornell Lycope... 69 1e-11
      emb|AW981615|AW981615 PC14F10 Pine TriplEx pollen cone library P... 70 2e-11
      emb|AI727213|AI727213 BNLGHi7517 Six-day Cotton fiber Gossypium ... 70 2e-11
      emb|AW218481|AW218481 EST303664 tomato radicle, 5 d post-imbibit... 70 2e-11
      gb|BE124891|BE124891 EST393926 GVN Medicago truncatula cDNA clon... 70 2e-11
15
      emb|AI731895|AI731895 BNLGHil1234 Six-day Cotton fiber Gossypium... 70 2e-11
      emb|AW459552|AW459552 sh44b12.y1 Gm-c1017 Glycine max cDNA clone... 70 2e-11
      emb|AI897158|AI897158 EST266601 tomato ovary, TAMU Lycopersicon ... 70 2e-11
      emb|AW219915|AW219915 EST302398 tomato root during/after fruit s... 70 2e-11
      emb|AW100926|AW100926 sd63c08.yl Gm-c1008 Glycine max cDNA clone... 70 2e-11
20
      gb|BE055048|BE055048 GA_Ea0001G22f Gossypium arboreum 7-10 dpa ... 70 2e-11
      emb|AW667875|AW667875 GA_Ea0011A20 Gossypium arboreum 7-10 dpa ... 70 2e-11
      emb|AI442790|AI442790 sa26el1.x1 Gm-c1004 Glycine max cDNA clone... 70 2e-11
      emb|AW559695|AW559695 EST314687 DSIR Medicago truncatula cDNA cl... 70 2e-11
      emb|AW441213|AW441213 EST310609 tomato fruit red ripe, TAMU Lyco... 70 2e-11
25
      emb|AW219914|AW219914 EST302397 tomato root during/after fruit s... 70 2e-11
      emb|AW108574|AW108574 gate0001G22f Gossypium arboreum 7-10 dpa f... 70 2e-11
      emb|AI725540|AI725540 BNLGHi12062 Six-day Cotton fiber Gossypium... 70 2e-11
      emb|AI162536|AI162536 A019P13U Hybrid aspen plasmid library Popu... 70 2e-11
      emb|AV422720|AV422720 AV422720 Lotus japonicus young plants (two... 69 3e-11
30
     emb[Y14573]HVCH4H Hordeum vulgare DNA for chromosome 4H.
                                                                     69 3e-11
      emb|AW348721|AW348721 GM210003A22A2R Gm-r1021 Glycine max cDNA 3... 69 3e-11
      emb|Al900335|Al900335 sc04c07.yl Gm-c1012 Glycine max cDNA clone... 69 3e-11
      emb|AW746279|AW746279 WS1 40 F11.g1 A002 Water-stressed 1 (WS1) ... 69 4e-11
     emb|AW981608|AW981608 PC14F03 Pine TriplEx pollen cone library P... 69 4e-11
     emb|AW685535|AW685535 NF028H02NR1F1000 Nodulated root Medicago t... 69 4e-11
      emb|AI726225|AI726225 BNLGHi5312 Six-day Cotton fiber Gossypium ... 69 4e-11
      emb|AW980916|AW980916 EST392069 GVN Medicago truncatula cDNA clo... 68 5e-11
      emb|AI441828|AI441828 sa47h04.yl Gm-c1004 Glycine max cDNA clone... 68 5e-11
      emb|AI897713|AI897713 EST267156 tomato ovary, TAMU Lycopersicon ... 68 7e-11
40
      emb|AI485408|AI485408 EST243729 tomato ovary, TAMU Lycopersicon ... 68 7e-11
      emb|AI483478|AI483478 EST249299 tomato ovary, TAMU Lycopersicon ... 68 7e-11
      emb|AW031045|AW031045 EST274352 tomato callus, TAMU Lycopersicon... 68 7e-11
     emb|AI483537|AI483537 EST249386 tomato ovary, TAMU Lycopersicon ... 68 7e-11
     gb|BE034706|BE034706 ML03C10 ML Mesembryanthemum crystallinum cD... 68 1e-10
45
     emb|AW980667|AW980667 EST391820 GVN Medicago truncatula cDNA clo... 67 le-10
      emb|AW349023|AW349023 GM210003B22B3R Gm-r1021 Glycine max cDNA 3... 67 1e-10
      emb|AI794756|AI794756 sb68g04.yl Gm-c1019 Glycine max cDNA clone... 67 le-10
      emb|AW984973|AW984973 NXNV 118 A01 F Nsf Xylem Normal wood Verti... 66 3e-10
     emb|AW737702|AW737702 EST339129 tomato flower buds, anthesis, Co... 66 3e-10
50
     emb|AW666412|AW666412 sk36c04.y1 Gm-c1028 Glycine max cDNA clone... 66 3e-10
     gbBE034328BE034328 MH03C07 MH Mesembryanthemum crystallinum cD... 66 3e-10
     Query= X86958.1_at 14763_at /id source genbank /description
     emb|caa60521.1| (x86958) protein kinase catalytic domain (fragment)
55
      [arabidopsis thaliana] /blast_score 1.00e-25 /ec_number /family
     kinase/chip nova/gb link
     http://www3.ncbi.nlm.nih.gov/htbin-
     post/entrez/query?db=n&form=6&dopt=g&uid=gb|x86958|/ncgi
     http://www.ncgr.org/cgi-bin/ff?x86958
60
          (168 letters)
```

5

Database: plantfungal 661,018 sequences; 426,114,510 total letters

Searching......done

Score E

Sequences producing significant alignments:

(bits) Value

emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 114 3e-26 10 emb|AW719817|AW719817 LjNEST10E2r Lotus japonicus nodule library... 113 6e-26 emb|AI727531|AI727531 BNLGHi8333 Six-day Cotton fiber Gossypium ... 107 3e-24 emb|AW266829|AW266829 L48-172T3 Ice plant Lambda Uni-Zap XR expr... 102 1e-22 emb|AW756795|AW756795 sl27c08.yl Gm-c1027 Glycine max cDNA clone... 102 2e-22 emb|AI901283|AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone... 98 3e-21 15 gb[BE021054[BE021054 sm47c02.yl Gm-c1028 Glycine max cDNA clone ... 97 8e-21 emb|AW597214|AW597214 si71g06.yl Gm-c1031 Glycine max cDNA clone... 94 5e-20 emb|AI781266|AI781266 EST262145 tomato susceptible, Cornell Lyco... 92 1e-19 gb|BE058691|BE058691 sn19e05.yl Gm-c1016 Glycine max cDNA clone ... 91 3e-19 20 emb|AW279355|AW279355 sf65g10.yl Gm-c1013 Glycine max cDNA clone... 91 5e-19 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 90 9e-19 emb|AW982539|AW982539 HVSMEg0003116f Hordeum vulgare pre-anthesi... 89 2e-18 emb|AI728857|AI728857 BNLGHi11808 Six-day Cotton fiber Gossypium... 89 2e-18 emb|AW329840|AW329840 N201116e rootphos(-) Medicago truncatula c... 88 2e-18 25 emb|AW509134|AW509134 sh30e11.yl Gm-c1017 Glycine max cDNA clone... 87 6e-18 emb[AW687262]AW687262 NF007G02RT1F1018 Developing root Medicago ... 86 1e-17 emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycope... 86 1e-17 emb|AW687777|AW687777 NF013D03RT1F1028 Developing root Medicago ... 86 1e-17 emb|AW667985|AW667985 GA Ea0012C15 Gossypium arboreum 7-10 dpa ... 85 2e-17 30 emb|AW979578|AW979578 EST341174 tomato root deficiency, Cornell ... 85 2e-17 emb|AW223870|AW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 85 3e-17 emb|AW306841|AW306841 sf49d02.yl Gm-c1009 Glycine max cDNA clone... 85 3e-17 gb[BE058485]BE058485 sn16g12.y1 Gm-c1016 Glycine max cDNA clone ... 51 6e-17 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 59 7e-17 35 emb|AW761546|AW761546 sl69a09.y1 Gm-c1027 Glycine max cDNA clone... 83 7e-17 emb|AW982145|AW982145 SsS0075 Suaeda salsa ZAP cDNA library Suae... 83 1e-16 emb|AI938653|AI938653 sb56g02.yl Gm-c1018 Glycine max cDNA clone... 82 1e-16 emb|AW132502|AW132502 se04h04.y1 Gm-c1013 Glycine max cDNA clone... 82 1e-16 emb|AW092144|AW092144 EST285240 tomato mixed elicitor, BTI Lycop... 81 3e-16 40 emb|AW040672|AW040672 EST283536 tomato mixed elicitor, BTI Lycop... 81 3e-16 emb|AW039328|AW039328 EST281585 tomato mixed elicitor, BTI Lycop... 81 3e-16 emb|AW220489|AW220489 EST297042 tomato fruit mature green, TAMU ... 81 4e-16 emblAW220490|AW220490 EST297043 tomato fruit mature green, TAMU ... 81 4e-16 emb|AW220491|AW220491 EST297044 tomato fruit mature green, TAMU ... 81 4e-16 45 emb|AW758828|AW758828 NXNV_091_B05_F Nsf Xylem Normal wood Verti... 52 4e-16 emb|AI896462|AI896462 EST265893 tomato callus, TAMU Lycopersicon... 81 5e-16 emb|AW394569|AW394569 sh32f08.yl Gm-c1017 Glycine max cDNA clone... 81 5e-16 emb|AJ271954|TCA271954 Theobroma cacao microsatellite DNA, clone... 65 6e-16 emb|AW685205|AW685205 NF026F12NR1F1000 Nodulated root Medicago t... 79 1e-15 50 emb|AW568064|AW568064 si68a06.yl Gm-r1030 Glycine max cDNA clone... 53 2e-15 emb|AF131222|AF131222 Lophopyrum elongatum protein serine/threon... 78 2e-15 gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 78 3e-15 emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 78 3e-15 emb|AW684940|AW684940 NF023C12NR1F1000 Nodulated root Medicago t... 77 4e-15 emb|AW284352|AW284352 LG1 275 D12.g1 A002 Light Grown 1 (LG1) So... 77 4e-15 55 emb|AI896953|AI896953 EST266396 tomato callus, TAMU Lycopersicon... 57 5e-15 emb|AI727374|AI727374 BNLGHi7892 Six-day Cotton fiber Gossypium ... 77 6e-15 emb[AW926765]AW926765 HVSMEg0008C18 Hordeum vulgare pre-anthesis... 77 6e-15 emb[AW278089]AW278089 sf39e12.y1 Gm-c1009 Glycine max cDNA clone... 50 6e-15 60 emb|AI794805|AI794805 sb70f02.yl Gm-c1019 Glycine max cDNA clone... 50 7e-15 emb[AW774553]AW774553 EST333704 KV3 Medicago truncatula cDNA clo... 76 8e-15

	emb AW509847 AW509847 ga66e01.yl Moss EST library PPU Physcomitr 76 8e-15
	emb AI967314 AI967314 Ljimpest00-017 Ljimp Lambda HybriZap two 50 1e-14
	emb AW980333 AW980333 EST391486 GVN Medicago truncatula cDNA clo 76 1e-14
	emb AW925036 AW925036 WS1_74_F04.b1_A002 Water-stressed 1 (WS1) 76 2e-14
5	emb AW437900 AW437900 ST78A08 Pine TriplEx shoot tip library Pin 76 2e-14
	gb[U59318]LEU59318 Lycopersicon esculentum serine/threonine prot 51 2e-14
	gb U13923 LEU13923 Lycopersicon pimpinellifolium serine/threonin 50 2e-14
	emb AI960995 AI960995 sc93g03.y1 Gm-c1019 Glycine max cDNA clone 52 2e-14
	gb[U59317]LPU59317 Lycopersicon pimpinellifolium serine/threonin 50 4e-14
10	emb AW034255 AW034255 EST277826 tomato callus, TAMU Lycopersicon 74 6e-14
	emb[AW704952]AW704952 sk56f04.yl Gm-c1019 Glycine max cDNA clone 74 6e-14
	emb AI729561 AI729561 BNLGHi13630 Six-day Cotton fiber Gossypium 67 6e-14
	emb[AW233982]AW233982 sf32g05.yl Gm-c1028 Glycine max cDNA clone 73 8e-14
	gb[U93048]DCU93048 Daucus carota somatic embryogenesis receptor 73 8e-14
15	emb AW694732 AW694732 NF079D07ST1F1061 Developing stem Medicago 73 8e-14
13	emb AW621923 AW621923 EST312721 tomato root during/after fruit s 73 8e-14
	emb A67797 A67797 Sequence 2 from Patent WO9743427. 73 8e-14
	emb AW666082 AW666082 sk31h04.y1 Gm-c1028 Glycine max cDNA clone 73 8e-14
20	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei 73 8e-14
20	emb AW621294 AW621294 EST312092 tomato root during/after fruit s 73 8e-14
	emb AW648736 AW648736 EST327106 tomato germinating seedlings, TA 51 8e-14
	emb AI896006 AI896006 EST265449 tomato callus, TAMU Lycopersicon 50 9e-14
	emb AF220602 AF220602 Lycopersicon pimpinellifolium Rio Grande 7 50 9e-14
05	emb AF220603 AF220603 Lycopersicon esculentum VFNT Cherry Pto lo 50 9e-14
25	gb T14833 T14833 crs280 lambdaZAPST Ricinus communis cDNA clone 47 1e-13
	emb AI938710 AI938710 sb57g07.yl Gm-c1018 Glycine max cDNA clone 49 1e-13
	emb AI896277 AI896277 EST265720 tomato callus, TAMU Lycopersicon 73 le-13
	emb AW267961 AW267961 EST306183 DSIR Medicago truncatula cDNA cl 48 1e-13
••	emb AI781597 AI781597 EST262476 tomato susceptible, Cornell Lyco 72 1e-13
30	emb AW201545 AW201545 sf04d10.yl Gm-c1027 Glycine max cDNA clone 72 1e-13
	emb AW621706 AW621706 EST312504 tomato root during/after fruit s 72 2e-13
	emb A67796 A67796 Sequence 1 from Patent WO9743427. 72 2e-13
	emb AW429258 AW429258 EST306714 tomato flower buds 0-3 mm, Corne 72 2e-13
	emb AI898120 AI898120 EST267563 tomato ovary, TAMU Lycopersicon 48 3e-13
35	emb AW617954 AW617954 EST314028 L. pennellii trichome, Cornell U 71 3e-13
	emb AW029819 AW029819 EST273074 tomato callus, TAMU Lycopersicon 48 3e-13
	emb AI485223 AI485223 EST243527 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI485585 AI485585 EST243906 tomato ovary, TAMU Lycopersicon 71 4e-13
40	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI483733 AI483733 EST249604 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI484550 AI484550 EST242780 tomato ovary, TAMU Lycopersicon 71 4e-13
45	emb AI487264 AI487264 EST245586 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb Al898374 Al898374 EST267817 tomato ovary, TAMU Lycopersicon 71 4e-13
	emb AI483732 AI483732 EST249603 tomato ovary, TAMU Lycopersicon 71 4e-13
	Query= M96073.6_s_at 14838_s_at /id_source genbank /description
50	gb aaa32835.1 (m96073) phosphoribosylanthranilate transferase
	[arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
	/gb_link /ncgi
	(1602 letters)
55	Database: plantfungal
	661,018 sequences; 426,114,510 total letters
	Searchingdone
	-
60 i	Score E
	Sequences producing significant alignments: Ohits) Value

```
emb|AW687938|AW687938 NF001B11ST1F1000 Developing stem Medicago ... 393 e-108
      emblAW039382|AW039382 EST281639 tomato mixed elicitor, BTI Lycop... 369 e-101
      emb|AW096850|AW096850 EST46F4 potato shoot cDNA library Solanum ... 263 2e-69
      emblAW688778|AW688778 NF011E05ST1F1000 Developing stem Medicago ... 244 1e-65
      emb|AW906002|AW906002 EST342043 potato stolon, Cornell Universit... 234 6e-63
      emb|AI855689|AI855689 sc23a07.yl Gm-c1013 Glycine max cDNA clone... 191 1e-47
      emb|AW622744|AW622744 EST306881 tomato flower buds 3-8 mm, Corne... 171 2e-41
      emb|AW041025|AW041025 EST283889 tomato mixed elicitor, BTI Lycop... 171 2e-41
10
      emb|AL023554|SPBC16G5 S.pombe chromosome II cosmid c16G5.
      gb|BE035432|BE035432 MO05D07 MO Mesembryanthemum crystallinum cD... 111 1e-23
      emb|AJ273068|AJ273068 AJ273068 Metarhizium anisopliae ARSEF 2575... 54 2e-16
      emb|AV412566|AV412566 AV412566 Lotus japonicus young plants (two... 78 2e-16
15
      emb|AV421776|AV421776 AV421776 Lotus japonicus young plants (two... 72 4e-13
      gb[U28372[YSCD9476 Saccharomyces cerevisiae chromosome IV cosmid... 49 8e-09
      emb[X04273|SCTRP4 Yeast TRP4 gene for anthranilate phosphoribosy... 49 9e-09
      emblAO874893|AO874893 V118C3 mTn-3xHA/lacZ Insertion Library, st... 49 1e-07
      emb|AJ228925|AJ228925 AJ228925 Barley leaf, 8 day old seedling H... 57 4e-07
20
      emb|AW220409|AW220409 EST302892 tomato root during/after fruit s... 53 5e-06
      emb|AW737074|AW737074 CAF50 Peronospora parasitica cDNA-AFLP fra... 46 8e-04
      emb|X73297|SCSETRP4 S.cerevisiae spacer element.
                                                             29 0.002
      gb[U10274|SCU10274 Saccharomyces cerevisiae thioredoxin reductas... 44 0.004
      emb|AW933535|AW933535 EST359294 tomato fruit mature green, TAMU ... 38 0.016
25
      emblAW922212|AW922212 DG1 17 B11.b1 A002 Dark Grown 1 (DG1) Sorg... 41 0.027
      gb|BE125449|BE125449 DG1 25 B11.b1 A002 Dark Grown 1 (DG1) Sorgh... 41 0.027
      emb|AV407038|AV407038 AV407038 Lotus japonicus young plants (two... 40 0.037
      emb|AI730383|AI730383 BNLGHi6768 Six-day Cotton fiber Gossypium ... 40 0.037
      emb|AW201070|AW201070 se97e05.yl Gm-c1027 Glycine max cDNA clone... 40 0.050
30
      dbj|E08275|E08275 cDNA encoding cystathionine gamma-lyase.
                                                                 37 0.46
      dbj|E08276|E08276 gDNA encoding cystathionine gamma-lyase.
      emb|AL113519|CNS01AXJ Botrytis cinerea strain T4 cDNA library un... 36 0.88
      emb|Z31724|PCREPELEM P.chrysosporium DNA for repetitive element.
      emb|AW695815|AW695815 NF099E03ST1F1021 Developing stem Medicago ... 34 1.4
35
      emb|A46806|A46806 Sequence 3 from Patent EP0684312.
                                                                35 1.7
      emb|Z37978|NTCYCMRN Nicotiana tabacum mRNA for cyclin B1 (cycB1 ... 35 1.7
      emb|A46810|A46810 Sequence 7 from Patent EP0684312.
      emblAL354572|LMFL5808 Leishmania major Friedlin chromosome 19 co... 35 2.3
40
      emb|AW661030|AW661030 832009F12.x1 C. reinhardtii CC-125 nutrien... 34 3.1
      emb|AQ447557|AQ447557 mgxb0008C17f CUGI Rice Blast BAC Library P... 34 3.1
      emb|AW257438|AW257438 EST305575 KV2 Medicago truncatula cDNA clo... 34 3.1
      emb|AW563834|AW563834 LG1 272 A11.b1 A002 Light Grown 1 (LG1) So... 34 3.1
45
      emb|AQ654417|AQ654417 Sheared DNA-20C20.TF Sheared DNA Trypanoso... 34 4.3
      emb|AW756224|AW756224 sl17f04.yl Gm-c1036 Glycine max cDNA clone... 34 4.3
      emb|X89715|SCAOGENES S.cerevisiae AOB567, AOF1001, AOE110, AOE26... 34 4.3
      emb|AF134853|AF134853 Cuphea hookeriana acyl-ACP carrier protein... 34 4.3
      emb|Z74896|SCYOL154W S.cerevisiae chromosome XV reading frame OR... 34 4.3
50
      gb[U15935]CWKAS3A Cuphea wrightii beta-ketoacyl-ACP synthase III... 34 4.3
      gb|BE033595|BE033595 MF04D10 MF Mesembryanthemum crystallinum cD... 34 4.3
      emb|AQ952764|AQ952764 Sheared DNA-43G7.TR Sheared DNA Trypanosom... 33 5.9
      emb[X61281]PBPOLII9 P.berghei RNA polymerase largest subunit.
      emb|Z36097|SCYBR228W S.cerevisiae chromosome II reading frame OR... 33 5.9
55
      emb|AL113095|CNS01ALR Botrytis cinerea strain T4 cDNA library un... 33 5.9
      gb[U36470[NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu... 33 5.9
      emb|Z78011|ANAXHA A.niger CBS 120.49 axhA gene.
                                                                33 5.9
      gb|BE023153|BE023153 sm79a01.yl Gm-c1015 Glycine max cDNA clone ... 33 5.9
      emb|X71807|ANUAPA A.nidulans uapA gene for uric acid-xanthine pe... 33 5.9
60
      emb|AI213031|AI213031 y6f05a1.rl Aspergillus nidulans 24hr asexu... 33 5.9
      emb|AQ874871|AQ874871 V117H8 mTn-3xHA/lacZ Insertion Library, st... 26 6.5
```

-WO-02/22675 - -PCT/US01/28506

```
gb[U18839]SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 33 8.1
      emb|AF006304|AF006304 Saccharomyces cerevisiae protein tyrosine ... 33 8.1
      gb|U18814|SCE3612 Saccharomyces cerevisiae chromosome V lambda c... 33 8.1
      emb|AW719293|AW719293 LjNEST C6r Lotus japonicus nodule library,... 33 8.1
      emb|AI441951|AI441951 sa83b07.y1 Gm-c1004 Glycine max cDNA clone... 33 8.1
      emblAI443684|AI443684 sa50b09.yl Gm-c1004 Glycine max cDNA clone... 33 8.1
      emb|AW932067|AW932067 EST357910 tomato fruit mature green, TAMU ... 33 8.1
      emb|AW720549|AW720549 LjNEST10b1rc Lotus japonicus nodule librar... 33 8.1
      emb|AW706285|AW706285 sj54d11.yl Gm-c1033 Glycine max cDNA clone... 33 8.1
10
      emb|Z69368|SPAC27F1 S.pombe chromosome I cosmid c27F1.
      emb|X55664|SVPEPCA Sorghum vulgare mRNA for phosphoenolpyruvate ... 33 8.1
      emb|AW299016|AW299016 EST305690 KV2 Medicago truncatula cDNA clo... 33 8.1
      emb|AW171746|AW171746 N100640e rootphos(-) Medicago truncatula c... 33 8.1
      emb|AI960269|AI960269 sc81b07.y1 Gm-c1018 Glycine max cDNA clone... 27 9.1
      Query= X98676.2_at 15778_at /id_source genbank /description
15
      emb|caa67234.1| (x98676) zinc finger protein [arabidopsis thaliana]
      /blast score 8.00e-87 /ec number /family /chip nova /gb link
      http://www3.ncbi.nlm.nih.gov/htbin-
      post/entrez/query?db=n&form=6&dopt=g&uid=gb|x98676| /ncgi
20
      http://www.ncgr.org/cgi-bin/ff?x98676
          _(643_letters)__
      Database: plantfungal
            661,018 sequences; 426,114,510 total letters
25
      Searching......done
                                          Score
                                                 E
      Sequences producing significant alignments:
                                                         (bits) Value
30
      gb|L46574|L46574 BNAF1975 Mustard flower buds Brassica rapa cDNA... 84 2e-29
      emb|AB006600|AB006600 Petunia x hybrida mRNA for ZPT2-13, comple... 57 2e-25
      emb|AB006599|AB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 57 5e-23
      emb|AI485362|AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... 64 4e-22
35
      emb|AI898309|AI898309 EST267752 tomato ovary, TAMU Lycopersicon ... 63 8e-22
      emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon ... 64 2e-21
      emb|AB006604|AB006604 Petunia x hybrida mRNA for ZPT2-9, complet... 102 2e-21
      emb|AW030869|AW030869 EST274159 tomato callus, TAMU Lycopersicon... 61 4e-21
      emb|AI485555|AI485555 EST243876 tomato ovary, TAMU Lycopersicon ... 55 7e-21
40
      emb|AB000451|AB000451 Petunia hybrida mRNA for PEThy;ZPT2-5, com... 62 2e-20
      emb|AI486627|AI486627 EST244948 tomato ovary, TAMU Lycopersicon ... 55 2e-20
      emb|AI486228|AI486228 EST244549 tomato ovary, TAMU Lycopersicon ... 55 2e-20
      emb|AI771123|AI771123 EST252223 tomato ovary, TAMU Lycopersicon ... 55 6e-20
      emb|AB006601|AB006601 Petunia x hybrida mRNA for ZPT2-14, comple... 62 6e-20
45
      emb|AI488341|AI488341 EST246663 tomato ovary, TAMU Lycopersicon ... 55 8e-20
      emb|AI959966|AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone... 60 le-19
      emb|AI966235|AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone... 60 1e-19
      emb|AI897376|AI897376 EST266819 tomato ovary, TAMU Lycopersicon ... 64 2e-19
      emb|AB006603|AB006603 Petunia x hybrida mRNA for ZPT2-8, complet... 61 4e-19
50
      emb|AW033868|AW033868 EST277439 tomato callus, TAMU Lycopersicon...
      emb|AI894711|AI894711 EST264154 tomato callus, TAMU Lycopersicon... 61 1e-18
      emb|AI485123|AI485123 EST243427 tomato ovary, TAMU Lycopersicon ... 60 2e-18
      emb|AI771824|AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... 59 5e-18
      emb|AW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 59 9e-18
55
      emb|AW216442|AW216442 EST295072 tomato callus, TAMU Lycopersicon... 57 1e-17
      emb|AW684455|AW684455 NF017B06NR1F1000 Nodulated root Medicago t... 62 5e-17
      emb|AW687462|AW687462 NF009H03RT1F1031 Developing root Medicago ... 57 8e-17
      emb|AV422177|AV422177 AV422177 Lotus japonicus young plants (two... 56 8e-17
      emb|AB006602|AB006602 Petunia x hybrida mRNA for ZPT2-7, complet... 60 2e-16
60
      dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 56 3e-16
      dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 56 3e-16
```

	emb AW680050 AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S 57 1e-15
	emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon 53 2e-15
	emb AI487993 AI487993 EST246315 tomato ovary, TAMU Lycopersicon 53 2e-15
	emb AW034640 AW034640 EST278324 tomato callus, TAMU Lycopersicon 53 2e-15
5	emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon 53 3e-15
	emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon 53 3e-15
	emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon 53 3e-15
	emb[AI771191]AI771191 EST252387 tomato ovary, TAMU Lycopersicon 53 3e-15
	emb[AW032357[AW032357 EST275811 tomato callus, TAMU Lycopersicon 53 3e-15
10	emb AI489727 AI489727 EST248066 tomato ovary, TAMU Lycopersicon 55 4e-15
10	
	emb AF053077 AF053077 Nicotiana tabacum osmotic stress-induced z 51 1e-14
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon 53 4e-14
	emb AI488445 AI488445 EST246784 tomato ovary, TAMU Lycopersicon 55 2e-13
	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge 53 2e-13
15	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet 53 2e-13
•	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds. 47 3e-13 dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13
	emb AW924420 AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) 48 5e-13
	emb AI778714 AI778714 EST259593 tomato susceptible, Cornell Lyco 52 7e-13
20	emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop 52 7e-13
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon 52 9e-13
	emb AI487287 AI487287 EST245609 tomato ovary, TAMU Lycopersicon 52 1e-12
	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon 50 2e-12
	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA 52 2e-12
25	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon 53 2e-12
	emb[AW153229]AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone 51 3e-12
	emb[AW625323]AW625323 EST319146 tomato radicle, 5 d post-imbibit 52 3e-12
	emb AW924443 AW924443 WS1 69 C08.gl A002 Water-stressed 1 (WS1) 57 3e-12
	emb[Y16131]Y16131 Y16131 young root nodules Medicago sativa subs 49 3e-12
30	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge 50 4e-12
50	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple 50 4e-12
	emb[Y18788]MSY18788 Medicago sativa mRNA for putative TFIIIA (or 49 4e-12
35	emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon 52 5e-12
33	emb AW560934 AW560934 EST315982 DSIR Medicago truncatula cDNA cl 49 6e-12
	emb AW781249 AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone 49 6e-12
	gb U68763 GMU68763 Glycine max putative transcription factor SCO 48 8e-12
	emb AI988657 AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone 49 8e-12
40	gb[BE059872[BE059872 sn38c04.yl Gm-c1016 Glycine max cDNA clone 48 8e-12
40	dbj D26086 PETZFP4 Petunia zinc-finger protein gene. 50 1e-11
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s 52 1e-11
	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR 52 2e-11
	emb AW729218 AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa 48 2e-11
	emb AW279005 AW279005 sg04d04.yl Gm-c1019 Glycine max cDNA clone 51 2e-11
45	emb AW164639 AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone 51 2e-11
	gb BE095284 BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two 50 2e-11
	emb AW102472 AW102472 sd88f02.yl Gm-c1009 Glycine max cDNA clone 54 2e-11
	emb AB000455 AB000455 Petunia hybrida mRNA for PEThy;ZPT4-1, com 51 4e-11
	emb AW775559 AW775559 EST334624 DSIL Medicago truncatula cDNA cl 46 4e-11
50	gb BE123920 BE123920 EST394045 DSIL Medicago truncatula cDNA clo 46 4e-11
	emb AW278572 AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone 51 4e-11
	emb AW706944 AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone 47 4e-11
-	emb AW219736 AW219736 EST302218 tomato root during/after fruit s 52 4e-11
	dbj D26085 PETZFDB3 Petunia zinc-finger DNA binding protein gene. 46 5e-11
55	emblAW777036 AW777036 M111167e DSIR Medicago truncatula cDNA clo 59 2e-10
	emb[AW032112]AW032112 EST275566 tomato callus, TAMU Lycopersicon 43 4e-10
	emb[AT000773]AT000773 AT000773 Brassica rapa guard cell Brassica 65 4e-10
60	
UU	gb[BE058334]BE058334 sn14g01.yl Gm-c1016 Glycine max cDNA clone 48 1e-08
	CHINA PROPERTY AND DESCRIPTION OF THE PROPERTY

emblAV426673|AV426673 AV426673 Lotus japonicus young plants (two... gb|BE125698|BE125698 DG1 54 B08.g1 A002 Dark Grown 1 (DG1) Sorgh... 57 1e-07 emblAF119050lAF119050 Datisca glomerata zinc-finger protein 1 (z... 56 3e-07 emb[AW030314]AW030314 EST273569 tomato callus, TAMU Lycopersicon... 53 4e-07 emb[X60700]PHEPF1 P.hybrida EPF1 gene for DNA-binding protein. 55 7e-07 emb|AW620780|AW620780 sj09e02.yl Gm-c1032 Glycine max cDNA clone... 54 9e-07 emb|AI960244|AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone... 54 9e-07 emb|AB000452|AB000452 Petunia hybrida mRNA for PEThy;ZPT2-6, com... 54 9e-07 10 Ouery= X98676.2 g at 15779 g at /id source genbank /description emb|caa67234.1| (x98676) zinc finger protein [arabidopsis thaliana] /blast score 8.00e-87 /ec number /family /chip nova /gb_link /ncgi (643 letters) 15 Database: plantfungal 661,018 sequences; 426,114,510 total letters Searching......done 20 \mathbf{E} Score -- Sequences producing significant alignments: (bits) _Value gb|L46574|L46574 BNAF1975 Mustard flower buds Brassica rapa cDNA... 84 2e-29 emb|AB006600|AB006600 Petunia x hybrida mRNA for ZPT2-13, comple... 57 2e-25 25 emblAB006599lAB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 57 5e-23 emb|AI485362|AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... 64 4e-22 emb|A1898309|A1898309 EST267752 tomato ovary, TAMU Lycopersicon ... 63 8e-22 emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon ... 64 2e-21 emb|AB006604|AB006604 Petunia x hybrida mRNA for ZPT2-9, complet... 102 2e-21 30 emb[AW030869]AW030869 EST274159 tomato callus, TAMU Lycopersicon... 61 4e-21 emb|AI485555|AI485555 EST243876 tomato ovary, TAMU Lycopersicon ... 55 7e-21 emb|AB000451|AB000451 Petunia hybrida mRNA for PEThy; ZPT2-5, com... 62 2e-20 emb|AI486627|AI486627 EST244948 tomato ovary, TAMU Lycopersicon ... 55 2e-20 emb|AI486228|AI486228 EST244549 tomato ovary, TAMU Lycopersicon ... 55 2e-20 35 emb|AI771123|AI771123 EST252223 tomato ovary, TAMU Lycopersicon ... 55 6e-20 emb|AB006601|AB006601 Petunia x hybrida mRNA for ZPT2-14, comple... 62 6e-20 emb|AI488341|AI488341 EST246663 tomato ovary, TAMU Lycopersicon ... 55 8e-20 emb|AI959966|AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone... 60 1e-19 emb|AI966235|AI966235 sc35g05.yl Gm-c1014 Glycine max cDNA clone... 60 1e-19 40 emb|AI897376|AI897376 EST266819 tomato ovary, TAMU Lycopersicon ... 64 2e-19 emb|AB006603|AB006603 Petunia x hybrida mRNA for ZPT2-8, complet... 61 4e-19 emb|AW033868|AW033868 EST277439 tomato callus, TAMU Lycopersicon... 62 1e-18 emb|AI894711|AI894711 EST264154 tomato callus, TAMU Lycopersicon... 61 le-18 emb|AI485123|AI485123 EST243427 tomato ovary, TAMU Lycopersicon ... 60 2e-18 45 emb|AI771824|AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... 59 5e-18 emblAW685937|AW685937 NF031H10NR1F1000 Nodulated root Medicago t... 59 9e-18 emb|AW216442|AW216442 EST295072 tomato callus, TAMU Lycopersicon... 57 le-17 emb|AW684455|AW684455 NF017B06NR1F1000 Nodulated root Medicago t... 62 5e-17 emb|AW687462|AW687462 NF009H03RT1F1031 Developing root Medicago ... 57 8e-17 50 emb|AV422177|AV422177 AV422177 Lotus japonicus young plants (two... 56 8e-17 emb|AB006602|AB006602 Petunia x hybrida mRNA for ZPT2-7, complet... 60 2e-16 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 56 3e-16 dbi|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 56 3e-16 emb|AW680050|AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S... 57 1e-15 55 emb|AW033574|AW033574 EST277145 tomato callus, TAMU Lycopersicon... 53 2e-15 emb|AI487993|AI487993 EST246315 tomato ovary, TAMU Lycopersicon ... 53 2e-15 emb|AW034640|AW034640 EST278324 tomato callus, TAMU Lycopersicon... 53 2e-15 emb|AI896031|AI896031 EST265474 tomato callus, TAMU Lycopersicon... 53 3e-15 emb|AW030858|AW030858 EST274148 tomato callus, TAMU Lycopersicon... 53 3e-15 60 emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 53 3e-15 emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 53 3e-15

	emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon 53 3e-15
	emb AI489727 AI489727 EST248066 tomato ovary, TAMU Lycopersicon 55 4e-15
	emb AF053077 AF053077 Nicotiana tabacum osmotic stress-induced z 51 1e-14
	emb AW030876 AW030876 EST274166 tomato callus, TAMU Lycopersicon 53 4e-14
5	
3	emb AI488445 AI488445 EST246784 tomato ovary, TAMU Lycopersicon 55 2e-13
	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge 53 2e-13
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet 53 2e-13
	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds. 47 3e-13
	dbj[D16416[WHTWZF1B Wheat mRNA for WZF1, complete cds. 47 3e-13
10	emb AW924420 AW924420 WS1_69_C08.b1_A002 Water-stressed 1 (WS1) 48 5e-13
	emb AI778714 AI778714 EST259593 tomato susceptible, Cornell Lyco 52 7e-13
	emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop 52 7e-13
	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon 52 9e-13
	emb AI487287 AI487287 EST245609 tomato ovary, TAMU Lycopersicon 52 1e-12
15	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon 50 2e-12
	gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA 52 2e-12
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon 53 2e-12
	emb AW153229 AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone 51 3e-12
	emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit 52 3e-12
20	emb AW924443 AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) 57 3e-12
20	
	emb Y16131 Y16131 Y16131 young root nodules Medicago sativa subs 49 3e-12
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge 50 4e-12
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple 50 4e-12
	emb Y18788 MSY18788 Medicago sativa mRNA for putative TFIIIA (or 49 4e-12
25	emb AI988290 AI988290 sc98f10.yl Gm-c1020 Glycine max cDNA clone 50 5e-12
	emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon 52 5e-12
	emb AW560934 AW560934 EST315982 DSIR Medicago truncatula cDNA cl 49 6e-12
	emb AW781249 AW781249 sk67b08.yl Gm-c1016 Glycine max cDNA clone 49 6e-12
	gb U68763 GMU68763 Glycine max putative transcription factor SCO 48 8e-12
30	
30	emb A1988657 A1988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone 49 8e-12
	gb BE059872 BE059872 sn38c04.yl Gm-c1016 Glycine max cDNA clone 48 8e-12
	dbj D26086 PETZFP4 Petunia zinc-finger protein gene. 50 1e-11
	emb AW219517 AW219517 EST301915 tomato root during/after fruit s 52 1e-11
	gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR 52 2e-11
35	emb AW729218 AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa 48 2e-1
	emb AW279005 AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone 51 2e-11
	emb AW164639 AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone 51 2e-11
	gb BE095284 BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two 50 2e-11
	emb AW102472 AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone 54 2e-11
40	emb AB000455 AB000455 Petunia hybrida mRNA for PEThy;ZPT4-1, com 51 4e-11
70	
	emb AW775559 AW775559 EST334624 DSIL Medicago truncatula cDNA cl 46 4e-11
	gb BE123920 BE123920 EST394045 DSIL Medicago truncatula cDNA clo 46 4e-11
	emb AW278572 AW278572 sf46c03.yl Gm-c1009 Glycine max cDNA clone 51 4e-11
	emb AW706944 AW706944 sk08e10.yl Gm-c1023 Glycine max cDNA clone 47 4e-11
45	emb AW219736 AW219736 EST302218 tomato root during/after fruit s 52 4e-11
	dbj D26085 PETZFDB3 Petunia zinc-finger DNA binding protein gene. 46 5e-11
	emb AW777036 AW777036 M111167e DSIR Medicago truncatula cDNA clo 59 2e-10
	emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon 43 4e-10
	emb AT000773 AT000773 AT000773 Brassica rapa guard cell Brassica 65 4e-10
50	emb AW216968 AW216968 EST295682 tomato callus, TAMU Lycopersicon 53 4e-09
30	
	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA 52 6e-09
	gb BE058334 BE058334 sn14g01.yl Gm-c1016 Glycine max cDNA clone 48 1e-08
	emb A1966679 A1966679 sc55a11.yl Gm-c1015 Glycine max cDNA clone 54 3e-08
	emb AV426673 AV426673 AV426673 Lotus japonicus young plants (two 48 4e-08
55	gb BE125698 BE125698 DG1 54 B08.g1 A002 Dark Grown 1 (DG1) Sorgh 57 1e-07
	emb AF119050 AF119050 Datisca glomerata zinc-finger protein 1 (z 56 3e-07
	emb AW030314 AW030314 EST273569 tomato callus, TAMU Lycopersicon 53 4e-07
	emb[X60700]PHEPF1 P.hybrida EPF1 gene for DNA-binding protein. 55 7e-07
60	emb AW620780 AW620780 sj09e02.y1 Gm-c1032 Glycine max cDNA clone 54 9e-07
60	emb AI960244 AI960244 sc80g07.yl Gm-c1018 Glycine max cDNA clone 54 9e-07
	COMPANIE AND THE PROPERTY OF T

Query= AL080252.77 s at 16232 s at /id source genbank /description emb|cab45796.1| (al080252) putative protein [arabidopsis thaliana] /blast_score 1.00e-119 /ec number /family /chip nova /gb link /ncgi (639 letters) Database: plantfungal 661,018 sequences; 426,114,510 total letters 10 Searching......done Score E Sequences producing significant alignments: (bits) Value 15 emb[Y11607[MSMP2C M.sativa mRNA for protein phosphatase 2C. emb|AJ242803|SST242803 Sporobolus stapfianus partial mRNA for pu... 154 4e-61 emb|AI055336|AI055336 coau0003L08 Cotton Boll Abscission Zone cD... 163 7e-56 emb|AI488711|AI488711 EST247050 tomato ovary, TAMU Lycopersicon ... 158 5e-46 20 emb|AI489841|AI489841 EST248180 tomato ovary, TAMU Lycopersicon ... 173 1e-42 emb|AW832587|AW832587 sm14b05.yl Gm-c1027 Glycine max cDNA clone... 119 5e-40 emb|AW676724|AW676724 DG1_13_B08.g1_A002 Dark Grown 1 (DG1) Sorg... 152 2e-36 emb|AW423616|AW423616 sh69d07.y1 Gm-c1015 Glycine max cDNA clone... 110 3e-36 emb|AW278110|AW278110 sf39h03.y1 Gm-c1009 Glycine max cDNA clone... 119 2e-35 25 emb|AW698103|AW698103 NXNV_066_C09_F Nsf Xylem Normal wood Verti... 120 2e-33 emb|AI489730|AI489730 EST248069 tomato ovary, TAMU Lycopersicon ... 62 3e-29 emb[AV428740]AV428740 AV428740 Lotus japonicus young plants (two... 59 2e-19 emb|AF092431|AF092431 Lotus japonicus nodule-enhanced protein ph... 64 1e-18 emb|AF092432|AF092432 Lotus japonicus protein phosphatase type 2... 73 8e-18 30 emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 80 4e-16 emb|AW458317|AW458317 sh86c05.y1 Gm-c1016 Glycine max cDNA clone... 77 7e-16 emb|AW035781|AW035781 EST281935 tomato callus, TAMU Lycopersicon... 84 1e-15 emb|AW647646|AW647646 EST307124 tomato germinating seedlings, TA... 84 1e-15 emb|AW621460|AW621460 EST312258 tomato root during/after fruit s... 84 1e-15 35 emb|AW776573|AW776573 EST335638 DSIL Medicago truncatula cDNA cl... 78 2e-15 emb|AW164504|AW164504 se73e07.yl Gm-c1023 Glycine max cDNA clone... 76 5e-15 gb|H07534|H07534 cbn054 BNL2 Brassica napus cDNA 5'/3', mRNA seq... 82 5e-15 emb|AJ277743|FSY277743 Fagus sylvatica mRNA for ABA induced prot... 68 6e-15 emb[AW164369]AW164369 se71f04.y1 Gm-c1023 Glycine max cDNA clone... 81 7e-15 40 emb|AW035694|AW035694 EST281848 tomato callus, TAMU Lycopersicon... 81 7e-15 emb|AW683894|AW683894 NF003B07NR1F1000 Nodulated root Medicago t... 71 9e-15 emb|AW201723|AW201723 sf06e04.y1 Gm-c1027 Glycine max cDNA clone... 73 9e-15 emb|AW704555|AW704555 sk38f02.y1 Gm-c1028 Glycine max cDNA clone... 73 9e-15 emb|AI812394|AI812394 1H12 Pine Lambda Zap Xylem library Pinus t... 75 le-14 45 emb|AI486266|AI486266 EST244587 tomato ovary, TAMU Lycopersicon ... 75 2e-14 emb|AW429253|AW429253 EST306709 tomato flower buds 0-3 mm, Corne... 67 3e-14 emb|AA080599|AA080599 EST054 Sugarcane leaf roll Saccharum sp. c... 74 3e-14 emb|AW328993|AW328993 N200187e rootphos(-) Medicago truncatula c... 78 8e-14 emb|AW926387|AW926387 HVSMEg0007B08 Hordeum vulgare pre-anthesis... 78 8e-14 50 emb|AW560026|AW560026 EST315074 DSIR Medicago truncatula cDNA cl... 77 1e-13 emb|AW981447|AW981447 EST392609 DSIL Medicago truncatula cDNA cl... 77 1e-13 emb|AW775291|AW775291 EST334356 DSIL Medicago truncatula cDNA cl... 77 1e-13 emb|AW223860|AW223860 EST300671 tomato fruit red ripe, TAMU Lyco... 69 1e-13 emb|AW930922|AW930922 EST356765 tomato fruit mature green, TAMU ... 69 1e-13 55 emb|AW126261|AW126261 N100368e rootphos(-) Medicago truncatula c... 71 3e-13 emb|AW217002|AW217002 EST295716 tomato callus, TAMU Lycopersicon... 75 6e-13 emb|AW560025|AW560025 EST315073 DSIR Medicago truncatula cDNA cl... 74 8e-13 emb|A1855433|A1855433 sc16a02.yl Gm-c1013 Glycine max cDNA clone... 73 1e-12 gb|BE057188|BE057188 sm97g04.yl Gm-c1015 Glycine max cDNA clone ... 55 3e-12 60 emb|A1898557|A1898557 EST268000 tomato ovary, TAMU Lycopersicon ... 66 6e-12 gb|BE055043|BE055043 GA Ea0031H07f Gossypium arboreum 7-10 dpa ... 71 1e-11

emblAI895824|AI895824 EST265267 tomato callus, TAMU Lycopersicon... 66 1e-11 emblAF075580|AF075580 Mesembryanthemum crystallinum clone Mpc5 p... 47 2e-11 emb|AW309195|AW309195 sg05e02.y1 Gm-c1019 Glycine max cDNA clone... 62 2e-11 emblAW934653|AW934653 EST353545 tomato flower buds 0-3 mm, Come... 69 3e-11 emb|AW736469|AW736469 EST332483 KV3 Medicago truncatula cDNA clo... 69 3e-11 emb[AI052979]AI052979 Mpc9 Ice plant seedlings, RT-PCR, pCRII M... 63 3e-11 gb|BE049699|BE049699 NXNV 142 B11 F Nsf Xylem Normal wood Vertic... 63 3e-11 emb|AW224147|AW224147 EST300958 tomato fruit red ripe, TAMU Lyco... 69 3e-11 10 emb|AW623772|AW623772 EST321717 tomato flower buds 3-8 mm, Corne... 68 5e-11 emb|AW929331|AW929331 EST338119 tomato flower buds 8 mm to pre-a... 68 5e-11 gb|BE057801|BE057801 sn07d10.y1 Gm-c1016 Glycine max cDNA clone ... 68 5e-11 emb|AW648269|AW648269 EST326723 tomato germinating seedlings, TA... 68 5e-11 emb|AW755847|AW755847 s110a10.y1 Gm-c1036 Glycine max cDNA clone... 68 5e-11 15 emb|AW290631|AW290631 NXNV044C04F Nsf Xylem Normal wood Vertical... 68 5e-11 emb|AI489668|AI489668 EST248007 tomato ovary, TAMU Lycopersicon ... 68 7e-11 emb|AI052978|AI052978 Mpc7 Ice plant seedlings, RT-PCR, pCRII M... 36 1e-10 emb|AI900423|AI900423 sc05e10.y1 Gm-c1012 Glycine max cDNA clone... 44 2e-10 emb|AW567769|AW567769 si54f05.yl Gm-r1030 Glycine max cDNA clone... 44 2e-10 emblAI489404|AI489404 EST247743 tomato ovary, TAMU Lycopersicon ... 66 2e-10 20 emb|AW096523|AW096523 EST289703 tomato mixed elicitor, BTI Lycop... 66 3e-10 emb|AW442288|AW442288 EST311684 tomato fruit red ripe, TAMU Lyco... 66 3e-10 emb|AW039555|AW039555 EST281836 tomato mixed elicitor, BTI Lycop... 66 3e-10 emb|AW094483|AW094483 EST287663 tomato mixed elicitor, BTI Lycop... 66 3e-10 25 emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 48 6e-10 emblAW279540|AW279540 sf90h08.y1 Gm-c1019 Glycine max cDNA clone... 64 8e-10 emb|AW101459|AW101459 sd78e02.yl Gm-c1009 Glycine max cDNA clone... 55 2e-09 emb|AJ277744|FSY277744 Fagus sylvatica mRNA for ABA and calcium ... 46 3e-09 emb|AF075579|AF075579 Mesembryanthemum crystallinum clone Mpc2 p... 62 4e-09 30 emb|AW265949|AW265949 L30-2480T3 Ice plant Lambda Uni-Zap XR exp... 62 4e-09 emb|AW054059|AW054059 L30-2031T3 Ice plant Lambda Uni-Zap XR exp... emb|AW830157|AW830157 sm23g12.y1 Gm-c1028 Glycine max cDNA clone... 62 6e-09 emb|AW934014|AW934014 EST359857 tomato fruit mature green, TAMU ... 61 8e-09 emb|AF211780|AF211780 AF211780 34.1B Nicotiana tabacum cDNA clon... 61 1e-08 35 emb|AW739238|AW739238 gb39a01.y1 Moss EST library PPN Physcomitr... 59 3e-08 emblAW396505|AW396505 sh28f03.yl Gm-c1016 Glycine max cDNA clone... 44 4e-08 emblAI488611|AI488611 EST246950 tomato ovary, TAMU Lycopersicon ... 59 4e-08 emb|AF079355|AF079355 Mesembryanthemum crystallinum protein phos... 45 5e-08 emb|AW164418|AW164418 se72c06.y1 Gm-c1023 Glycine max cDNA clone... 47 5e-08 40 emb|AW687126|AW687126 NF006C06RT1F1049 Developing root Medicago ... 46 7e-08 emb|AW560258|AW560258 EST315306 DSIR Medicago truncatula cDNA cl... 46 7e-08 emb|AW923104|AW923104 DG1 49 F11.b1 A002 Dark Grown 1 (DG1) Sorg... emb|AI812431|AI812431 10H3 Pine Lambda Zap Xylem library Pinus t... 57 1e-07 emb|AW680755|AW680755 WS1 7 A11.b1 A002 Water-stressed 1 (WS1) S... 39 2e-07 45 emblAW781533|AW781533|sl81d01.v1 Gm-c1037 Glycine max cDNA clone... 57 2e-07 emb|AF097667|AF097667 Mesembryanthemum crystallinum protein phos... 38 2e-07 emb|AI773148|AI773148 EST254248 tomato resistant, Cornell Lycope... 56 3e-07 emb[AV424435]AV424435 AV424435 Lotus japonicus young plants (two... 40 5e-07 gb[L33918]USMUAC1A Corn smut fungus uac1 gene, complete cds. 41 5e-07 50 emb|AW278161|AW278161 sf40e04.y1 Gm-c1009 Glycine max cDNA clone... 55 7e-07 emb[AI060326]AI060326 Mpc5 Ice plant seedlings, RT-PCR, pCRII M... 37 8e-07 emb|AW616138|AW616138 EST296905 L. hirsutum trichome, Cornell Un... 54 9e-07 emblAW119467|AW119467 sd47d10.yl Gm-c1016 Glycine max cDNA clone... 54 9e-07 emb|Z48008|SC8119 S.cerevisiae chromosome IV cosmid 8119. 53 2e-06 55 Query= AC004138.105 at 16257 at /id source genbank /description

Query= AC004138.105_at 16257_at /id_source genbank /description gb|aac32915.1| (ac004138) putative nucleoside triphosphatase [arabidopsis thaliana] /blast_score 0 /ec_number ec_3.6.1.42 /family diphosphatase /chip nova /gb_link

http://www3.ncbi.nlm.nih.gov/htbinpost/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi 5

15

20

25

30

35

40

45

55

60

http://www.ncgr.org/cgi-bin/ff?ac004138 (1551 letters)

```
Database: plantfungal
       661,018 sequences; 426,114,510 total letters
```

Searching......done

10

E Score Sequences producing significant alignments: (bits) Value gb|U58597|STU58597 Solanum tuberosum ATP-diphosphohydrolase (RRO... 66 1e-31 emb|Z32743|PSNTPASE P.sativum (Alaska) NTPase mRNA for nucleosid... 64 1e-30 emb|AB022319|AB022319 Pisum sativum mRNA for apyrase, complete cds. 64 le-30 emb|AB027616|AB027616 Pisum sativum mRNA for apyrase, partial cd... 64 2e-29 emb|AW925295|AW925295 HVSMEg0001H23 Hordeum vulgare pre-anthesis... 69 2e-29 emb|AF156782|AF156782 Medicago sativa nod factor binding lectin-... 66 8e-29 emb|AW983120|AW983120 HVSMEg0008D22f Hordeum vulgare pre-anthesi... 70 2e-28 emb|AI771115|AI771115 EST252215 tomato ovary, TAMU Lycopersicon ... 71 4e-28 emb|AW934554|AW934554 EST353446 tomato flower buds 0-3 mm, Corne... 71 8e-26 emb|AW621504|AW621504 EST312302 tomato root during/after fruit s.... 62_7e-25 emb|AF156780|AF156780 Lotus japonicus nod factor binding lectin-... 60 2e-23 emb|AW618513|AW618513 EST320499 L. pennellii trichome, Cornell U... 67 5e-22 emb|AF139807|AF139807 Dolichos biflorus nod factor binding lecti... 65 6e-22 emb|AW928903|AW928903 EST337691 tomato flower buds 8 mm to pre-a... 71 7e-22 emb|AB032754|AB032754 Solanum melongena EEF45 mRNA, partial cds. emb|AW428956|AW428956 EST306496 tomato flower buds 0-3 mm, Corne... 68 1e-19 emb|AW201606|AW201606 sf05b09.yl Gm-c1027 Glycine max cDNA clone... 57 8e-18 emb|AV421159|AV421159 AV421159 Lotus japonicus young plants (two... 62 8e-18 emb|AL121741|SPAC824 S.pombe chromosome I cosmid c824. emb|AL121783|SPCC11E10 S.pombe chromosome III cosmid c11E10. emb|AZ048365|AZ048365 LMAJFV1 lm77d11.x1 Leishmania major FV1 ra... 65 2e-16 emb|AI900961|AI900961 sc17g01.yl Gm-c1013 Glycine max cDNA clone... 61 4e-16 emb|AW233919|AW233919 sf32a09.y1 Gm-c1028 Glycine max cDNA clone... 72 6e-16 emb|AI729322|AI729322 BNLGHi13103 Six-day Cotton fiber Gossypium... 56 4e-15 gb[U18779|SCE8199 Saccharomyces cerevisiae chromosome V cosmid 8... 47 9e-15 gb[L19560[YSCGUANDIP Saccharomyces cerevisiae guanosine diphosph... 47 1e-14 emb|AI855475|AI855475 sc16e11.yl Gm-c1013 Glycine max cDNA clone... 56 6e-13 emb|AI488582|AI488582 EST246921 tomato ovary, TAMU Lycopersicon ... 60 8e-13 emb|AJ388942|AJ388942 AJ388942 Medicago truncatula R108 Medicago... 63 1e-12 emb|AW620334|AW620334 sj03g08.yl Gm-c1032 Glycine max cDNA clone... 61 2e-12 emb|AF156781|AF156781 Dolichos biflorus apyrase mRNA, complete cds. 62 7e-12 emb|AA660474|AA660474 00360 MtRHE Medicago truncatula cDNA 5' si... 65 7e-12 emb|AI441990|AI441990 sa82g03.y1 Gm-c1004 Glycine max cDNA clone... 60 2e-11 emb|AW696828|AW696828 NF109D12ST1F1101 Developing stem Medicago ... 57 2e-11 gb/BE059022/BE059022 sn24b03.yl Gm-c1016 Glycine max cDNA clone ... 53 4e-11 emb|AW306606|AW306606 se53a03.y1 Gm-c1017 Glycine max cDNA clone... 56 8e-11 emb|AI490444|AI490444 EST248770 tomato ovary, TAMU Lycopersicon ... 61 2e-10 emb|AW564791|AW564791 LG1_301_H10.b1_A002 Light Grown 1 (LG1) So... 51 2e-10 emb|AI771846|AI771846 EST252946 tomato ovary, TAMU Lycopersicon ... 61 3e-10 emb|AI897295|AI897295 EST266654 tomato ovary, TAMU Lycopersicon ... 61 3e-10 emb|AI485852|AI485852 EST244173 tomato ovary, TAMU Lycopersicon ... 61 3e-10 emb|AI899079|AI899079 EST268522 tomato ovary, TAMU Lycopersicon ... 61 3e-10 emb|AW922880|AW922880 DG1 47 F10.b1 A002 Dark Grown 1 (DG1) Sorg... 48 4e-10 emb|AI490499|AI490499 EST249033 tomato ovary, TAMU Lycopersicon ... 61 5e-10 emb|AI488302|AI488302 EST246624 tomato ovary, TAMU Lycopersicon ... 60 1e-09 emb|AV418181|AV418181 AV418181 Lotus japonicus young plants (two... 57 2e-09 emb|AW924275|AW924275 WS1 52 E03.b1 A002 Water-stressed 1 (WS1) ... 64 3e-09 emb|AW257004|AW257004 EST305141 KV2 Medicago truncatula cDNA clo... 48 8e-09 emb[A1771696]A1771696 EST252796 tomato ovary, TAMU Lycopersicon ... 61 3e-08

emb|AW623313|AW623313 EST321258 tomato flower buds 3-8 mm, Corne... 58 2e-07

	emb AA231755 AA231755 CDO38.R cDNA from oat Avena sativa cDNA cl 56 7e-07
	emb AW736308 AW736308 EST332392 KV3 Medicago truncatula cDNA clo 54 4e-06
	emb AW563435 AW563435 LG1 214 E12.b1 A002 Light Grown 1 (LG1) So 38 4e-05
	emb AB010444 AB010444 Neospora caninum mRNA for NTPase, complete 41 1e-04
5	emb AL160371 LMFLCHR15 Leishmania major Friedlin assembled chrom 44 0.004
_	emb AF203695 AF203695 Saccharomyces cerevisiae golgi nucleoside 43 0.005
	gb[U18778]SCE9537 Saccharomyces cerevisiae chromosome V cosmids 43 0.005
	emb AZ124337 AZ124337 T223080b Medicago truncatula BAC library M 41 0,026
10	emb AW225681 AW225681 ST70C07 Pine TriplEx shoot tip library Pin 41 0.026
10	emb AW774350 AW774350 EST333501 KV3 Medicago truncatula cDNA clo 41 0.026
	emb AI974272 AI974272 T110271e KV0 Medicago truncatula cDNA clon 40 0.035
	emb AL049184 PFMAL13P3 Plasmodium falciparum chromosome 13 strai 39 0.13
	emb AI728079 AI728079 BNLGHi9928 Six-day Cotton fiber Gossypium 29 0.23
	emb X61608 BNLHCB3A B.napus gene for LHCII Type III chlorophyll 37 0.33
15	emb AW671082 AW671082 LG1_284_C02.b1_A002 Light Grown 1 (LG1) So 37 0.33
	emb AZ124338 AZ124338 T223081b Medicago truncatula BAC library M 36 0.85
	emb AF188744 AF188744 Brassica napus high-affinity ammonium tran 35 1.2
	dbj[D37795]D37795 Ipomoea nil Tpn1 gene. 35 1.2
	dbj E08493 E08493 gDNA encoding transposable element, Tpn1 which 35 1.2
20	
20	emb AL356192 NCB24B19 Neurospora crassa DNA linkage group II BAC 30 1.3
	emb AF106939 AF106939 Phanerochaete chrysosporium 1,4-benzoquino 29 1.4
	emb AL163492 LMFL787 Leishmania major Friedlin chromosome 19 cos 35 1.5
	emb AW234282 AW234282 sf23d03.yl Gm-c1028 Glycine max cDNA clone 35 1.6
	emb AL116534 CNS01D9A Botrytis cinerea strain T4 cDNA library un 35 1.6
25	emb AW428880 AW428880 Ljirnpest25-999-b7 Ljirnp Lambda HybriZap 35 1.6
	gb[N60092]N60092 TgESTzylld09.rl TgRH Tachyzoite cDNA Toxoplasma 35 2.2
	emb AW056764 AW056764 ST55E11 Pine TriplEx shoot tip library Pin 35 2.2
	gb[N81562]N81562 TgESTzy59h03.rl TgRH Tachyzoite cDNA Toxoplasma 35 2.2
	emb AW286610 AW286610 LG1 335 A07.g1 A002 Light Grown 1 (LG1) So 35 2.2
30	emb AQ656308 AQ656308 Sheared DNA-27M14.TR Sheared DNA Trypanoso 35 2.2
	emb AL162692 SPBP4H10 S.pombe chromosome II P1 clone p4H10. 34 3.0
	emb AQ652731 AQ652731 Sheared DNA-18C6.TR Sheared DNA Trypanosom 34 3.0
	emb AF016222 AF016222 Schizosaccharomyces pombe Rsvlp (rsvl) gen 34 3.0
	emb AW350237 AW350237 GM210008A10B2R Gm-r1021 Glycine max cDNA 3 34 4.1
35	emb AQ943814 AQ943814 Sheared DNA-34A9.TF Sheared DNA Trypanosom 34 4.1
"	
	emb AW666160 AW666160 sk32h08.y1 Gm-c1028 Glycine max cDNA clone 34 4.1
	emb AL109736 SPCC18B5 S.pombe chromosome III cosmid c18B5. 27 4.6
	emb AW441608 AW441608 EST311004 tomato fruit red ripe, TAMU Lyco 33 5.7
40	emb AL035476 PFMAL4P3 Plasmodium falciparum chromosome 4 strain 33 5.7
40	emb AW398001 AW398001 sg71a06.y1 Gm-c1007 Glycine max cDNA clone 33 5.7
	emb AW933585 AW933585 EST359428 tomato fruit mature green, TAMU 33 5.7
	emb AI069343 AI069343 mgae0006cG03f Magnaporthe grisea Appressor 33 5.7
	emb[X62697]NCACU3 N.crassa acu-3 gene for isocitrate lyase. 26 5.7
	emb AI488866 AI488866 EST247205 tomato ovary, TAMU Lycopersicon 31 6.2
45	emb Z79690 ANPFKA A.niger pfkA gene. 26 7.3
	emb X13508 HVGHRDSP Barley gene for storage protein gamma-hordein. 28 7.8
	gb M36378 BLYG1HORDA Barley gamma-1 hordein storage protein gene 28 7.8
	emb AF114171 AF114171 Sorghum bicolor BAC clone 25.M18, complete 33 7.8
	emb AI900865 AI900865 sb95d08.yl Gm-c1012 Glycine max cDNA clone 33 7.8
50	emb AZ124341 AZ124341 T223084b Medicago truncatula BAC library M 33 7.8
<i>-</i>	Children 124341 12230040 Medicago dunicatula DAC notaly M 55 7.6
	One AT 025/70 144 -417/52 -4/11 - 1 - 1 /1 - 1 /1
	Query= AL035679.144_at 17653_at /id_source genbank /description
	emb cab38823.1 (al035679) putative protein [arabidopsis thaliana]
	/blast_score 0 /ec_number /family /chip nova /gb_link
55	http://www3.ncbi.nlm.nih.gov/htbin-
	post/entrez/query?db=n&form=6&dopt=g&uid=gb al035679 /ncgi
	http://www.ncgr.org/cgi-bin/ff?al035679
	(1455 letters)
	· · · · · · · · · · · · · · · · · · ·

Database: plantfungal
661,018 sequences; 426,114,510 total letters

5 Sequences producing significant alignments: (bits) Value emblAW091895|AW091895 EST285075 tomato mixed elicitor, BTI Lycop... 306 3e-82 emb|AW040183|AW040183 EST282682 tomato mixed elicitor, BTI Lycop... 306 3e-82 emb|AW776130|AW776130 EST335195 DSIL Medicago truncatula cDNA cl... 204 2e-51 10 emb|AI897609|AI897609 EST267052 tomato ovary, TAMU Lycopersicon ... 182 4e-45 emb|AI055000|AI055000 coau0002L23 Cotton Boll Abscission Zone cD... 90 1e-42 emb|AI055639|AI055639 coau0004K19 Cotton Boll Abscission Zone cD... 107 2e-22 emb|AW693198|AW693198 NF061D12ST1F1000 Developing stem Medicago ... 66 6e-10 emb|AW684256|AW684256 NF014F09NR1F1000 Nodulated root Medicago t... 43 0.007 15 emb|AW667681|AW667681 GA_Ea0010D15 Gossypium arboreum 7-10 dpa ... 43 0.007 emb|AW736130|AW736130 EST332126 KV3 Medicago truncatula cDNA clo... 39 0.12 emb|AW683515|AW683515 NF015C12LF1F1097 Developing leaf Medicago ... 36 0.21 emb|AI781902|AI781902 EST262781 tomato susceptible, Cornell Lyco... 36 0.57 gb[U12141|SCU12141 Saccharomyces cerevisiae chromosome XIV left ... 35 0.73 20 emb|AW277626|AW277626 sf84e07.yl Gm-c1019 Glycine max cDNA clone... 36 0.79 emb|Z71330|SCYNL054W S.cerevisiae chromosome XIV reading frame O... 35 0.80 emb|AW692595|AW692595 NF057C11ST1F1000 Developing stem Medicago ... 35 1.1 emb[X54145]ANPECT A.niger gene for pectinesterase. 35 1.5 35 1.5 emb|A35008|A35008 A.niger PE gene. 25 emb|A34997|A34997 A.niger pectinesterase coding sequence. 35 1.5 emb|AQ162316|AQ162316 mgxb0012I08r CUGI Rice Blast BAC Library P... 34 2.8 emb|AF132029|AF132029 Hortonia floribunda chloroplast atpB-rbcL ... 34 2.8 emb|AW567917|AW567917 si67c02.yl Gm-r1030 Glycine max cDNA clone... 34 2.8 emb|AO951657|AO951657 Sheared DNA-48F5.TR Sheared DNA Trypanosom... 34 2.8 30 gb[U81520|CIU81520 Cichorium intybus sucrose:sucrose 1-fructosyl... 34 3.9 emb]AZ047925]AZ047925 LMAJFV1 lm68e11.x1 Leishmania major FV1 ra... 34 3.9 emb|AI730144|AI730144 BNLGHi6313 Six-day Cotton fiber Gossypium ... 34 3.9 emb|AQ942723|AQ942723 Sheared DNA-42J12.TR Sheared DNA Trypanoso... 34 3.9 gb[U05812|HMU05812 Herpetomonas muscarum ATCC 30261 kinetoplast ... 34 3.9 emb|AW681095|AW681095 WS1_8_B09.g1_A002 Water-stressed 1 (WS1) S... 34 3.9 35 emb|AL049180|PFMAL13P1 Plasmodium falciparum chromosome 13 strai... 27 4.9 emb|AW832107|AW832107 sm30e05.y1 Gm-c1028 Glycine max cDNA clone... 33 5.3 gb[N82224]N82224 TgESTzy37d01.rl TgRH Tachyzoite cDNA Toxoplasma... 33 5.3 emb|A94222|A94222 Sequence 5 from Patent EP0952222. 40 emb|AA741851|AA741851 LmLv39p3/584B Leishmania major promastigot... 33 5.3 emb|AW728096|AW728096 GA_Ea0029O02 Gossypium arboreum 7-10 dpa ... 33 7.3 emb|AW278032|AW278032 sf89g07.yl Gm-c1019 Glycine max cDNA clone... 33 7.3 gb[N82117]N82117 TgESTzy36b06.rl TgRH Tachyzoite cDNA Toxoplasma... 33 7.3 emb|AL355930|NCB2O8 Neurospora crassa DNA linkage group II BAC c... 32 10.0 45. emb|AW688738|AW688738 NF011A11ST1F1000 Developing stem Medicago ... 32 10.0 emb|AI781529|AI781529 EST262408 tomato susceptible, Cornell Lyco... 32 10.0 emb|Al397765|Al397765 NCC5Al1T7 Conidial Neurospora crassa cDNA ... 32 10.0 emb|AF127239|AF127239 Nicotiana tabacum cultivar Burley 21 argin... 32 10.0 emb[AW180260]AW180260 MgA0351f MgA Library Mycosphaerella gramin... 32 10.0 50 emb|AF127240|AF127240 Nicotiana tabacum cultivar Xanthi arginine... 32 10.0 gb|BE055666|BE055666 GA Ea0009H20f Gossypium arboreum 7-10 dpa ... 32 10.0 gb|BE036548|BE036548 MP01C02 MP Mesembryanthemum crystallinum cD... 32 10.0 emb|AW038750|AW038750 EST280611 tomato mixed elicitor, BTI Lycop... 32 10.0 emb|AL133484|LMFL236 Leishmania major Friedlin chromosome 19 cos... 32 10.0 gb|BE123936|BE123936 EST394061 DSIL Medicago truncatula cDNA clo... 32 10.0

10

15

20

25

30

Example 4

Immediate Early Transcriptional Responses Controlled
by a Salicylic Acid Dependent Local Resistance Pathway

Salicylic Acid (SA) is an important mediator of local and systemic defense responses. In Arabidopsis, accumulation of SA is essential for local resistance against many pathogens including Peronospora parasitica (Peronospora) isolates. Furthermore, numerous defense-related genes can be activated by SA treatment. In addition to local resistance, SA-accumulation is required for systemic acquired resistance (SAR). In the SAR pathway, SA has been shown to act upstream of NPR1, which is also essential for SAR. Short application of the SA analog BTH (e.g., 4 hours) to plant tissue appears to simulate local defense responses to Peronospora parasitica, whereas sustained SA treatment (e.g., 48 hours) elicits SAR-related plant responses (Maleck et al., 2000).

A previous cDNA microarray study identified a cluster of roughly 30 coregulated genes that appear to be specifically involved in resistance of the *Arabidopsis* ecotype WS against the *Peronospora* isolate Noco2 (Maleck et al., 2000). These genes are strongly activated in response to infection with Noco2 (incompatible interaction) and 4 hours after BTH treatment. However, these genes were not markedly activated during a compatible interaction with the *Peronospora* isolate Emwal or an incompatible interaction with *Pseudomonas syringaea* (DC3000 avrRpt2) bacteria. BTH treatment for 48 hours (that simulates SAR) even strongly repressed these genes. Thus, a rapid and transient SA peak may control Noco2 triggered defense genes.

Resistance of the Arabidopsis ecotype Col-0 against the *Peronospora* isolate Emoy2 appears to be regulated by a similar pathway that also is dependent on accumulation of SA. Emoy2 resistance in Col-0 is controlled by the resistance gene *RPP4*. To further explore early SA-dependent gene regulatory events and to relate these to *Peronospora*-induced resistance responses, immediate-early target genes of SA were identified using Affymetrix chip experiments with the protein biosynthesis inhibitor cycloheximide (CHX). Genes of this category likely are linked to transcriptional regulators acting closely downstream of SA. Results from these "SA-chip" experiments were combined with those from a set of chip experiments examining expression

profiles triggered in the *Arabidopsis* ecotype Col-0 by the *Peronospora* isolate Emoy2 to identify clusters of co-regulated *RPP4* controlled SA-dependent immediate early genes.

Results

5

10

15

20

30

35

To identify genes controlled by the RPP4 pathway, interactions between the Peronospora isolate Emoy2 and Col-0 wild type plants, the defense mutants ndr1, npr1 and pad4 as well as transgenic NahG plants were examined by chip experiments. The interactions between Emoy2 and Col-0, ndr1 or npr1 are incompatible (plant is disease resistant), whereas the interactions involving pad4 and NahG are compatible (plant is susceptible, i.e., disease develops). For each interaction three different time points were analyzed: 0, 12 and 48 hours post infection with 50,000 Emoy2 spores/ml. Genes that were at one or more time points more strongly expressed in Col-0, ndr1 and npr1 as compared to pad4 and NahG were considered as controlled by the RPP4 pathway. Genes represented by 271 probe sets showed at least one 2-fold expression difference in comparison between Col-0 and pad4 or NahG and were selected for further analysis.

To identify immediate early target genes of SA, Col-0 wt seedlings were pretreated with CHX or mock treated 15 minutes before spraying with 2 mM SA or water and harvested 2 hours later (Table 28).

	Table 28	
	<u>Plants</u>	Treatment
	Col-0	untreated (mock)
25	Col-0	+SA
	Col-0	+SA+CHX
	Col-0	+ CHX

271 probe sets were found to be upregulated in a *RPP4* pathway-specific manner (SEQ ID NOs: 400-684). Emoy2-induced upregulation of these genes is compromised in pad4 and *NahG* plants. These RPP4 controlled genes were further analyzed concerning their responses to SA, CHX and SA + CHX. The 271 probe sets were subcategorized by K-means clustering over the SA/CHX data set. Nine K-means clusters comprised three subgraphs. For each of these subgraphs, the first data point represented the untreated control value, the second data point represented the response to combined SA/CHX treatment, the third

--WO 02/22675 --- PCT/US01/28506

data point represented CHX treatment alone and the fourth data point represented SA treatment alone. K-means clustering defined two categories of RPP4 controlled CHX/SA-responsive genes: immediate early genes (SA-responsive, not CHX affected) and super-induced genes (additive effects of SA and CHX).

Two K-means clusters represent *RPP4*-controlled SA-induced immediate early genes (Table 29; SEQ ID NOs: 150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615 and 526). *RPP4*-controlled upregulation of these genes is SA dependent and SA induction is not compromised by CHX, which blocks or reduces protein biosynthesis. Thus, all essential regulators that mediate SA-responsiveness of these genes must be already preformed and, hence, are likely to act closely downstream of SA. This set of 15 genes includes seven potential regulator genes that may be involved in the control of secondary response genes (which require protein biosynthesis) or other late responses.

15

5

Table 29

	12354 <u>g</u> at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
20	14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase
	15479_at	emb CAB39671.1 (AL049483) putative protein
	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
	16061_s_at	gb AAB97145.1 (AF000977) MEK1
	16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase
25	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
	16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-
		D-glucosyltransferase
	17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
	17930_s_at	emb CAA07352.1 (AJ006960) peroxidase
30	18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase
	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak
		similarity to NF-kappa-B
	20685_at	emb CAB41928.1 (AL049751) short-chain alcohol
		dehydrogenase like protein
35	13702_s_at	emb CAA19683.1 (AL024486) putative protein
	14704_s_at	gb AAD15461.1 (AC006067) unknown protein
	To fu	rther subcategorize these genes and to more precisely define a
	cluster of stri	ctly co-regulated genes, the set of 15 genes was analyzed by K-
	means cluster	ring over the RPP4 data set (Emoy2 infections). This allows to use
40	RPP4 trigger	ed expression timing as an additional criterion for subclustering.

Normalized absolute expression levels at 0, 12 and 48 hpi in Emoy2 infected

Col-0 (w.t.), ndr1, npr1, pad4 and NahG plants are displayed. Genes that share a pronounced almost linear and sustained expression increase were chosen for further analysis. These 5 genes (Table 30, which show a pronounced Emoy2-induced SA-dependent but npr1-independent linear expression increase and which encode potential regulators) are upregulated by the RPP4 pathway, respond to Emoy2 recognition with a steep, sustained, almost linear expression increase. This pronounced "upregulation" is SA dependent and independent of de novo protein biosynthesis. Transcription factors that mediate this response must be present when SA is perceived and may act closely downstream of SA.

The mechanism that switches these genes on may involve posttranslational modifications of such preformed transcription factors.

Τ	al	Ы	e.	3	0

12354_g_at gb|AAC23641.1| (AC004684) putative receptor-like protein kinase

15616_s_at emb|CAA08794.1| (AJ009696) wall-associated kinase 1

16140_s_at emb|CAB42872.1| (AJ012423) wall-associated kinase 2

17499_s_at gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel 20429_s_at emb|CAB10219.1| (Z97336) hypothetical protein - weak similarity to NF-kappa-B

To identify the potential binding sites of such key transcription factors, the promoters of these five genes were searched for conserved compact sequence motifs (Table 31; SEQ ID NOs: 757-764; SEQ ID NO:765 is a consensus sequence). Using the program "AlignACE", a strikingly conserved motif was found that is present in all five promoters. This motif resembles the described consensus binding site of WRKY transcription factors, W box. However, the W box core motif, TGAC, is followed by an "A". The permutation TGACA has never been associated with WRKY binding. In addition to this, four more positions are highly conserved. This motif may be the specific binding site of an unconventional WRKY transcription factor or a factor of a novel so far unknown type. Yeast one hybrid screens can reveal the identity of this factor.

Table 31

25

30

W box-like Motif
35 MAP Score: 4.4
ACAGTGACA 0 391 1 (12345) SEQ ID NO:757
ACAGTGACA 1 236 1 (16140) SEQ ID NO:758

	ACAGTGACA 1 317 1	(16140)	SEQ ID NO:759
	ACAGTGACA 2 281 1	(15616)	SEQ ID NO:760
	ACAGTAACA 3 84 1	(17498)	SEQ ID NO:761
	AAAGTAACA 3 1557 0	(17498)	SEQ ID NO:762
5	AAAGTGACA 4 1840 0	(20429)	SEQ ID NO:763
*	AAAGTGACA 4 2131 0	(20429)	SEQ ID NO:764
	ACAGTGACA A		SEQ ID NO:765

10 Expt. Frequency: 0.02/1kb Obs. in SOMc7: 0.06/lkb Obs. in this cluster: 0.50/1kb

15 One K-means cluster of the 271 RPP4 controlled probe sets represents RPP4-controlled SA/CHX super-induced genes (Table 32; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). RPP4-controlled upregulation of these genes is SA-dependent; these genes are weakly inducible upon both SA and CHX treatment alone. The response to 20 combined treatment with SA and CHX is stronger than the response to either single treatment. Induction of genes in response to CHX alone has been described before and has been attributed to hypothetical proteins that are rapidly turned over and either repress transcription of the respective gene or control degradation of the respective mRNA. Block of synthesis of such hypothetical 25 proteins may lead to increased mRNA levels by either increased transcription or reduced mRNA degradation. Like the set of immediate early SA responsive genes shown before, genes of this set also appear not to require de novo protein biosynthesis for their response to SA. In contrast to the previous gene set, however, the observed CHX-induced up-regulation may point to a de-repression 30 mechanism.

Table 32

	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box
		zinc finger protein
35	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of
	•	unknown function
	14116 at	gb AAC26243.1 (AF077407) contains similarity to sugar
	_	transporters
	14170 at	gb AAF29406.1 AC022354 5 (AC022354) unknown protein
40	14223 at	emblCAA19683.11 (AL024486) putative protein

```
gb|AAD31062.1|AC007357 11 (AC007357) Strong similarity to
     14248 at
                   gb|X97864 cytochrome P450
     14608 at
                   gb|AAD31074.1|AC007357 23 (AC007357) Similar to
                   gb|AF038007 FIC1, member of the PF|00122 E1-E2 ATPase
 5
                   family.
     14614 at
                   gb|AAC16958.1| (AC004165) putative glucosyltransferase
     15646 s at
                   gb|AAC37474.1| (L42212) serine acetyltransferase
     16054 s at
                   emb|CAA74639.1| (Y14251) glutathione S-transferase
     16105_s_at
                   gb|AAC31756.1| (U68017) heat shock transcription factor 4
10
     16968 at
                   emb|CAA17559.1| (AL021961) glucosyltransferase -like protein
     18235 at
                   gb|AAB61480.1| (AC000348) T7N9.4
     18567 at
                   gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase
     18591 at
                   emb|CAA52772.1| (X74756) ATAF2
     19845 g at
                   emb|CAB37510.1| (AL035540) monooxygenase 2 (MO2)
15
     20017 at
                   gb[AAC16079.1] (AC004521) unknown protein
            To further subcategorize these genes based on RPP4 triggered expression
     timing, the set of 17 SA/CHX super induced genes was K-means clustered over
     the RPP4 (Emoy2) data set (Table 33; SEQ ID NOs: 214, 621, 71, 439, 78, 80,
     264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). A group of five
20
     genes was identified that consistently respond quickly ("fast", within 12 hpi) and
     that have elevated expression ground states in the npr1 mutant. The fast
```

inducibility may point to an NPR1-dependent repression mechanism. Since NPR1 has been shown previously to act closely at the level of transcriptional regulation, a NPR1 dependent repressor may shut expression of these genes down. Upon CHX treatment this hypothetical repressor is not synthesized anymore and expression of these genes is elevated. This repressor may also participate in RPP4 triggered activation of these genes and allow Emoy2-

response is SA dependent (is abolished or attenuated in pad4 and NahG). The

elevated expression ground states in npr1 together with the observed CHX

30 induced de-repression.

Table 33

	18591_at	emb CAA52772.1 (X74756) ATAF2
	14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to
35		gb X97864 cytochrome P450
	14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
	15646_s_at	gb AAC37474.1 (LA2212) serine acetyltransferase
	16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4

To identify binding sites of activating or repressing factors responsible for the co-regulation of this small cluster, the promoters of these genes were searched for conserved compact motifs with "AlignACE" (Table 34; SEO ID NOs: 766-772, SEQ ID NO:773 is a consensus sequence). One strictly

conserved octameric motif was found, which, however, is absent in one of the promoters. Yeast one hybrid screens can identify factors binding to this motif.

Table 34

Random20:

SOMc3:

SOMc1:

25

30

0.00/lkb

0.10/1kb

0.10/lkb

'
_

As described hereinbelow, sets of genes specifically controlled by the RPP7 and RPP8 pathways were defined. Similarly a set of RPP4 pathway controlled genes was defined (see Figure 4). Figure 4 shows a "Venn diagram" including only the transcription factor genes of these RPP4, RPP7 and RPP8 controlled genes. Three transcription factor genes were found to be specifically upregulated by each of the three Peronospora defense pathways: AtERF1. HSF4, ATAF2. Furthermore, ERF transcription factors appear to play an 35. important role in controlling defense responses directed against Peronospora in general. Table 35 gives four potential target genes of ERF transcription factors. These genes contain ERF binding motifs in their promoters.

Table 35

40 Genes with potential ERF binding sites (GCCGCC or GCCGAC):

thioredoxin (13189) RPP7/RPP8 and (weakly) RPP4 controlled C2H2 zinc finger (15665) RPP7/RPP4 and (weakly) RPP8 controlled SigA binding protein (14148) RPP7/RPP4 controlled HSP70 (13284) RPP7/RPP8 controlled

These genes are specifically controlled by at least two different *Peronospora* defense pathways and show an almost linear increase of transcript levels during incompatible Hiks1 interactions (K-means clusters 3+5).

6 potential ERF binding sites in K-means cluster 3+5: 0.5 motifs /

10 1kbExpected: 0.1 motif / 1kb; Enrichment in K-means cluster 3+5: 5-fold

SEO ID NO:789

MPTSATAVAPSTGSVQKKDQDWRAILSPEQFRVLREKGTENRGKGEYT KLFDDGIYSCAGCATPLYKSTTKFDSGCGWPSFFDAIPGAIKQTDMFGSN

15 AADGSIVTSGLDYILISINEKLKAYT

SEO ID NO:790

- 1 tgcattcttt tgaggggttt aattttctgc atagctttgt ctaatctctt agagctcaat
- 61 aagagaagat ggatgttcca cggccagctt tcaaatgttt tgatgacgat ggccggctta
- 20 121 aacgttcagg gacggtttgg accgcgagtg cgcatatcat aaccgccgtg attggatctg
 - 181 gtgttctatc gcttgcgtgg gctataggtc aactcggttg gatcgcaggt cctacagtga

 - 241 tgttgttgtt ctcttttgtc acttactact cttccacgct tcttagcgac tgctacagaa
 - 301 coggagatee tgtetetggg aagagaaact atacttacat ggaegetgte egateaatee
 - 361 taggtggctt taggttcaag atttgtgggc tgattcagta tttgaatctg tttggtatca
 - 421 eggtegggta cacaategea geatetataa gtatgatgge gateaagagg tecaaetgtt
 - 481 tecaegagag eggagggaaa aaccegtgte acatgtegag caatecatae atgateatgt
 - 541 ttggtgtgac cgagatettg eteteteaga teaaagattt tgaccagatt tggtggetet
 - 601 ccattgtcgc tgctatcatg tccttcacat actctgcaat cggtttagct ctcggaatca
 - 661 ttcaagtcgc ggcaaatgga gttgtcaagg gaagtctcac cggaattagc atcggcgcag
- 721 tgactcagac ccaaaaaata tggagaacct ttcaagcact tggagacatt gcctttgctt 30
 - 781 atteatacte tettettett atteaaatte aggacactet aagateteea ceageagaat
 - 841 caaaaacgat gaagategee acaagaatea geategetgt tacaacgaea ttttacatge
 - 901 tatgtggttg tatgggctat gcggccttcg gagataaagc accgggaaac ctcttaaccg
 - 961 gttttggttt ctacaatccg ttttggctcc ttgacgtggc taacgctgcc atagttatcc
- 35 1021 accttgtagg agcttatcaa gtctttgctc agcccatctt cgcctttatt gagaaacaac
 - 1081 tggccgctag gtttcccgac agtgacttgg tgaccaagga atacgaaatc cgaatccctg
 - 1141 gttttaggte accgtacaaa gtcaacgttt teagageagt ttacegaage gggtttgtgg
 - 1201 ttttgaccac tgtgatatcc atgcttatgc cgtttttcaa cgacgtcgta gggattttag
 - 1261 gtgcgttagg gttttggcct ttgacggttt actttccggt ggagatgtat ataagacaga
- 40 1321 ggaaggttga gagatggagt atgaagtggg tttgtctgca gatgttgagc tgtggttgtt
 - 1381 tgatgatcac gttggtcgcc ggagttggct ccatcgccgg agtaatgcta gaccttaagg
 - 1441 tttacaagec gttcaagact acttactaaa caaaccatga tgatagatga agaagaagaa
 - 1501 ggtggtggag aaaaaaaaca aaagatataa attttaatga tgattttcat tggggaaatg
 - 1561 tgaataatgt aaaagttett egtttegtat aatttttate ttgegtaatt tatataeat

45

SEQ ID NO:791

MVKNLKVDPLAKVTASTTSMVIKILSSLFITDDSYVLVSAKENKNQSEAE PSYYETLETYQGLPCPYGGYYGYYYPGLDGSVGEAKDNGYYGYGTEVQ YPVMQGENGSVIYLMPGFQSYDASQTYMPINPVGVSSQALHSPMYAAQ GYYQNQFGYADVSSPTYLWDPVGDRYVYGVASYTPPLKQNISSSSHNH

- 5 NNYYSKSKNSFTGHGMGDRPKTPRKASQNSYAPPPLLNQEKGRIAYPM DPVKKKSGALNRDETEKAKARTKENGTSMNDLANGQDHITNGECESCS LDAEGNERSNGVGSVIRRDQYNLPSFQTKYEEAIFFVIKSYSEDDIHKSIK YNVWSSTLNGNKKLDSAYQESQKKAADKSGKCPVFLFFSVNASGQFCG VAEMIGRVDYEKSMEFWQQDKWTGYFPVKWHIIKDVPNPQLRHIILEN
- 10 NENKPVTNSRDTQEVRLPQGNEVLNIFKNYAAKTSILDDFDFYENREKV MVQKKLRFPPVLKKKEEDLVADFKTMEMSNTVEEGNTELTGTVS

SEQ ID NO:792

- 1 cgatcacgga tetggettgg tteatacaaa accgeegttg eegeggeaeg ggeetaegat
- 15 61 acceptigg tittactiacy tegic tetre gegagactea attracetiga agaggietti
 - 121 aaggatggaa acggcggtga aggcttagga ggagatatgt ctccgacgtt gatacggaag
 - 181 aaggeggetg aggtgggage tagagtegae geagagttge ggttagagaa taggatggtt
 - 241 gagaacttag acatgaataa gttgccggag gcatatggat tgtaatttat agtttggtag
 - 301 tttataggtt ggagattgcc cggagacaga gtcaaacaga ggttctctga ctcatatgag
- 20 361 gcataatata gttaatatag taatttttgt tttgagcata gtaattatgt cataacc

SEQ ID NO:793

- 1 gggcaatgat tattcgttcg ccggaaccag aagtcaaaat tttggtagat agggatccca
- 61 taaaaacttc tttcgaggaa tgggctaaac ccggtcattt ctcaagaaca atagctaagg
- 25 121 gacctgatac taccacttgg atctggaacc tacatgctga tgctcacgat tttgatagtc
 - 181 ataccagtga tttggaggaa atctctcgaa aagtatttag tggccatttc ggccaactct
 - 241 ctatcatctt tetttggetg agtggeatgt atttccatgg tgetegtttt tecaattatg
 - 301 aagcatgget gagtgateet acteacattg gacetagtge teaggtggtt tggecaatag
 - 361 tgggccaaga aatcctgaat ggagtagtgg gcggaggctt ccgaggaata caaataacct
- 30 421 caggettitt teagattigg egageateeg gaataactag tgaattacaa etttattgta
 - 481 ccgcaattgg cgcattggtc ttcgcagcct taatgctttt tgctggttgg ttccattatc
 - 541 acaaagcage tecaaaattg gettggttee aagatgtaga atetatgttg aateaccatt
 - 601 tagcaggget actaggactt gggteeettt ettgggeagg acateaagta eatgtatett
 - 661 atccgattaa ccaatttcta aacgctggag tagatcctaa agaaataccg cttcctcatg
- 35 721 aatttatett gaategggat ettttggete aactttatee aagttttget gaaggageaa
 - 781 ctcccttttt taccttaaat tggtcaaaat actcggaatt tcttactttt cgtggcggat
 - 841 tagatccagt gactgggggt ctatggttaa ccgatatagc acatcatcat ttacgtatcg
 - 901 caattetttt tetaategeg ggteatatgt ataggaceaa etggggtatt ggteatggta
 - 961 taaaagatat tttagaggct cataaaggtc catttacagg ccaaggccat aaaggcctat
- 40 1021 atgaaattct aacaacatca ttgccc

SEO ID NO:794

- MEGSSSSSSLISKSDAELEEMLDRMLTRLALCDDSKLESLVSNLLPLTISS LSSQSPVVRNKAMCVDFIFQVLEILSHVNKRVKHQHEIGLPLLALWKLY
- 45 TDPAAAPMVRNFAIVYVEMAFERAPAKVIGECHASKISDDVSAKYRSLIT SQDKDLFLDFCLHMLLYQPSSQGGGSSPGLSVFQVNRIIGKQALKGDTLT RRKLPSNTFLTKNYHFLKINQFLKQLGILNVIGNMDLPGESVYPLYIAAS VDRVGMDLLVKIHSSQEPVAKRGEELLKKIASGTNLDDPKLINRLFLLFN GTTGTENVAPEHNVAPGNISLKMKLMSGFCRSIAAANSFPATLQCIFGC
- 50 MYDILFLLNLTFREKTEMAVRLFDALKLETQSLRSTIQEAIVSLAAAYKD

SPENILRDLEVLLLANSLAEQNEARFCALRWATSLYNSHHCPSLYICMLS AADPKLDIREIALEGLFLKEEGRSIVSNHDHKYPKFIEMLEYILKQOPKLL DSSEMRSQKLLFPSQVYLVMIKFLVKCFELEMEESNTQAVGTEFLDSAQ KMCSLLEHSLAFEGSAELHACASKALVSVGSYLPEMVELYFSRKIVWLR 5 SLLSHTDLSTRESVSRLLGMASCALSDAESCSLLSELISSISQPQKLRFEAQ HGGLCAVGFVSAHCLHRIPTVSKAVTQNAVKYLVEVVNLETAPLASVA MEALGHIGICGALPFLVNDSSPGTQVLEILQERLSKLLSGDDIKSVQKIAL SLGHICSNETSSSHLKIALDLLFSLSRSKAEEILFAAGEALSFLWGGVPVT ADMILKTNYTSLSTDSNFLMKEVKSLSDVKTDTEEDSRTTTRETITGKLF 10 DTLLYSSRKEERCAGTVWMLSLTMYCGQQPSIQLMLPKIQEAFSHLLGD **QNELTQELASQGMSIIYELGDASMKKSLVDALVNTLTGTSKRKRAIKLV** EESEVFQEGTIGESPSGGKISTYKELCNLANEMGQPDLIYKFMDLANHQA SLNSKRGAAFGFSKIAKQAGDALRPHLRLLIPRLIRYQYDPDKNVQDAM AHIWKALIQDPKKAVDEHLNHIFDDLLVQCGSRLWRSREASCLALADIIQ 15 GRKFDQVKEHLKKLWIAAFRAMDDIKETVRNAGDKLCRAVTSLTIRICD VTLTELADAKOAMDIVLPFLLSEGIMSKVNSVRKASIGVVMKLAKFYSK HEIINQFELLASFGELNVLLGNIYDPLSDFVLFVTVCRLHAANIGIETEKLE , NLRISISKGSPMWETLDLCINIVDIESLEOLIPRLTOLVRGGVGLNTRVGV ASFISLLVQKVGSEIKPFTGMLLRLLFPVAKEEKSSAAKRAFSSACGIVLK 20 YSSPSQAQSLIEETAALHSGDRSSQIACASLFKSFSSTAADIMSSHQSAIVP AIFISRFEDEKOISSLFEEVWEDITSGERVTLOLFLOEIVNHICESITSSSRFK LSFSLGKDALLDALGALSVACHEAITKEDPTTPTTILSLICSACKKKLKKY RESAFSCLEKVIIAFGDPKFFHAVFPMLYEMCNTASIKTNTQVQAASDAV KTESENGEDGHVPLEKIMECVKSCIQVATIDDILSAKADLIHVLIISLSPGF 25 LWTVKMSGISCVGKLCSRFPSLWTDSMDDLSPSDATKFVHELFHSLVPK LLECIHTVKIAQFHVAASQCLLELIELYSTISSLHPVEVDFKAEVVSLLELE

SEQ ID NO:795

KSEEAKSLLRKSRDALANLPSLN

- 30 MDKETEILSRLAANHLHLAQFEPLKATLLALRVRNPDLALTILQTIVSNA GRFDNVLWSRSCPSPSLLSFLSTIELLRFENPTSPWGFDSETLSLRADFLL MVQVLIDRVTERIKEDEESEDENSGLGNCLRVLQGVLELGVERLKFVVD TSSSEGSNKIEEDAVVSLRSIVLDYSDVFDALCCNIQRQLAGCESYGTCL VEEVQGEEQRKEMNEATCIGSPELDNINVFALIQRNVQLAQLDAMKTKL
- 35 DEGDERGAADRIRYLHLDYGVEKENYHAVLKALLSRVMEKKDEYGDS
 WHMVRQNLLFMYKEALSSNCGDLVQMIQGIQDDMLLPHSQLHLSLDNE
 QIPLPLECFRRYLVDLKTERNIEDKSSPMSRAINSCLRDMYHYARISGSHV
 LECVMCAALSSVKKEKLQEANDVLTLFPRLRPLVASMGWDLLPGKTAT
 RRKLMRLLWTSDSQALRLEESSLYGNQTDELELASFAACVNSGKSWTP
- 40 KASFLMHGNVSSAHDDAEVDPFVENLVLERLSAQSPLRVLFDVVPGIKF QDAISLISMQPIASTAEAWKRIEDIELMHMRYALEAIVLALGAMEEAMK DETDASHRVVFYHLKDLTNHLEAIKNVPRKIMMVNIVISLLHIDDIRLSST QSASSACFSEKSNTPGLDPGDLGTEGEKEIVISFTKQLLDVLRRNLPSHPIE QECQLDGNYSTDGRQALEWRVSMAKRFIEDCEWRLSVMQHLLPLSERQ
- 45 WGLKEVLSILRAAPEKLLNLCMQRAKYDIGEEAVNRFALSAEDKATLEL AEWVDNAFKGTLVEDVMSRTAEGAAAVQDLDFHSLGSQLSPLAMVLLF AQSQVMLSEIYPGGAPKVGFTYWDQVHEVAIISVLRRILKRLQEFLEQDD PQILQASFSGDTIISSCTESHRQGQKDRALAMLHQMIEDAHRGKRQFLSG KLHNLARALADEKPEVDVLKGDGSDMAVEKDGVLGLGLKYTKQSPGS
- 50 ANRAVDGNPVSHETEDKGKKSFGPLSNKTSTYLSQFILYTAAIGDIVDGT

DTTHDFNFFSLVYEWPKDLLTRLVFDRSSTDAAAKVAEVMSADFVHEVI SACVPPVYPPRSGHGWACIPVIPTTPCSHSEGKVLSPSIEAKPNCYVRSSA TPGVPLYPLOLDVIRHLVKISPVRAVLACVFGGSILYNGSDSIISSSLNDEF PSSPDADRLFYEFSLDQSERYPTLNRWIQMQTNLHRVSEFVVTPKQKPD DTRIKPDERTGIKRLLEHDSDSESDTEETFSKNNIQPALTDGSARDGGSFE NGVCRTDPTVFLSFDWENEVPYEKAVNRLIDEGKLMDALALSDRFLRN GASDWLLQLLIKSREENPSTSGRSQGYGGQSNSWQYCLRLKDKQLAAT LALKCCIGDKLCRSTATYFRQMIAIIAGKRLSFFLLFEIMFGSWYARCVTL KNLNGKOVEAECKEDPEGLALRLAGKGAVSAALEVAESAGLSIDLRREL 10 QGRQLVKLLTTDPLNGGGPAEASRFLSSLQDSADALPVVMGAMQLLPD LRSKQLLILKEFPALRDNNVIMAYAAKAISVTIIPPPREPRITVSASRLROK SRAGPAVKASFTSSLSNFQREARRAFSWAPRNAENRTTSKDVYRKRKNS GLGASERAAWEAMTGIQEDQGSSYSADGQDRLPSVSIAEEWMLTGDKT KDEGVRASHKYESTPDIILFKALLSLCSDELVSARSAMDLCISOMKNVLS 15 SKQLSEGASVETIGRAYHATEAFVQGLSYAKSLLRKLLGTTESTNNNGE RSRDVDDISSDAGSSSVGSQSTDEPSDVLSLTEIWLGRAELLQSLLGSGIS TSLDDIADOLSSECLRDRLISDERYSMAVYMCKKCKIDVFPVWKAWGL ALLRMERYAQARVKFKQAFQLKGEDIPDVIQEIINTIEGGPPVDVSIVRS MYDHLAKSAPTILDDSLSADSYLNVLHMPSTFPRSERSRRSLESEKNSSV 20 PGSDFEDGPRSNLDTTRYSECTNYLQEHARQNLLGFMFRHGHFKDACM

LFFPQSGLPPPLQTSSVGAVSTSSSPQRTDPLATEYGTIESLCEFCVGYGAI
SSLEEVITERLESAKNQDQAINQYIAGALTRICAFFEINRHFNYLYKFLVL
KKDYVTSGYCCIQLFMNSTTQEDAVRHLEHAKKYWSLTILGVQAHFEE
ALTARHRGSDSKKLVTKGVRGKSAAEKLSEETLVKLSSRVKMQIDVVK
25 SFSDSEGAPWKHSLFGNPNDSETSRRRCEIVETLVEKNFDLAYSVIYEFK

LSAVDIYAGVATSLADRKKGSQLTELFKNIKGTIQDDDWDQVLNIADTG KARSVWLIFCEMLQVLGAAINIYANKHKERPDRLIDMLTSSHRKVLACV VCGRLKSAFQIASKSGSVADVQYVAHQALHANSHTVLDMCKQWLAKY M

30

References

Aarts et al., Proc Natl Acad Sci 95:10306 (1998).

Allison et al., (1986).

Altschul et al., J. Mol. Biol. 215:403 (1990).

35 Altschul et al., <u>Nucleic Acids Res.</u> 25:3389 (1997).

An et al., EMBO J. 4:277 (1985).

Aoyama T. et al., N-H Plant Journal, 11:605 (1997).

Bailey and Elkan In: Proceedings of the second international Conference on Intelligent Systems for Molecular Biology (Altman, R., ed), pp 28-36, AAAI

40 press (1994).

Ballas et al., Nucleic Acids Res. 17:7891 (1989).

Bansal et al., Proc. Natl. Acad. Sci. USA, 89:3654 (1992).

Batzer et al., Nucleic Acid Res., 19:5081 (1991).

-WO-02/22675 ---- PCT/US01/28506

Beals et al., Plant Cell, 9:1527 (1997).

Belanger et al., Genetics, 129:863 (1991).

Bevan et al., Nature, 304:184 (1983).

Blochinger & Diggelmann, Mol Cell Biol, 4:2929.

5 Bourouis et al., EMBO J., 2:1099 (1983).

Boyes et al., Proc Natl Acad Sci USA, 95:15849 (1998).

Byrne et al. Plant Cell Tissue and Organ Culture, 8:3 (1987).

Campbell and Gowri, Plant Physiol., 92:1 (1990).

Cao et al., Plant Cell, 6:1583 (1994).

10 Cao et al., <u>Cell</u>, 88:57 (1997).

Century et al., Science, 278:1963 (1997).

Chandler et al., Plant Cell, 1:1175 (1989).

Christou et al., Biotechnology, 9:957 (1991).

Christou et al., Plant Physiol., 87:671 (1988).

15 Cordero et al., Plant J., 6:141 (1994).

Corpet et al., Nucleic Acids Res. 16:10881 (1988).

Crameri et al., Nature Biotech., 15:436 (1997).

Crameri et al., Nature, 391:288 (1998).

Creelman et al., Annu Rev Plant Physiol Plant Mol Biol 48:355 (1997).

20 Crossway et al., BioTechniques, 4:320 (1986).

Czako et al., Mol. Gen. Genet. 23 5 (1), 33-40 (1992).

Datta et al., Bio/Technology, 8, 736 (1990).

Dayhoff et al., Atlas of Protein Sequence and Structure, Natl. Biomed. Res.

Found., Washington, C.D. (1978).

25 De Blaere et al., Meth. Enzymol. 143:277 (1987).

de Framond, FEBS, 290:103 (1991).

Delaney et al., Proc. Natl. Acad. Sci. USA 92:6602 (1995).

Della-Cioppa et al., Plant Physiology, 84:965 (1987).

Dennis et al., Nucleic Acids Res., 12:3983 (1984).

30 Dong et al., Curr Opin Plant Biol 1:316 (1998).

Dzelkalns et al., Plant Cell, 5:855 (1993).

Eisen et al., Proc. Natl. Acad. Sci. USA, 95:14863 (1996)

Eisen et al., Trends in Plant Sci. 95:14863 (2000).

Ellis and Jones, Curr Opin Plant Bio 1:288 (1998).

Elroy-Stein et al., PNAS USA, 86:6126 (1989).

English, et al., Plant Cell 8:179 (1996).

Eulgem et al., Trends in Plant Sci. 5:199 (2000).

Falk et al., Proc Natl Acad Sci USA 96:3292 (1999).

5 Feys et al., <u>Plant Cell</u> 6:751 (1994).

Franken et al., EMBO J., 10:2605 (1991).

Fromm et al., Bio/Technology 8:833 (1990).

Gallie et al., Molecular Biology of RNA, 237 (1989).

Gallie et al., Nucl. Acids Res., 15:8693 (1987).

10 Gan et al., <u>Science</u> (1995), 270 (5244), 1986-8).

Gatz Current Opinion in Biotechnology, 7:168 (1996).

Gatz, C., Annu. Rev. Plant Physiol. Plant Mol. Biol., 48:89 (1997).

Gelfand, eds., PCR Strategies (Academic Press, New York (1995)).

Glazebrook et al., Genetics 143:973 (1996).

15 Glazebrook et al., <u>Proc. Natl. Acad. Sci. USA</u> 91:8955 (1994).

Gordon-Kamm et al., Plant Cell, 2, 603 (1990).

Graham et al., Biochem. Biophys. Res. Comm., 101:1164 (1981).

Graham et al., J. Biol. Chem., 260:6555 (1985).

Graham et al., J. Biol. Chem., 260:6561 (1985).

20 Guerineau et al., Mol. Gen. Genet. 262:141 (1991).

Hammond-Kosack and Jones, <u>Ann. Rev. Plant Physiol. Plant Mol. Biol.</u>, 48:575 (1997).

Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA, 89:10915 (1989).

Hiei et al., Plant J. 6:271 (1994).

25 Higgins et al., <u>Gene</u> 73:237 (1988).

Higgins et al., CABIOS 5:151 (1989).

Hinchee et al., Biotechnology, 6:915 (1988).

Hoekema, In: <u>The Binary Plant Vector System</u>. Offset-drukkerij Kanters B.V.

30 Huang et al., <u>CABIOS</u> 8:155 (1992).

Hudspeth & Grula, Plant Molec. Biol., 12:579 (1989).

Huffman et al., J. Cell. Biochem., 17B: Abstract.

Hunt et al., Mol. Plant-Microbe Int. 9:261 (1997).

Ingelbrecht et al., Plant Cell, 1:671 (1989).

Innis et al., eds., <u>PCR Protocols: A Guide to Methods and Applications</u> (Academic Press, New York (1995).

Innis and Gelfand, eds., <u>PCR Methods Manual</u> (Academic Press, New York) (1999).

5 Jobling et al., <u>Nature</u>, 325:622 (1987).

John et al., Proc. Natl. Acad. Sci. USA 89(13):5769 (1992).

Jones et al., Adv Bot Res 24:89 (1997).

Joshi et al., Nucleic Acid Res. 15:9627 (1987).

Joshi, NAR, 15:6643 (1987).

10 Karlin and Altschul, Proc. Natl. Acad Sci. USA 872264 (1990).

Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873 (1993).

Keller et al., Genes Dev., 3:1639 (1989).

Kirsh et al., Plant J. 26:217 (2001).

Klein et al., Bio/Technology, 6:559 (1988).

15 Klein et al., Nature (London) 327:70 (1987).

Klein et al., Plant Physiol., 91:440 (1988).

Klein et al., Proc. Natl. Acad. Sci. USA, 85:4305 (1988).

Kohler et al., Plant Mol. Biol., 29:1293 (1995).

Knauf, et al., Genetic Analysis of Host Range Expression by Agrobacterium

20 In: Molecular Genetics of the Bacteria-Plant Interaction, Puhler, A. ed., Springer-Verlag, New York, 245 (1983).

Koziel et al., Biotechnology, 11:194 (1993).

Kridl et al., Seed Science Research, 1:209 (1991).

Kriz et al., Mol. Gen. Genet., 207:90 (1987).

25 Kunkel, Proc. Natl. Acad. Sci. USA, 82:488 (1985).

Kunkel et al., Methods in Enzymol., 154:367 (1987).

Langridge et al., Cell, 34:1015 (1983).

Lindstrom et al., Der. Genet., 11:160 (1990).

Lommel et al., Virology, 81:382 (1991).

30 Lorz et al. Mol. Gen. Genet. 199:178 (1985).

Macejak et al., Nature, 353:90 (1991).

Maleck et al., Nature Genetics, 26:403 (2000).

Mansson et al., Gen. Genet., 200:356 (1985).

Martin and Paz-Ares, Trends in Genetics 13:67 (1997).

Martinez et al., J. Mol. Biol., 208:551 (1989).

McBride et al., Proc. Natl. Acad. Sci. USA, 91:7301 (1994).

McCabe et al., Bio/Technology, 6:923 (1988).

McDowell et al., Plant J. 22:523 (2000).

5 McDowell et al., Plant Cell 10:1861 (1998).

McNellis et al., Plant J. 1998, 14:247-257.

Meinkoth and Wahl, Anal. Biochem., 138:267 (1984).

Messing & Vierra, Gene, 19:259 (1982).

Mogen et al., Plant Cell 2:1261 (1990).

10 Moore et al., <u>J. Mol. Biol.</u>, 272:336 (1997).

Munroe et al., Gene 91:151 (1990).

Murray et al., Nucleic Acids Res., 17:477 (1989).

Myers and Miller, CABIOS 4:11 (1988).

Needleman and Wunsch, J. Mol. Biol. 48:443 (1970).

15 Odell et al., Nature, 313:810 (1985).

Odell et al., Nature, 313:810 (1985).

Ohtsuka et al., J. Biol. Chem., 260:2605 (1985).

Okamuro et al., Biochemistry of Plants, 15:1 (1989).

Paszkowski et al., EMBO J., 3:2717 (1984).

Pacciotti et al. Bio/Technology 3:241 (1985).

Park et al., J. Plant Biol. 38(4):365 (1985).

Pearson et al., Meth. Mol. Biol. 24:307 (1994).

Pearson and Lipman, Proc. Natl. Acad. Sci. 85:2444 (1988).

Penninck et al., Plant Cell 8:2309 (1996).

25 Perlak et al., <u>Proc. Natl. Acad. Sci. USA</u>, 88:3324 (1991).

Pieterse et al., Plant Cell, 10:1571 (1996).

Pieterse et al., Plant Cell, 8:1225 (1998).

Potrykus Mol. Gen. Genet. 199:183 (1985).

Proudfoot, <u>Cell</u> 64:671 (1991).

30 Quigley et al., J. Mol. Evol., 29:412 (1989).

Ralston et al., Genetics, 119:185 (1988).

Reina et al., Nucleic Acids Res., 18:6425 (1990).

Reina et al., Nucleic Acids Res., 18:7449 (1990).

Riggs et al., Proc. Natl. Acad. Sci. USA, 83:5602 (1986).

Rochester et al., (1986).

Ronald, Curr Opin Plant Bio1 1:294 (1998).

Rossolini et al., Mol. Cell. Probes, 8:91 (1994).

Roth et al., Nature Biotechnology, 16:939 (1998).

Ruiz et al., <u>Plant Cell</u> 10:937 (1998).

Ryals et al., Plant Cell 8:1809 (1996).

Ryals et al., Plant Cell 9:425 (1997)

Sambrook et al., <u>Molecular Cloning: A Laboratory Manual</u> (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York) (1989).

10 Sanfacon et al., Genes Dev. 5:141 (1991).

Sanford et al., Particulate Science and Technology, 5:27 (1987).

Schernthaner et al., EMBO J., 7:1249 (1988).

Schindler et al., Plant Cell 4:1309 (1992).

Schwob et al., Plant J., 4:423 (1993).

15 Shah et al., Mol. Plant-Microbe Interact. 10:69 (1997).

Shimamoto et al., Nature; 338:274 (1989).

Shirasu et al., Plant Cell 9:261 (1997).

Shulaev et al., Plant Cell 7:1691 (1995).

Simpson, Plant Mol. Biol., 19:699 (1985).

20 Skuzeski et al., <u>Plant Molec. Biol.</u>, 15:65 (1990).

Slater et al., <u>Plant Mol. Biol.</u>, 5:137 (1985).

Smith et al., Adv. Appl. Math. 2:482 (1981).

Smith et al., Planta 168:94 (1986).

Spencer et al., Theor Appl Genet, 79:625 (1990).

25 Staswick et al., Proc. Natl. Acad. Sci. USA 89:6837 (1992).

Staub et al., EMBO J., 12:601 (1993).

Staub et al., Plant Cell, 4:39 (1992).

Stemmer, Nature, 370:389 (1994).

Stemmer, Proc. Natl. Acad. Sci. USA, 91:10747 (1994).

30 Sukhapinda et al. <u>Plant Mol. Biol.</u> 8:209 (1987).

Sullivan et al., Mol. Gen. Genet., 215:431 (1989).

Svab et al., Proc. Natl. Acad. Sci. USA, 87:8526 (1990).

Svab et al., Proc. Natl. Acad. Sci. USA, 90:913 (1993).

Tijssen, <u>Laboratory Techniques in Biochemistry and Molecular Biology-</u>
<u>Hybridization with Nucleic Acid Probes</u>, part I chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays"

Elsevier, New York (1993).

5 Turner et al., Molecular Biotechnology, 3:225 (1995).

VanTunen et al., EMBO J., 7:1257 (1988).

Vasil et al., Biotechnology, 11:1553 (1993).

Vernooij et al., Plant Cell 6:959 (1994).

Vodkin, Prog. Clin. Biol. Res., 138:87 (1983).

10 Vogel et al., EMBO J., 11:157 (1992).

Walker and Gaastra, eds., <u>Techniques in Molecular Biology</u>, MacMillan Publishing Company, New York (1983).

Wandelt et al., Nucleic Acids Res., 17:2354 (1989).

Waterman, M.S. Introduction to Computational Biology: Maps, sequences

and genomes. Chapman & Hall. London (1995).

Weeks et al., Plant Physiol., 102:1077 (1993).

Weissinger et al., Annual Rev. Genet., 22:421 (1988).

Wenzler et al., Plant Mol. Biol., 13:347 (1989).

Weymann et al., Plant Cell 7:2013 (1995).

20 White et al., Nucl Acids Res, 18:1062 (1990).

Willitset al., Mol Plant-Microbe Interact 11:795 (1998).

Xie et al., Science 280:1091 (1998).

Yamamoto et al., Nucleic Acids Res., 18:7449 (1990).

Yang & Klessig, PNAS 93:14972 (2000).

25 Yu et al., <u>Proc Natl Acad Sci USA</u> 95:7819 (1998).

Zhang et al., Proc. Natl. Acad. Sci. USA, 94:4504 (1997).

Zhou et al., Plant Cell 10:1021 (1998).

Zhou et al., Plant Cell 8:2235 (1996).

All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the

details described herein may be varied considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

- 1. An isolated polynucleotide comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 or the complement of the open reading frame, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
- 2. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which is substantially similar to an *Arabidopsis* nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
- 3. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
- 4. The isolated polynucleotide of claim 1, 2, or 3 which is DNA.
- 5. The isolated polynucleotide of claim 1, 2, or 3 which is RNA.
- 6. The isolated polynucleotide of claim 1 wherein the nucleotide sequence encodes a polypeptide having at least 90% amino acid sequence identity to the *Arabidopsis* polypeptide encoded by the open reading frame.
- 7. The isolated polynucleotide of claim 1 wherein the nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

8. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a dicot.

- 9. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a monocot.
- 10. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a cereal plant.
- 11. An isolated polypeptide encoded by the polynucleotide of claim 1, 2, or 3.
- 12. An expression cassette comprising the polynucleotide of claim 1, 2, or 3 operably linked to suitable regulatory sequences.
- 13. The expression cassette of claim 12 wherein the polynucleotide is linked to a promoter for expression in a plant.
- 14. A recombinant vector comprising the polynucleotide of claim 1, 2, or 3.
- 15. A host cell comprising the expression cassette of claim 12.
- 16. A host cell comprising the polynucleotide of claim 1, 2, or 3.
- 17. The host cell of claim 15 or 16 which is selected from the group consisting of yeast, bacteria and plant.
- 18. A transformed plant, the genome of which is augmented with the polynucleotide of claim 1, 2, or 3 or a polynucleotide which comprises one of SEQ ID NOs: 1-684 and 789-795 which is expressed in an amount which confers resistance or tolerance to the plant to pathogen infection.

- 19. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene corresponding to the polynucleotide of claim 1, 2, or 3 or a gene corresponding to one of SEQ ID NOs: 1-684 and 789-795.
- 20. The plant of claim 19 which is altered by T-DNA insertion, transposon insertion, or targeted DNA insertion.
- 21. The plant of claim 19 in which expression is inhibited by transcription or post-transcriptional mechanisms.
- 22. The plant of claim 18 or 19 which is a monocot.
- 23. The plant of claim 18 or 19 which is a dicot.
- 24. The plant of claim 18 or 19 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
- 25. A method of expressing a polynucleotide in a cell, comprising: introducing the polynucleotide of claim 1, 2, or 3 into a cell so as to express the open reading frame.
- 26. The method of claim 25 wherein the cell is a plant cell.
- 27. The method of claim 25 wherein the cell is a monocot cell.
- 28. The method of claim 25 wherein the cell is a dicot cell.
- 29. A composition comprising the polynucleotide of claim 1, 2, or 3 or comprising the polypeptide of claim 11.

30. A method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by comprete infection of the cell, comprising:

- a) contacting a plurality of isolated nucleic acid samples on a solid substrate with a probe comprising plant nucleic acid corresponding to RNA isolated from plant cells infected with an oomycete, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
- b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising plant nucleic acid corresponding to RNA from uninfected plant cells or from mutant plant cells which have a response to pathogen infection that is different that the plant cells in a), so as to identify which samples corresponding to genes having an open reading frame, the expression of which is altered in response to oomycete infection, wherein the genes comprise orthologs of *Arabidopsis* genes comprising one of SEQ ID NOs: 1-684 and 789-795.
- 31. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is induced in response to infection.
- 32. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is decreased in response to infection.
- 33. The method of claim 30 wherein the probe comprises nucleic acid from a dicot.
- 34. The method of claim 30 wherein the probe comprises nucleic acid from a monocot.

----WO 02/22675 -----PCT/US01/28506

35. An isolated polynucleotide comprising an open reading frame of a gene identified by the method of claim 30.

- 36. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
 - a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by a nucleic acid sequence comprising an open reading frame comprising one of SEQ ID NOs: 1-684 and 789-795 so as to yield transformed plant cells; and
 - b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to the pathogen relative to a corresponding plant which does not comprise the expression cassette.
- 37. The method of claim 36 wherein the polynucleotide hybridizes under moderate hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
- 38. The method of claim 36 wherein the polynucleotide hybridizes under stringent hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
- 39. A transformed plant prepared by the method of claim 36.
- 40. A seed of the plant of claim 39.
- 41. A progeny plant of the plant of claim 39.
- 42. A method for identifying a plant cell infected with a pathogen, comprising:

a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence substantially similar to one or more of SEQ ID NOs:1-184, 301-494 or 500-803, or a portion thereof so as to yield an amplified product; and

- b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the product is indicative of pathogen infection.
- 43. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising at least one of SEQ ID NOs: 685-788.
- 44. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which nucleotide sequence hybridizes under high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788 or which nucleotide sequence hybridizes under very high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788.
- 45. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, wherein the plant nucleotide sequence comprises SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 764 or SEQ ID NO: 773.
- 46. The isolated polynucleotide of claim 43, 44, 45 or 46 wherein the nucleotide sequence which directs transcription is 25 to 2000 nucleotides in length.

47. A recombinant vector comprising the polynucleotide of claim 43, 44, 45 or 46.

- 48. The vector of claim 47 which is a plasmid.
- 49. An expression cassette comprising the polynucleotide of claim 43, 44, 45 or 46 operatively linked to an open reading frame.
- 50. The expression cassette of claim 49 operably linked to other suitable regulatory sequences.
- 51. A host cell comprising the expression cassette of claim 49.
- 52. A transformed plant, the genome of which is augmented with the expression cassette of claim 49.
- 53. A plant cell containing the expression cassette of claim 49.
- 54. A transformed plant comprising transformed plant cells, the transformed plant cells containing the expression cassette of claim 49.
- 55. The transformed plant of claim 54 wherein the plant is a dicot.
- 56. The cell of claim 53 which is a dicot cell.
- 57. The transformed plant of claim 54 wherein the plant is a monocot.
- 58. The cell of claim 53 which is a monocot cell.
- 59. The transformed plant of claim 54 which is a cereal plant.
- 60. A method of augmenting a plant genome, comprising:
 - a) contacting plant cells with the expression cassette of claim 49 so
 as to yield transformed plant cells; and

b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.

- 61. A transformed plant prepared by the method of claim 60.
- 62. A seed of the plant of claim 61.
- 63. A progeny plant of the plant of claim 61.
- 64. A method of using a plant promoter, comprising: introducing the expression cassette of claim 49 to a plant cell and detecting the expression of the product of the open reading frame.
- 65. A recombinant vector comprising the expression cassette of claim 49.
- 66. A plant cell comprising the vector of claim 65.
- 67. A transformed plant, the cells of which comprise the vector of claim 65.
- 68. The plant of claim 52, 54, 61 or 67 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
- 69. The expression cassette of claim 49 wherein the open reading frame is in an antisense orientation.
- 70. The expression cassette of claim 49 wherein the open reading frame is in a sense orientation.
- 71. A transformed plant, the genome of which is augmented with a polynucleotide which is substantially similar to any one of SEQ ID NOs:

--WO 02/22675 ---- PCT/US01/28506

1-684 and 789-795 and which is expressed in an amount which inhibits or prevents pathogen infection.

- 72. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene comprising a polynucleotide substantially similar to any one of SEQ ID NOs: 1-684 and 789-795.
- 73. The plant of claim 71 or 72 wherein the polynucleotide is substantially similar to SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 792, SEQ ID NO: 57, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 102, SEQ ID NO: 111, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 682, SEQ ID NO: 129, SEQ ID NO: 137, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 161, SEQ ID NO: 165, SEQ ID NO: 170, SEQ ID NO: 174, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 184, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 197, SEQ ID NO: 208 or SEQ ID NO: 211.
- 74. The method of claim 36 wherein the polynucleotide is substantially similar to SEQ ID NO: 308, SEQ ID NO: 300, SEQ ID NO: 272, SEQ ID NO: 362, SEQ ID NO: 265, SEQ ID NO: 241, SEQ ID NO: 261, SEQ ID NO: 380, SEQ ID NO: 228, SEQ ID NO: 658, SEQ ID NO: 243, SEQ ID NO: 254, SEQ ID NO: 216, SEQ ID NO: 225, or one of SEQ ID NO: 400-684.
- 75. The expression cassette of claim 12 wherein the polynucleotide is in antisense orientation.
- 76. The expression cassette of claim 12 wherein the polynucleotide is in sense orientation.

- 77. A method for identifying a plant cell infected with a pathogen, comprising:
 - a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to an Arabidopsis polypeptide encoded by an open reading comprising sequences selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 so as to form a complex; and
 - b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
- 78. A method for identifying a plant cell infected with a pathogen, comprising:
 - a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe comprising at least a portion of a polynucleotide that is substantially similar to any one of SEQ ID NOs: 1-684 and 789-795 under conditions effective to form a specific complex between the probe and the nucleic acid; and
 - b) detecting and determining the presence or amount of complex formation wherein the presence or amount of complex formation is indicative of pathogen infection.
- 79. A computer-readable medium having stored thereon a data structure comprising:
 - a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
 - a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

80. The computer readable medium of claim 79 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.

- 81. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
 - a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
 - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
- 82. The computer readable medium of claim 81 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
- 83. The method of claim 42, 60, 77 or 78 wherein the cells are dicot cells.
- 84. The method of claim 42, 60, 77 or 78 wherein the cells are monocot cells.
- 85. The method of claim 42, 60, 77 or 78 wherein the cells are maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat cells.

RPP-DEPENDENT DEFENSE PATHWAYS

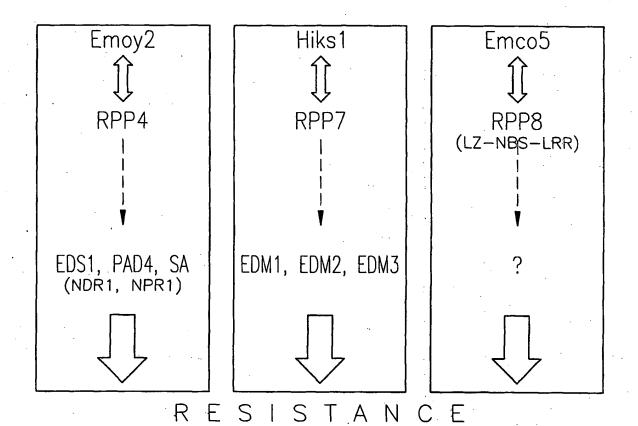


FIG. 1

motifs:

Motif 1/ MAP Score: 6.87857

CAACAATGAC

TT TT

Motif 2 MAP Score: 2.22382

GATGGGNCNAA

TT A

C

Known stress-responsive cis-elelemts:

ttgacc, ttgact, ggtcaa and agtcaa W box

ttgaca and tgtcaa W box-like

tgacg and cgtca TGA-bZIP binding site

acgt bZIP binding site core

cacgtg G Box

geegee and ggegge GCC box

| Subcluster A 17014 ribonuclease RNS1

SEQ ID NO:

FIG. 2A

14609 putative cytochrome P450

SEQ ID NO:

tttgctcagccttttgtggtctctaccgcttaggaccacttactgcaaatctagaaaat taaaatata<u>tgac</u>tagctaaaatgtgaggtatattgagaagtgagttcttaaaactact tggacttgtctacttagaatttgagacattataagtacaattgatgttaatctaaaagt gtagaacattgttaatttettgaacagetgttage<u>eaacaatgae</u>ggaegataegatea ttgatcgaagaggcgattttgtttcacatcgatcagtggatctctttggcgaagtaca<u>tg</u> accaaccaccagatgatcagaagcattcaacacctctctatttatcccaatttgtaagt acatatatgtatgatagtatgtatgtatatattatgagtacatatacattagaaa atactattaactttcaagtcgttatagtaatggacaatattattcgtaattatcaaaag cgctttttcattttctatctgaacctaatgcctagcgagttgaaaacatagctacctaa taggctactactacacaatcttgaagcacaaataatacaacgaaACGTcccttgggtat gagattatttagaagtttcataagattctagtccttattcaattgtgcccatcaagcac aaagtacggaagcgataggaaggACGTCAcagtcctgttttgataatctaatgatcgta gaaagcGTTGGGtgcttttaagttttttctttcgcctaaatattttaaggtcttttgcc aggaatagaaatatgataaagtetattgagtttgtaagaeetatgtatattgggteegg atgcaatgcttttttactcatgcgcattcaatagaagaatttgttatcagtgaacgagt acaaTGTCAAtatatttaacaaattatttaaaaccttttaaaatatgtgcatagtttttt ttcgtactcggatagaaattaataataacaaaaattactgatttgataaaatgaatttc gctttgtaaataaattatatatattcaaaatcctcatcgtcgaaaacaattttaaaaat aaaacaaccaaagatattttccacaaattaaattaattttagttttgaattcagatata ttatttattaatttggatatacttattaccgaaataaaggattgtttatttcttacaac tcgtcttattagtgttgcatagcataacaaggtgaaagagaaaacatq

16649 putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase (function:disease SEQ ID NO: resistance) (promoter up to next ORF)

776

catgtctcttgagtctcgtggttgtgtgcaaattgttcgttgttataaacgagagatgt atgtcaatatatattggcttctggtcaaactaattgagctactaataagacccaaat taaggactaacaccaattgatcttatccatgacttttcaaccatgggactagaaaat caattatctagacagtacttgatgcgaatatattaacgtttatgtttcttaaggatttt

ttttctctcttaaggttgcatacaaatgttgaaatatgcaagcaggcgaacagtttgca atgtagttttattgactaatataaatttggtatgtgagatttaaaatgcaaaaaagta tatagtatagaattatttaaagaatatatcaaattgaaggtactaaaaaaacggatttg aattcgaatgctaacataacgaataccagcataaatctccaaagatgattcaaattttg cagtttcaatccctcaatccgcttcaacggatgaaacaataataatattcaacatgttc taacaatttttcaagtatgcatgaagaaatcacttaaaaaattccaagatatgtattta aaagcaaaaacaaaagttacagaatgtcttgaggagaggattcctcaaacctcctaaga aaagatottttgggtttttgtaatotgtoattgtaagttaagcaaagtttgttgaataa gtgttccagagatatgataagttgaccttttggattgtctaatctggaatcttttagtt tatggtgaactctcaccccaagctcaatgtgatgtccatgtaactaatcttaggcaaca tgatgtggcataggagattgggcatcctcatcatcaagatccctaaatgacgaaatgat tttaaaataataattcctaagatttcacatccttaaacccttattaagtcctaacattc gaaaatacacaacattcatttgatttaatttaaattttatattaacttctctattttc attaaaaattgtaaaatatttttttattgtcgtaaaatgttttacttttctatttccat ctg**ttgggccaaa**ga

17653 (similarity to DNA damage inducible) (promoter up to next ORF)

SEQ ID NO:

acaataatttccataattcaaatgctttcagaaaggatttctcaatacaggttaaaaat atcaatctaatctttgcaaactcattaaactaatttagttactttccttaactttaaga aacggtctgaaagaggacaaaaagattttcacaagtgtacaccaataaaagaaaatcgt ttttttcccttataaaatgacaaaaattaccaagaaattaaatggaacataacttacga cgaaatttacctgacgattttttttccttactgaaaattaccaagaaatcgcgtggaag aaagtcaaccttttgggaaaattgtcgtctttgacatcagaagagattcaaactaaaat gaatgagtacgttacttgcgttatggttgggttttcctttttaattttagaaacttttc ttacttatattttgaatcaacagttgataacacaagtataaattattattttcgccatc acactggagtcaagctcgagagagacttgtttcctaatttaattcataaacttgtttcg acaatagtcttataatttattcacacttaaaattaacaatacaagtcttttcaa agtcttttaattatataaacaatagaagtctttttcattgtctctttttgactaattaa taaagaccatgaaaagacttgtattgtaagttttgagtgtaaattgtaataaattacta tggttttgttttatatttctgccatctaaataattacattatatgataaaataat taccctagcgacaaatgacagctagaaatgtaataagaacaccaactaaataattatgc aggttaataatggagcaagtgatgttctttctatatactgtacattttcttttaaaaa attatgtaatttcgcagaagagaaaagaaaaacacgtggtgattagagagtagtataaa gatagttggttgggttctgtttttttctgtatctcgaggcgccaaaaacaacaacaaa aaaacttcagagcggtgatcagattcaccgatttttctcaaaatg

17008 putative tyrosine aminotransferase

SEQ ID NO: 778

cataggactactacaatcagTTGAGAgagacgacgatctggttaatggccatggccactg agtttgatagcttccttggagatggca<u>tgac</u>gatcatagaaaccttttagtcTGTCAAa tatttcttgtaccactgattcgtcggttcctatcgatatcctcacccaattctctgccc attgatcataattaacgatgcaaatttataaattaaaatcatatgtaagaaga<u>tgac</u>ta tgggagccccaagttcttaagatgttgtatattgttaaagagatcaatacctggtataa ggataagactctcctcactaactagcttcgTGACGaaatcaaaatcatttttgatatta tt<u>caacattgatg</u>TGTCAAgcttcaactgtaaaataaatcgtttaagctaatcatttat caagaaaaagaattaaagtacccataaataagaacaagattcgggtttcttgggacaaa agagacaaggaatatccttgagcctctcacatgaaagctcgACGTtgcgtctcatggct ttgatcttcttctcgaagaactctttaggtgttttctccaatatatcaggaagtgcttc ctatcaaaatccataatatctcacattatttagagaaccaaaacttatagcttacgat gatagtgagagattacaaacctggagaataaatgaaggctgtggagttaaatcaagaaa ttettaattggtgeggtaatettattttaagtaaaaetatagtgtttagaagTTGAC<u>T</u>g <u>ac</u>ccctgtagatacaaagataccattaggatcgttcatggcgatccagccaactctcca gcctgggTTGACCcatcctttggatatggatccgagcgtgatcaccggagctattgatg caaacttccccatgggaataaaaggcttgtctccatatacaacatgatcatatacttcg teggatattateattatacegagttttetageeateteegegaeetaaagattagtega $\verb|tatattaccaaaaaaACGT| tagttgttttacacttcaaaaaaacttatattacattaaat|$

15042 cinnamyl alcohol dehydrogenase-like protein (promoter up to BAC end)

SEQ ID NO: 779

<u>cat</u>tttttgatgattctttcttcttcttatcttgatctgctgctttcacgcttttgct gtttatgtgtgtgtattactatatatatatagagaaagttggaaacgtaacgtatgc gtatgtgtgatgaaataattggtgtttctgcatagcacacatttgatggctataattga gtgtaaatttgtgtatattattgacaaaattagtcaaaagcttaaaatcttttttagtc gttgaaagatccttctagaaaaagacattttttttttcttcttcttttcatacgatggctc atggctgtgtagtttattagaattttaggtgaaaaaatattagaagccaacaaaactt aaatgaaatttatttgcattcataattcattttaccagtttataacaacaacgtaatcc aaaaagtaaaatgagaaagaatggaatttgtgtactttgaaaggaagaaaaaccactat gtctaatcgtgtgtttgctttggtttaaaatcatggttggccacgtgttgattcttgac ctctctctgacatgaaactgtagcattgacggcccagatcagctgcgagaatacttccc acaaccatggaaattttacggcccagatcaacaagaatcgatttgctctttactattt cgaagaacaaagagtgacagttatgaataatagaaaagaaggacaaagagtgtgtgaat ggcttcacattaaaacaaaagcccattatgaatgacccattcacatttcacacccagtt tgaaaaatcgaccgtccaattaagtaacattcaaaaacccaaaagataaacctctaatt cacgaatcacaacagcagcatgagccgtttcatcacgacgttatctcagagtttcttgg aaataatttgttgtagcggacttgtggctgtaa<u>atggggccaa</u>tgcttaaatttacttg

12778 Lipase/Acylhydrolase with GDSL-motif family SEQ ID NO: (promoter up to next ORF) 780

<u>cat</u>catttagagagaggagaaacagaactgtgaaaagagaagaagattgcttttgtgc cttagctcgtagaccgattcgttatatttatattgcaagtactacaatttggcaatgaa aataatagttcattttactatacaaataataacgtgtagcgcgaggttcattttactat acacctatttaacgcactagcaaacgattatcgatcaattatattatatagttcgctta atcacgtctgacgcattactggtttctcttctactttatttttaattctcaacaaaata acttacaattacacaagagtctgaatacacataagctttaacccaatccggcaatatag aatacaatttgggatcataattcagaaaagaaagagattccctagcaattctatctgcc acacaattcccttctcatcgggtaaaagtcactttaacctcttcgaagtgctgaaaaga tcgtgcatttagaggcaagaagtagaattaaacatacaaatttcacggaaatatagggt gtaaatggtaacactaaaccagattcagtaatttctgcagtaaccatttgcataaaact aaattttgctgactagccaaattcaacaaaaaatttcaacaccaacatatacgtagat atgtttatttctgctaaaacttttggataatttacgagtacacaactcgaattaaaata tttttaatatcaaatacatatcaaatagatatttttaaataagtcagattatactgat acgatatatgaataatatagatacataaaatatcactaccagaatagacaagagacgaa tatgttcggataattatagataatttggataataattttaataacgtttagataactta aatcaattattaaaattttgcaaaaacaactcatacctatgctaagatattctttaaaa gataaattatagtaatttccttaatcatcctcatcatattattgattaaattacttgaa attttcttaatagtgttttgacaaagattttcgttaattatttacatatttttaatagt tcaaatttaaataagaaagaataactcaattttgcgttgacacaatcttaatagtatag

|| Subcluster B 20245 glutathione-conjugate transporter AtMRP4

SEQ ID NO: 781

atttttctaataagacttttcttattctcatagactcttcttattcatcttattc $\verb|aattcgaccaactcagtggaagacaaatctcacacgaccctttccactttttggtaact|\\$ ttattattaattattagtatggtgtagttcctttcttcttctgctgatctTGTCAAc aaaatactaaatttttcctaagcggctgtttatatattattaacaaaggtttccgcgtg tctcttgtttaactagtagactaaaaacaaatcgtaaactcgattttctcaaccaaatt tagaagatactacggcatgtaattagctaatgataaaagattcgaattttcgttccaat ggatttgtcttttcttttgcccaaaaccaagaatttgtcttctcttggcagtatttagc tagacaacgcatatagctatattttgtgtacactGGTCAAggtcgtggatACGTCAt taataatattatttccaataagtcctattaaaacattaaacaactttgagttttaaaac aaacttagtgtaaagaaaataaaaatagcagacagtttacgggtaagactaga<u>tgac</u>ca aagattattagttgttggaaatcagcttagcgtaatcttcgagaaaa<u>tgac</u>tctaatgc taaaatactgatttaatcaattttctaatggtTTGACCCAACagacttttttttttt ctatcctctaataatatataatcatatagtagtaattatttagtagataatatgattaa <u>cACGTq</u>aatagcaaagtttctatcatttttattcaaaaaaagattcataagtaataaaa tgatAGTCAActtttcttttttttttgtgttttggccttttgtTGACGC<u>GTCAttgttg</u>

17051 CTF2B involved in hydroxylation and oxidation of an aromatic ring

SEQ ID NO: 782

<u>cat</u>agccgcgttccaagaggaGGTCAAgtggattcacttttctataatcaatattaaat tgtagtcacaaaattcaagaaacttatatagaccttattttatttttgaacatcaatag $\verb|ttgtcgttgaaaagtatcttggggatatttagatttagcatatgA| \verb|GTCAATGTTG| ggtc|$ $\verb"cttaagagttgaggctacaaatttataactcagaaaaagtgtatatgccctttaattt$ ${\tt tggcctattggtcttttatgg} \textbf{CGTCA} {\tt actccaatttcagtttgaaaagaaaTGTCAAta}$ actaacaatgttgtcttTTGACTttgaaatcttagaagtttcgacttacccatttctac aagtgttaaatagcactgttattcaaaatcttatatttgttaattgtgcttaatattt ttaaaatttaaatacttcattaaaatccaatgttattcaaaactaaattacttttgaaa tatgtgtatatgaagtcatttgaaatgaaatctcataagtttcataagtaaattatta gaataaaaacccaaggtaattgtatagattttgaaatccacacaataatatcgaattgt agttagttgattgaatataaaagtaggaaagatgtgggattcatgtggtgg**tttggccc** atctccatgatctctagtgaatttcagctTGACGcaactttcgttaagatcttacttca ttgtgtgttggtgttgagcctcactggattggtgtgtcggctttttagttcactcagag ${\tt ataattcaaatggatctccttcattccatagttgcatTTGACAtttttatataaaactt}$ $\verb|gctgattatctaag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| teactag| t$ $\verb|atgtctaatagattaaaaattaaaagatagaaatgtctaatggattgaaatatataaag\underline{t}|$ gactcagccaaaaacatgttaactgaaaatcttgtataaaatggagattctctgataac

19640 putative glutathione S-transferase

SEQ ID NO:

aatgtagttttttctggttttgtggagttaatcactaccttttagcttggatttatagc
cttatggtgttgatggtcttgtgataaaacgacgacgaactttgccgttttatatggtc
ggcagtgtgatgtaaatgcgaagagtctagaaggaaacagatgTTGACTttacaacata
tttataACGTtccctttataattttttttttatctctttttttagtaagtggagatgtgtc
ctaattcctaaccttgccttatccctggagcatgtgtaccTTGACTtgatccattcatt
ttctgaagacaaccccatgcttCGTCAagaatttcttctgcttccccaattatacccat
cactttatcgtggttcttcataattgatccattttgtctgtgtatgaaacatcaacagc
tttaaaaccatttgtcattctcgtttgttatattgacgcccaagaaaacaacactct
atagtctgagctataaaaaaagaattagtactaatctgttatttgatgttccttttggc
atatattaaaaatgttgttgttataataggcgttggtttttccgtttctccatctacga
acttgtttgctgaattttccttccaacaatgttataaagtatcggtgaattttctatgg
ttacaagactcaccacctcacgatactaaaaaatatactaaagaaatttgttatattgtg
ccgcaacaaatagacccacatgtccgttgtactttcctctgtttacacaacttcttACG
TgtcgaaatacatgttcacatttaatcatagtggttttttataagaaggatggtTTG

ACTaaattatagcttttatctacttttctttcatatgaaaactccaggtttatgaacca atttcttatgatttgtaagaaattgaatactactacatttaaaatgtttataataatta aTTGACAttagaatttagtaaaaacactaattgttcatacaaatgtttcatttattgtt catacaaactattataacaagattacacaaacatatagttaacatctactgatcgaaga gt<u>atcattgttg</u>tctcttaggctgatttgattctttctacaactttcttcatatg

14248 PAD3_at member of the PF | 00067 Cytochrome P450 family

SEQ ID NO:

gttctggtcgaaggatttgtcccggaatgccaatggcgattgctagtgtggaactagca ttgatgaatttgctttattattttgattggagtatgcctgatgggactaaaggtgaaga cattgatatggaagaagctggtaatatctctatTGTCAAgaaaatacctcttcaacttg tgcctgttcaACGTtattgatgagcaataatataagctcgataacatggaaagtgtatg aagcaaaaaacataagattctttagattttgttgtgttatataagaaaqaaatgttcca ataataaatcaagaaagaataacttttgttcatttacttaaaaactagatcataatcaa cacggattaagatctttttcattcaacaaaattctaaattttgttttttaagtaaaaa atgttatagcataaatgttcagatttttatgtcgtattatattqaattaaatataggac aataagatctagaacaaaaacgatacattcagattgattattgaaatcaaataatcgaa tttataattgaatttgatggaatttataatgtattttttgtcatggaaataataaagtt tggaagatgctggaatgatctctttttacaagaaagctcctctcattcttgttccggtt aaacaccattaatgacatcggcacacaaaaattcaaacaccqttqaaqattqtttqcta tactttatttttatcaataataagttgcggtacttggttaactgtatACGTacttctat ttcttatagttgtgcgataattaccacaagtccaaaaaagtaaaatatgaatttgataa agcagtgtaaacctgagattttcaagatttgggcctaaacccattagagaatgctACGT agagaaccattgggcccataaacttattttattcccgcaaagcctgagtggattcgaac cactaccacaaaagtaagagtttgggttatttgattttaatcattcactttgaattat tatagacaccggacagtgacttatgataaagagatttttaacctttaaaactaaaacac taaaatacataatccaaagaagacggaacaaaaaacaaaaacagagccaggaataatq

17500 athcallga_s_at calmodulin-like protein (promoter up to next ORF)

SEQ ID NO: 785

18928 putative endochitinase (promoter up to SEQ ID NO: next repeat region) 786

<u>cat</u>tttgtgtatggagggtgttgtgtgaagaaatgaagaaggtgtgttgatgtatttat agtgtaaatttggtctattcaaattgaaatattgatcagtgttagacatctttcacgat tattgattggctttttctgagtcaaagtcaatgccactttgtaccacttaacaaaagtc aatgacacagttttttctcttgtcgttatgagaaattccatgtcggtcatagatcagat caaaaacgaatatgtaatcaaaattttaaagagccaagttacttggatgaaaatcattc tcataaaaacttgattgagataatcaagtttagattagttcaaacgtttgagatttttc tattgaatagttccaagtttttgttaattagctcaaacgatattgttagctaatatagc attttttttggtcaactaatatagcatttagaacgttcttttaaagtcttactttgatt tttaacaaaaattgtatggaattgtgagaaaaatgactagtgaagccaaaatgtttcta tttataaatcaaaatcaaccaaaattagaaaaatccaactcaattattgcaatttccaa atagtcatgcgtcaaaattaaaccagcatatcaataaaaagcggtttagtcttaccaac cctggtctagagactctagaaccatcggagctcaagtgaaaaacgacgccgttaagctg catctttcaagatagataaaaacttttgtcgatcgcttcatctctcacagagtttcggc agcgaaactagggtttcgaaagtctctgtctcatcaaagcttcgaaaaggtagatttat ggtttcttactctctttctctatgatattccaatttcttgcgagcttgctcagtgttc ttaccttatatttaccgaaccagtgcctttatattctatcacattcgaagttattggtt tctggttacttatattgcttattgttctatgactacgatataattatcccaaagatttg ttcttttctccgaatttggattagaaatggatatactcaaattctgaacatgcccagaa gaatcct

14614 putative glucosyltransferase (promoter SEQ ID NO: up to next repeat region) 787

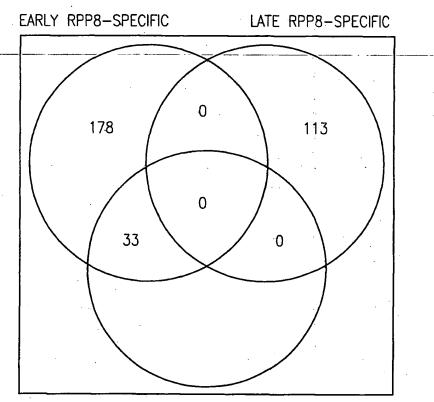
| | Additional genes showing early and transient RPP-triggered expression

13176 Contains Myb DNA-binding domain repeat signatures

SEQ ID NO: 788

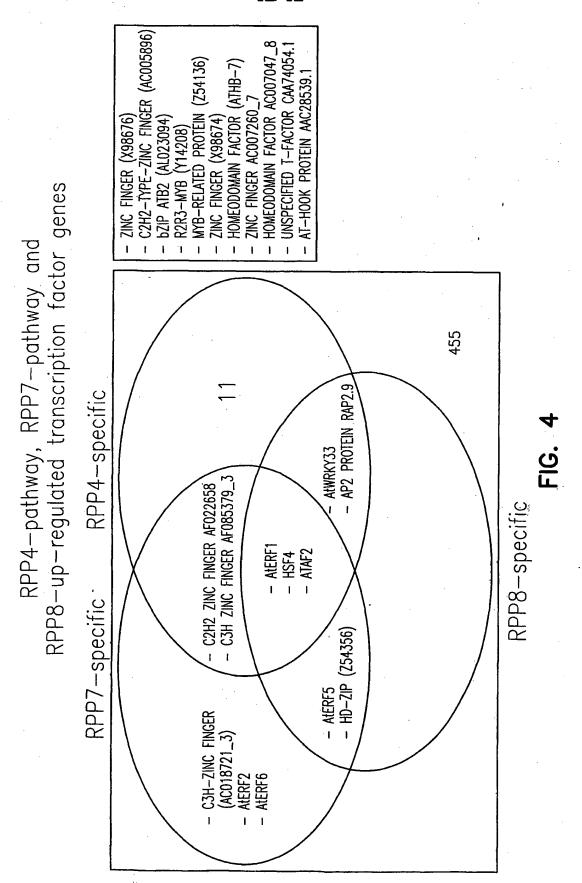
ttccaaaacttaaaccttaaatgaacttcaatctacaccatataaagagga ${\tt agagatataccttegccatCGTCAttggcccaaagaacaaaatgtacatactttacaag}$ ${\tt aggaatcaatattaaagtgtatataaccaa} \underline{{\tt tgac}} {\tt aaggctccaataatatcttctttgt}$ gtcctgaaaaaacacattaccaagttcaacaactcaatcagatcgaaaagtaaacaaca tgaagaagaagaagaacattcacacacaaatgctaacctcgatttcgtttttctgagtt ccaggaatctcaagagcatctacatcgaaagAGTCAAcggcagggctagtgcgaatcaa acgctgctccacattgtcatcctcctcatcggaatccatttccgggtgattatgctcat catatccatcatcgtcgtaatcttcattaacctcataatcatctttctcatcgaacacc catcgcgacaaTGACGTcgttgaatcgtctccgccaaactcctcatcaatctcagaccc atcgcctccactgctttcttcttc<u>cACGTg</u>aaacatcaatcaccgttggaaaacactga agatetegagattgtgatteagattegtatetetgateeaaggaaacaggattggaatt acctggcacgaatgagaaagaagcttacACGTgtccaatcatgattggattcgagactc acggtttaaggaaaaacaaaccagaccaaattaggcttaaccgctaaaaaaccgggttc tcgttttgaaagattgagagagacgatctacaaaggaggacaggacccggcacgaatga gaagaagcttacACGTgtccaatcaggattgaacgatttaatcaagcttaaccgtatgt aaaccggattttagctgggtccacaagtAGTCAAatatagattttttaatAGTCAAata attttcataggggcgaagttcaagatgagttactacactcatcaaagctcacaaaaaga gaagagaagagaggatcaatcaccattctcatq

26 Peronospora (Hiks1 and Emco5) induced RPP7, EDM1,2,3 and RPP8—Dependent genes



EARLY AND LATE RPP7-PATHWAY-SPECIFIC

FIG. 3



SUBSTITUTE SHEET (RULE 26)